

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 11, 2005, 03:18:50 ; Search time 7690.41 Seconds
(without alignments)
2375.375 Million cell updates/sec

Title: US-09-736-250-1
Perfect score: 1962
Sequence: 1 MKPFGPLENQLSLFLLEKAI.....LSRQEGHASPFPPLQPVSVM 377

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues
Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+p2n.model -DEV=xlh
-Q=/cgn2 1/USPTO spool/US09736250/runat 07022005 154924 20406/app query.fasta_1.718
-DB=GenEmbl -QMT=fastcap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFWT=ptp -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09736250_QCGN 1 1 3890 @runat 07022005 154924 20406 -NCPU=6 -ICPU=3
-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :				GenEmbl.*
				1: gb.ba.*
				2: gb.htg.*
				3: gb.in.*
				4: gb.on.*
				5: gb.ov.*
				6: gb.pat.*
				7: gb.ph.*
				8: gb.pl.*
				9: gb.pr.*
				10: gb.ro.*
				11: gb.sts.*
				12: gb.sy.*
				13: gb.un.*
				14: gb.vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

				SUMMARIES	
Result No.	Score	Query Match	Length DB ID	Description	
1	1962	100.0	1133	6 AR145734	AR145734 Sequence
2	1962	100.0	1260	6 AR087353	AR087353 Sequence
3	1962	100.0	1260	6 C0812312	C0812312 Sequence
4	1962	100.0	1260	6 AR281918	AR281918 Sequence

5	1962	100.0	1260	6 AR380354	AR380354 Sequence
6	1962	100.0	1260	9 HUMCYI	D50310 Human mRNA
7	1962	100.0	1384	9 AF135162	AF135162 Homo sapi
8	1962	100.0	1817	9 BC000420	BC000420 Homo sapi
9	1962	100.0	1889	6 CQ468129	CQ468129 Sequence
10	1962	100.0	1889	9 BC004975	BC004975 Homo sapi
11	1952	99.5	1131	9 CR541783	CR541783 Homo sapi
12	1851	94.3	1535	10 AF005886	AF005886 Mus muscu
13	1851	94.3	2348	10 BC003290	BC003290 Mus muscu
14	1841	93.8	2755	6 CQ414515	CQ414515 Sequence
15	1666.5	84.9	200850	2 AC101881	AC101881 Mus muscu
16	1666.5	84.9	202228	2 AC124646	AC124646 Mus muscu
17	1662	84.7	179333	2 AC117658	AC117658 Mus muscu
18	1325.5	67.6	1658	5 BC061670	BC061670 Xenopus l
19	1297.5	66.1	1553	5 BC075116	BC075116 Xenopus t
20	1176	59.9	690	6 CQ721727	CQ721727 Sequence
21	1013	51.6	2339	5 BC068369	BC068369 Danio rer
22	1011	51.5	2166	5 BC044400	BC044400 Danio rer
23	891	45.4	601	11 BV167473	BV167473 sqm5620
24	811	41.3	490	6 CQ685286	CQ685286 Sequence
25	795	40.5	29867	9 AY207372	AY207372 Homo sapi
26	795	40.5	35191	9 AC111196	AC111196 Homo sapi
27	795	40.5	178916	2 AP002874	AP002874 Homo sapi
28	795	40.5	179443	2 AC079051	AC079051 Homo sapi
29	770.5	39.3	2146	6 CQ414223	CQ414223 Sequence
30	763	38.9	804	6 BD079737	BD079737 Cancer-as
31	748	38.1	444	6 AX886044	AX886044 Sequence
32	748	38.1	444	6 BD025654	BD025654 Sequence
33	746.5	38.0	3597	5 BC081135	BC081135 Xenopus l
34	731	37.3	444	6 CQ671106	CQ671106 Sequence
35	727	37.1	11793	10 AF228739S2	AF228740 Mus muscu
36	727	37.1	153811	10 AC134827	AC134827 Mus muscu
37	705	35.9	241543	2 AC099472	AC099472 Rattus no
38	705	35.9	260517	2 AC111318	AC111318 Rattus no
39	705	35.9	270068	2 AC113213	AC113213 Rattus no
40	677	34.5	601	11 BV180201	BV180201 sqm10841
41	650	33.1	818	5 BX930648	BX930648 Gallus ga
42	642	32.7	790	5 BX930233	BX930233 Gallus ga
43	638	32.5	389	6 CQ661908	CQ661908 Sequence
44	625	31.9	369	6 CQ688465	CQ688465 Sequence
45	621	31.7	516	6 CQ410974	CQ410974 Sequence

ALIGNMENTS

RESULT 1	AR145734	AR145734	Sequence 2 from patent US 6218115.	1133 bp	DNA	linear	PAT 08-AUG-2001
LOCUS	AR145734	Sequence 2 from patent US 6218115.					
DEFINITION	AR145734	Sequence 2 from patent US 6218115.					
ACCESSION	AR145734	Sequence 2 from patent US 6218115.					
VERSION	AR145734.1	GI:15108923					
KEYWORDS	Unknown.						
SOURCE	Unknown.						
ORGANISM	Unknown.						
REFERENCE	1 (bases 1 to 1133)						
AUTHORS	Nakamura,T.						
TITLE	Human cyclin I and genes encoding same						
JOURNAL	Patent: US 6218115-A 2 17-APR-2001;						
FEATURES	Location/Qualifiers						
source	1..1133						
	/organism="unknown"						
	/mol_type="unassigned DNA"						

ORIGIN				Alignment Scores:			
Pred. No.:				1.22e-174	Length:	1133	
Score:				1962.00	Matches:	377	
Percent Similarity:				100.00%	Conservative:	0	
Best Local Similarity:				100.00%	Mismatches:	0	
Query Match:				100.00%	Indels:	0	
DB:				6	Gaps:	0	

```
US-09-736-250-1 (1-377) x AR145734 (1-1133)
Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle 20
Db 1 ATGAAGTTTCAGGGCCCTTTGGAAACACAGAGATTGCTTTCTGTTGGAAAGGCAATC 60
Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 61 ACTAGGAGACAGAGTGGAAAGTGAATGTGGGAAATGCTTCAATCAGAAATGTT 120
Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn 60
Db 121 TCTCCATCCACAGAGATGAGAGAAATCCAGATCAATGCTGCTTTTCTAGCTGCCAAG 180
Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 181 CTTTACCAGAAACATTGCTCTGGCTAGCAGTCTTTTGGATAGGTTTTTAGCTACCCTA 240
Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaAlaLys 100
Db 241 AAGGCTCATCCAAATACTTGGATTTGATTCGCAATCAGCTGTTTTTCTAGCTGCCAAG 300
Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 301 ACTGTTGAGGAAGATGAGAGAAATCCAGTACTAAAGGTATTGGCAAGAGACAGATTCTGT 360
Qy 121 GlyCysSerSerGluIleLeuArgMetGluArgIleLeuAspLysLeuAsnTrp 140
Db 361 GGATGTTCTCATCTGAAATTTGAGAAATGAGAGAAATTTCTGGAATGATTTTGGATGG 420
Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 421 GATCTTCACACAGACACACCATTTGATTTCTTCATATTTTCCATGCTGCAATGCTGCA 480
Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 481 ACTAGGCTCAGTTACTTTTTCAGTTTGGCCCAATTTAGCCCATCTCAACATTTGGCAGTC 540
Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
Db 541 CTTACCAAGCAACTACTTCTGATGCTGATGCTGCAACCACTTCTGCAATTCAGAGGATCC 600
Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
Db 601 ATGCTTGTCTGGCCATGTTAGTCTGGAATGGAGAACTCATTTCTGATTTGGCTTCT 660
Qy 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
Db 661 CTTACAAATTGAACCTCTTCAGAAAGCACAGATGGATAGCTCCAGTTGATCCATTTGTCGG 720
Qy 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
Db 721 GAGCTTGTGGACATCACCTTTTACTCTGAGTCTTCCGCTTCTGAAATTCGTTTAT 780
Qy 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db 781 GTCTACCGTCCCTCAAGCACACCTGCTGACCTGTGCAAGGAGTGTTCAGATTACAT 840
Qy 281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
Db 841 CCTCTCTGTCCTCCAGGCCAGACTTCTCCAGGACCAACAGCAAGCCAGAGTGCAGTC 900
Qy 301 ArgGlyThrAlaAlaPheTyrHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
Db 901 AGAGGTACAGACGCTTTTACCATCATCTCCAGCTGGCAGTGGGTGCAAGCAGACCTCT 960
Qy 321 ThrLysArgLysValGluGluMetGluValAspAspPheTyrAspGlyIleLysArgLeu 340
Db 961 ACTAAACGCAAGTAGAGAAATGGAAGTGGATGACTTCTATGATGGAATCAAAACGGCTC 1020
Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
Db 1021 TATAATGAAGATAATGTCTCAGAAATGTGGGTCTCTGTGTGGCAGCTGATTTATCAAGA 1080
```

361 GlnGluGlyHisAlaSerProCysProProLeuGlnProValSerValMet 377
1081 CAAGAGGACATGCTTCCCTTGTCCACCTTTGCAGCCTGTTCTGTGCATG 1131

RESULT 2
LOCUS AR087353 1260 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 5 from patent US 5986055.
ACCESSION AR087353
VERSION AR087353.1 GI:10014116
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1260)
AUTHORS Yang,M., Nandabalan,K. and Schultz,V.Peter.
TITLE CDK2 interactions
JOURNAL Patent: US 5986055-A 5 16-NOV-1999;
FEATURES Location/Qualifiers
1..1260
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.: 1..4e-174 Length: 1260
Score: 1962.00 Matches: 377
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-736-250-1 (1-377) x AR087353 (1-1260)

Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle 20
Db 1 ATGAAGTTTCAGGGCCCTTTGGAAACACAGAGATTGCTTTCTGTTGGAAAGGCAATC 60
Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 61 ACTAGGAGACAGAGTGGAAAGTGAATGTGGGAAATGCTTCAATCAGAAATGTT 120
Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn 60
Db 121 TCTCCATCCACAGAGATGAGAGAAATCCAGATCAATGCTGCTTTTCTAGCTGCCAAG 180
Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 181 CTTTACCAGAAACATTGCTCTGGCTAGCAGTCTTTTGGATAGGTTTTTAGCTACCCTA 240
Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaAlaLys 100
Db 241 AAGGCTCATCCAAATACTTGGATTTGATTCGCAATCAGCTGTTTTTCTAGCTGCCAAG 300
Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 301 ACTGTTGAGGAAGATGAGAGAAATCCAGTACTAAAGGTATTGGCAAGAGACAGATTCTGT 360
Qy 121 GlyCysSerSerGluIleLeuArgMetGluArgIleLeuAspLysLeuAsnTrp 140
Db 361 GGATGTTCTCATCTGAAATTTGAGAAATGAGAGAAATTTCTGGAATGATTTTGGATGG 420
Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 421 GATCTTCACACAGACACACCATTTGATTTCTTCATATTTTCCATGCTGCAATGCTGCA 480
Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 481 ACTAGGCTCAGTTACTTTTTCAGTTTGGCCCAATTTAGCCCATCTCAACATTTGGCAGTC 540
Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
Db 541 CTTACCAAGCAACTACTTCTGATGCTGATGCTGCAACCACTTCTGCAATTCAGAGGATCC 600
Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
Db 601 ATGCTTGTCTGGCCATGTTAGTCTGGAATGGAGAACTCATTTCTGATTTGGCTTCT 660
Qy 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
Db 661 CTTACAAATTGAACCTCTTCAGAAAGCACAGATGGATAGCTCCAGTTGATCCATTTGTCGG 720
Qy 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
Db 721 GAGCTTGTGGACATCACCTTTTACTCTGAGTCTTCCGCTTCTGAAATTCGTTTAT 780
Qy 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db 781 GTCTACCGTCCCTCAAGCACACCTGCTGACCTGTGCAAGGAGTGTTCAGATTACAT 840
Qy 281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
Db 841 CCTCTCTGTCCTCCAGGCCAGACTTCTCCAGGACCAACAGCAAGCCAGAGTGCAGTC 900
Qy 301 ArgGlyThrAlaAlaPheTyrHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
Db 901 AGAGGTACAGACGCTTTTACCATCATCTCCAGCTGGCAGTGGGTGCAAGCAGACCTCT 960
Qy 321 ThrLysArgLysValGluGluMetGluValAspAspPheTyrAspGlyIleLysArgLeu 340
Db 961 ACTAAACGCAAGTAGAGAAATGGAAGTGGATGACTTCTATGATGGAATCAAAACGGCTC 1020
Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
Db 1021 TATAATGAAGATAATGTCTCAGAAATGTGGGTCTCTGTGTGGCAGCTGATTTATCAAGA 1080


```
Db 541 CTTACCAAGCACTACTTCACTGTATGGCCCTGCAACCACTTCTGCAATTCAGAGATCC 600
Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
Db 601 ATGCTTGCTCTGGCCATGTTAGTCTGGAATGAGAAACTCAATTCCTGATTGCTTTCT 660
Qy 221 LeuThrIleGluLeuLeuGluAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
Db 661 CTTCAATTTGAATGCTTTCAAGAAACACAGATAGATAGCTCCCAAGTTGATCCATTGTCGG 720
Qy 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
Db 721 GAGCTTGGGCACATCACCTTTACTCTGAGATCTTCCCTGCTCTGAAATCCGTTTAT 780
Qy 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db 781 GTCTACCGTCCCTCAAGCACACCTGGTGTGACCTGTGACAAAGGAGTGTTCAGATTACAT 840
Qy 281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
Db 841 CCCTCCTCTGTCAGGCCAGACTTCTCCAAGGACACACAGCAAGCCAGAAAGTGCACGTC 900
Qy 301 ArgGlyThrAlaAlaPheTyrHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
Db 901 AGAGTCAGCAGCCTTTTACCATCATCTCCAGCTGCCAGTGGGTGCAAGCACCTCT 960
Qy 321 ThrLysArgLysValGluGluMetGluValAspPheTyrAspGlyValLeuArgLeu 340
Db 961 ACTAAACGCAAGTAGAGGAATGGAAGTGGATGATCTTATGATGGATCAACGGCTC 1020
Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
Db 1021 TATAATGAAGATAATGTCAGAAATATGGGTCTCTGTGTGGCACTGATTTATCAAGA 1080
Qy 361 GlnGluGlyHisAlaSerProCysProProLeuGlnProValSerValMet 377
Db 1081 CAAGAGGACATGCTTCCCTTGTCCACCTTTGCAGCCTGTTCTGTCTCATG 1131

RESULT 3
CQ812312 LOCUS CQ812312 1260 bp DNA linear PAT 24-MAY-2004
DEFINITION Sequence 64 from Patent WO2004038020.
ACCESSION CQ812312
VERSION CQ812312.1 GI:47601932
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Wittig R., Poustka A., Mollenhauer J. and Schadendorf D.
TITLE Target genes for the diagnosis and treatment of cancer
JOURNAL Patent: WO 2004038020-A 64 06-MAY-2004;
Deutsches Krebsforschungszentrum Stiftung des oeffentlichen n Rechtes
(DE)
FEATURES
source Location/Qualifiers
1..1260
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="caxon:9606"
misc_feature 1..1260
/note="D50310"
ORIGIN
Alignment Scores:
Pred. No.: 1.4e-174 Length: 1260
Score: 1962.00 Matches: 377
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-09-736-250-1 (1-377) x CQ812312 (1-1260)
```

```
Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle 20
Db 1 ATGAAGTTTCAGGGCCCTTTGGAAACACAGAGATTGTCTTCTCTGTGGTGGAAAGCGCAATC 60
Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 61 ACTAGGGAAGCACAGATGTGGAAGTGAATGTGGGAAATAGCCCTTCAATCAGATCAATCAAC 120
Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysLysTrpGlnPheAsn 60
Db 121 TCTCCATCCACAGAGATGAAGTAATTCATGGCTGGCCAAACTCAAGTACCAATTCAC 180
Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 181 CTTTACCAGAAAACATTTGCTCTGGCTAGCAGTCTTTTGGTAGTGTCTTCAATAGTACCGTA 240
Qy 81 LysAlaHisProLysTrpLeuSerCysIleAlaIleSerCysPhePheLeuAlaLys 100
Db 241 AAGGCTCATCCAAATACTTGAAGTTGATTGCAATCAGCTGTTTTTCTAGCTGCCAAG 300
Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 301 ACTGTTGAGGAGATGAGAGAAATTCAGTACTAAGGTATTGGCAGAGACAGATTTCTGT 360
Qy 121 GlyCysSerSerSerGluIleLeuArgMetGluArgIleLeuLeuAspLysLeuAsnTrp 140
Db 361 GGATGTTCTCATCTGAAATTTTGAAGATGGAGAAATTTCTGGATAAGTGAATGG 420
Qy 141 AspleuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 421 GATCTTCACACAGCACACCATTTGATTTTCTCATATTTTCCATGTCATTTGCCAGTGCA 480
Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 481 ACTAGGCTCAGTTACTTTTTCAGTTTGGCCAAATTTGAGCCCATCTCAACATTTGGCAGTC 540
Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
Db 541 CTTACCAAGCACTACTTCACTGTATGGCTGCAACCAACTTCTGCAATTCAGAGATCC 600
Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
Db 601 ATGCTTGCTCTGGCCATGTTAGTCTGGAATGAGAAACTCAATTCCTGATTGCTTTCT 660
Qy 221 LeuThrIleGluLeuLeuGluAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
Db 661 CTTCAATTTGAATGCTTTCAAGAAACACAGATAGATAGCTCCCAAGTTGATCCATTGTCGG 720
Qy 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
Db 721 GAGCTTGGGCACATCACCTTTTACTCTGAGTCTTCCCTGCTCTGAAATCCGTTTAT 780
Qy 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db 781 GTCTACCGTCCCTCAAGCACACCTGGTGTGACCTGTGACAAAGGAGTGTTCAGATTACAT 840
Qy 281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
Db 841 CCCTCCTCTGTCAGGCCAGACTTCTCCAAGGACACACAGCAAGCCAGAAAGTGCACGTC 900
Qy 301 ArgGlyThrAlaAlaPheTyrHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
Db 901 AGAGTTCAGCAGCCTTTTACCATCATCTCCAGCTGCCAGTGGGTGCAAGCACCTCT 960
Qy 321 ThrLysArgLysValGluGluMetGluValAspPheTyrAspGlyValLeuArgLeu 340
Db 961 ACTAAACGCAAGTAGAGGAATGGAAGTGGATGATCTTATGATGGATCAACGGCTC 1020
Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
Db 1021 TATAATGAAGATAATGTCAGAAATATGGGTCTCTGTGTGGCACTGATTTATCAAGA 1080
```

```
Qy 361 GlnGluGlyHisAlaSerProCysProLeuGlnProValSerValMet 377
Db 1081 CAAGAGGACATGCTTCCCTTGTCCACCTTGCAGCCCTGTTCTGTGTCATG 1131

RESULT 4
AR281918
LOCUS AR281918 1260 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 5 from patent US 6521412.
ACCESSION AR281918
VERSION AR281918.1 GI:29717848
KEYWORDS unknown.
SOURCE unknown.
ORGANISM unknown.
REFERENCE 1 (bases 1 to 1260)
AUTHORS Yang, M., Nandabalan, K. and Schulz, V.P.
TITLE HsReg1 and hSReg2 proteins and use thereof to detect CDK2
JOURNAL Patent: US 6521412-A 5 18-FEB-2003;
FEATURES
    Location/Qualifiers
        1..1260
            /organism="unknown"
            /mol_type="genomic DNA"

ORIGIN
Alignment Scores:
Pred. No.: 1.4e-174 Length: 1260
Score: 1962.00 Matches: 377
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-736-250-1 (1-377) x AR281918 (1-1260)

Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle 20
Db 1 ATGAAGTTTCAGGGCCCTTTCGAAACCCAGAGATTGCTTTCTCTGTTGGAAAGGCAATC 60

Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 61 ACTAGGAGACACAGATGTCGAAAGTGNATGTGGGAAATGCCCTTCATCATCAAGATGTT 120

Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn 60
Db 121 TCTCATCCACAGAGATGAAGTAATTCATATGGCTGGCCAACTCAAGTACCAATTCAC 180

Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 181 CTTTACCCAGAAACATTTGCTGTGGTAGCAGTCTTTTGGATAGGTTTTTAGCTACCGTA 240

Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaAlaLys 100
Db 241 AAGGCTCATCCAAATACCTTCAAGTGTATTCATCAATCAGCTGTTTTTTCCTAGCTGCCAG 300

Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 301 ACTGTTGAGGAAGATGAGAGAATTCAGTCTAAAGGTATTGGCAAGAGACAGATTCTGT 360

Qy 121 GlyCysSerSerGluIleLeuArgMetGluArgIleLeuAspLysLeuAsnTrp 140
Db 361 GGATGTTCTCATCTGAAATTTTGAAGATGAGAGAATTATCTGGATTAAGTTGAATGG 420

Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 421 GATCTTCACACAGCCACACCATTTGATTTTCTTATATTTTCCATGTCATTCAGTGTCA 480

Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 481 ACTAGGCTCATGTTACTTTTTCAGTTTGGCCAAATTTAGCCCATCTCAACATTTGGCAGTC 540

Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
Db 541 CTTACCAAGCAACTACTTCTACTGTATGCGCTGCAACCAACTTCTGCATTCAGAGATCC 600

Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
Db 601 ATGCTTGCTCTGGCCATGGTTAGTCTGAAATGAGAAATCAATCTCTGATTGCTTCT 660

Qy 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
Db 661 CTTACAATTGAACCTTCAGAAAGCACAGATGATAGTCCCAAGTTGATCCATTGTCGG 720

Qy 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
Db 721 GAGCTTGTGGCACATCACCTTTTACTCTGCGTCTTCCCTGCTCTGAAATTCGCTTAT 780

Qy 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db 781 GTCTACCGTCCCTCAAGCACACCTGTGTGACCTGTGACAAAGAGGTGTTTCAGATTACAT 840

Qy 281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
Db 841 CCTCTCTCTGTCCTCCAGGCCAGACTTCTCCAGGACAAACAGCAGCAGAGTCCAGTC 900

Qy 301 ArgGlyThrAlaAlaPheTyrHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
Db 901 AGAGGTACAGAGCCCTTTTACCATCATCTCCAGCTGCCAGTGGGTGCAGACACCTCT 960

Qy 321 ThrLysArgLysValGluGluMetGluValAspAspPheTyrAspGlyIleLysArgLeu 340
Db 961 ACTAAACGCCAAGTAGAGGAATGGAAGTGGATGACTTCTATGATGAATCAACAGGCTC 1020

Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
Db 1021 TATAATGAAGATAATGCTCAGAAATGTGGTCTCTGTGTGGCACTGATTATCAAGA 1080

Qy 361 GlnGluGlyHisAlaSerProCysProLeuGlnProValSerValMet 377
Db 1081 CAAGAGGACATGCTTCCCTTGTCCACCTTTCAGCCCTGTTCTGTGTCATG 1131

RESULT 5
AR380354
LOCUS AR380354 1260 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 899 from patent US 6607879.
ACCESSION AR380354
VERSION AR380354.1 GI:40087988
KEYWORDS unknown.
ORGANISM unknown.
REFERENCE 1 (bases 1 to 1260)
AUTHORS Cocks, B.G., Stuart, S.G. and Seilhamer, J.J.
TITLE Compositions for the detection of blood cell and immunological response gene expression
JOURNAL Patent: US 6607879-A 899 19-AUG-2003;
FEATURES
    Location/Qualifiers
        1..1260
            /organism="unknown"
            /mol_type="genomic DNA"

ORIGIN
Alignment Scores:
Pred. No.: 1.4e-174 Length: 1260
Score: 1962.00 Matches: 377
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-736-250-1 (1-377) x AR380354 (1-1260)

Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle 20
Db 1 ATGAAGTTTCAGGGCCCTTTCGAAACCCAGAGATTGCTTTCTCTGTTGGAAAGGCAATC 60

Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 61 ACTAGGAGACACAGATGTCGAAAGTGNATGTGGGAAATGCCCTTCATCATCAAGATGTT 120

Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn 60
Db 121 TCTCATCCACAGAGATGAAGTAATTCATATGGCTGGCCAACTCAAGTACCAATTCAC 180

Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 181 CTTTACCCAGAAACATTTGCTGTGGTAGCAGTCTTTTGGATAGGTTTTTAGCTACCGTA 240

Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaAlaLys 100
Db 241 AAGGCTCATCCAAATACCTTCAAGTGTATTCATCAATCAGCTGTTTTTTCCTAGCTGCCAG 300

Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 301 ACTGTTGAGGAAGATGAGAGAATTCAGTCTAAAGGTATTGGCAAGAGACAGATTCTGT 360

Qy 121 GlyCysSerSerGluIleLeuArgMetGluArgIleLeuAspLysLeuAsnTrp 140
Db 361 GGATGTTCTCATCTGAAATTTTGAAGATGAGAGAATTATCTGGATTAAGTTGAATGG 420

Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 421 GATCTTCACACAGCCACACCATTTGATTTTCTTATATTTTCCATGTCATTCAGTGTCA 480

Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 481 ACTAGGCTCATGTTACTTTTTCAGTTTGGCCAAATTTAGCCCATCTCAACATTTGGCAGTC 540

Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
Db 541 CTTACCAAGCAACTACTTCTACTGTATGCGCTGCAACCAACTTCTGCATTCAGAGATCC 600
```

|||||
61 ACTAGGAGGACACAGATGTGAAGTGAATGTGGAAATGCCTTCAATCAAGATGTT 120
Qy SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn 60
|||||
121 TCTCCATCCAGAGAGATGAAGTAACTCAATGGCTGGCCAACTCAAGTACCAATTCAC 180
Qy LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
181 CTTTACCAGAAACATTTGCTCTGGTAGCAGTCTTTTGGATAGTGTTTTACGTACCGTA 240
Qy LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaLys 100
241 AAGGCTCATCCAAATACTTCAGTGTATTCCAATCAGCTGTTCCTAGCTGCCAAG 300
Qy ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
301 ACTGTTGAGGAAGATGAGAGATTCAGTACTAAGGTATTGGCAAGACAGATTTCTGT 360
Qy GlyCysSerSerGluIleLeuArgMetGluArgIleLeuAspLysLeuAsnTrp 140
361 GGATGTTCTCATCTGAAATTTTGAATGAGAGATTAATCTGGATAAGTTGAATTGG 420
Qy AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
421 GATCTTACACAGCCACACCATTTGATTTCTTATATTTTCCATGTCATTCAGTGTCA 480
Qy ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
481 ACTAGGCTCAGTACTTTTCAAGTTGGCCAAATGAGCCCATCTCAACATTTGGCAGTC 540
Qy LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgLys 200
541 CTTACCAAGCAACTACTTCACTGTATGCTGCAACCACTTCTGCAATTCAGAGGATCC 600
Qy MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
601 ATGCTTGTCTGGCCATGTTAGTCTGGAAATGAGAAACACTCATTCCTGATTTGCTTCT 660
Qy LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
661 CTTACATTTGACCTGCTTCAGAAAGCAGATGATAGTCTCCAGTGTATCATTTGTCGG 720
Qy GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
721 GAGCTTGTGGCACATCACCTTTCTACTCTGCAGTCTTCCCTGCTCTGAAATTCGGTTAT 780
Qy ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
781 GTCTACCGTCCCTCAAGCACACCTTGGTGACCTGTGCAAAAGGAGTGTTCAGATTTACAT 840
Qy ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
841 CCTCTCTGTCCAGGCCAGACTTCTCCAGGACACAGCAAGCCAGAGTGCAGTC 900
Qy ArgGlyThrAlaAlaPheTyrHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
901 AGAGTACAGCAGCCTTTTACCATCATCTCCAGCTGCCAGTGGGTGCAAGCAGCTCT 960
Qy ThrLysArgLysValGluGluMetGluValAspAspPheTyrAspGlyIleLysArgLeu 340
961 ACTAAACCAAGTAGAGAAATGGAAGTGGATGACTTCTATGATGGAATCAAAAGCGGTC 1020
Qy TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
1021 TATATGAAGATATGCTTCAGAAATATGGGTCTCTGTGTGGCAGTATTTATCAAGA 1080
Qy GlnGluGlyHisAlaSerProCysProProLeuGlnProValSerValMet 377
1081 CAAGAGGACATGCTTCCCTTGTCCACTTTGAGCCTGTTCGTGTCATG 1131

RESULT 6
HUMCYI

LOCUS HUMCYI 1260 bp mRNA linear PRI 10-FEB-1999
DEFINITION Human mRNA for cyclin I, complete cds.
ACCESSION D50310
VERSION D50310.1 GI:1183161
KEYWORDS cyclin I.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (sites)
AUTHORS Nakamura,T., Sanokawa,R., Sasaki,Y.F., Ayusawa,D., Oishi,M. and Mori,N.
TITLE Cyclin I: a new cyclin encoded by a gene isolated from human brain
JOURNAL Exp. Cell Res. 221 (2), 534-542 (1995)
MEDLINE 96086776
PUBMED 7493655
REFERENCE 2 (bases 1 to 1260)
AUTHORS Nakamura,T.
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 1260)
AUTHORS Nakamura,T.
TITLE Direct Submission
JOURNAL Submitted (17-APR-1995) Takeshi Nakamura, Sumitomo Electric Industries, Biomedical R&D Department; 1, Taya-cho, Sakae-ku, Yokohama, Kanagawa 244, Japan (E-mail:tnakam@pele.sumiden.co.jp, Tel:045-853-7275, Fax:045-853-3528)
FEATURES
source
1..1260
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="FC6"
/tissue_type="Brain"
1..1134
/codon_start=1
/product="cyclin I"
/protein_id="BAA0849.1"
/db_xref="GI:1183162"
/translation="MKFPPGLENRQLSFLLEKAITREAOQKVNVRKMPNSQNVSPSQ RDEIVPLAKLYQFNLYPTFALASLLDRFLATVKAHKYLSIAISCFPLAAKTVD EDERIPVLALARDSFCGSSSEILMERIILDKNLDLHTATPLDPLHFLHAIVS TRQLFSLPKLSPSHLAVLTQQLHMACNQLQFRGSMALAMVSLMEKILPDW LSTIELLQKQMDSSQLIHCRELVHHLSTLQSSLSVYVTRPLKHLVTCDKGV FRIHPSPVGPFDISKNSKEPVRTGAFFYHLLPAASGCKQTSKTKRKEEMVEDDFY DGIRLYNEDNVSENVSGVGTDLRSQEGHASPCLPPLQPVSVM"
ORIGIN
Alignment Scores:
Pred. No.: 1.4e-174 Length: 1260
Score: 1962.00 Matches: 377
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
US-09-736-250-1 (1-377) x HUMCYI (1-1260)
Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuGluLysAlaIle 20
Db 1 ATGAAGTTTCAGAGCCCTTTGGAAACACAGAGATTGCTTCTTCCTGTTGGAAAGGCAATC 60
Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 61 ACTAGGGAAGCACAGATGTGAAAGTGAATGTGGGAAATGCCTTCAATCAGATGTT 120
Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn 60
Db 121 TCTCCATCCAGAGAGATGAAGTAACTCAATGGCTGGCCAACTCAAGTACCAATTCAC 180
Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 181 CTTTACCAGAAACATTTGCTCTGGTAGCAGTCTTTTGGATAGTGTTTTACGTACCGTA 240

```
Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaAlaLys 100
Db 241 AAGGCTCATCCAAATACTTGGAGTGTATTGCAATCAGCTGTTTCTTCTAGCTGCCAAG 300
Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 301 ACTGTTGAGGAAGATGAGAGAATTCAGTACTAAAGGTAATTGGCAAGACAGATTCTCTGT 360
Qy 121 GlyCysSerSerGluIleLeuArgMetGluArgIleLeuLeuAspLysLeuAsnTrp 140
Db 361 GGATGTTCTCATCTGAAATTTGAGATGAGAGAATTTCTGGATAAGTTGAAATGG 420
Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 421 GATCTTCACACAGCCACACCACTGGATTTCTTCATATTTCCATGCAATTCAGTGTCA 480
Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 481 ACTAGGCTCAGTTACTTTTTCAGTTTGCCAAATTTGAGCCCATCTCAACATTTGGCAGTC 540
Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuPheArgGlySer 200
Db 541 CTTACCAAGCAACTTCTCTGATGCTGCGCTGCAACCACTCTGCAATTCAGAGATCC 600
Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
Db 601 ATGCTTGCTCTGGCCATGTTAGTCTGGAATGAGAACTCATCTGATTGCTTTCT 660
Qy 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
Db 661 CTTACAAATTGAATGCTTCAGAAAGCACAGATGATAGTCTCCCACTTGCATTTGTCGG 720
Qy 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
Db 721 GAGCTTGGGCACATCAGCTTTCTACTCTGAGTCTTCCCTGCTCTGAAATTCGTTAT 780
Qy 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db 781 GTCTACGCTCCCTCAAGCACACCTGCTGACCTGTGACAAAGGAGTGTTCAGATTACAT 840
Qy 281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
Db 841 CCCTCTCTGTCAGGCGCCAGACTTCTCCAGGACACACAGCAAGAGTGTCCAGTC 900
Qy 301 ArgGlyThrAlaAlaPheTyrHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
Db 901 AGAGTACAGAGCCCTTTTACATCACTCCAGCTGCCAGTGGTGGCAACAGACCTCT 960
Qy 321 ThrLysArgLysValGluGluMetGluValAspAspPheTyrAspGlyIleLysArgLeu 340
Db 961 ACTAAACGCAAGTAGAGAAATGGAAGTGGATGACTTCTATGATGGAATCAACGGGTC 1020
Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
Db 1021 TATAATGAAGATAATGCTTCAGAAATGCGGTTCTGTGTGGCAGCTGATTTATCAAGA 1080
Qy 361 GlnGluGlyHisAlaSerProCysProLeuGlnProValSerValMet 377
Db 1081 CAAGAGGACATGCTTCCCTTGTCCACTTTCAGGCTGTTTCTGTGATG 1131

RESULT 7
AF135162 1384 bp mRNA linear PRI 17-MAR-2000
LOCUS Homo sapiens cyclin I (CYCL) mRNA, complete cds.
DEFINITION AF135162
ACCESSION AF135162
VERSION AF135162.1 GI:7259481
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1. (bases 1 to 1384)
AUTHORS Chen, J.H., Luo, W.Q., Zhou, Y., Zhou, H.J., Huang, X.W., Yuan, J.G. and
```

Qiang, B.Q.
Isolating a new cDNA coding for human cyclin protein
Unpublished
2. (bases 1 to 1384)
Chen, J.H., Luo, W.Q., Zhou, Y., Zhou, H.J., Huang, X.W., Yuan, J.G. and
Qiang, B.Q.
Direct Submission
Submitted (16-MAR-1999) Dept. of Biochemistry, Ins. of Basic Med.
Science, 5 Dong Dan 3 Tiao, Beijing 100005, P.R. China
Location/Qualifiers
1. 1384
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
1. 1384
/gene="CYCL1"
200. 1333
/genes="CYCL1"
/codon_start=1
/product="cyclin I"
/protein_id="AAP43786.1"
/db_xref="GI:7259482"
/translation="MRP PGELENQRISFLEKAITREAOQWKVNRMPNQNVSPSQ
RDEVIQWLAKLYQFNLPTFALASSLLDRFLATVKAHPKYLISLCISCFEFLAAKV
EEDERIPVLKVLARDSEFCGSSSEILMERIILDKLNDLHTATPDLDLFHFAIAYS
TRQLLFLPKLSPQHLAVTLKQLLHMACNQLQPRGSMALAMVLSLEMEKLIIDW
LSLTIELLOKQMDSSQLIHRELVAHLSTLQSSLPNSVYVVRPLKHLTVTCQKGV
FRLHPSVPGPDFSKNSKEVPVRGTAAFYVHLPRASGCKQTSKTRKEEMEVEDDYF
DGIRLYNEDNVSENVSGVCTDLRSQEGHSPCPPLQPVSVW"

ORIGIN

Alignment Scores:
Pred. No.: 1,57e-174 Length: 1384
Score: 1962.00 Matches: 377
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-736-250-1 (1-377) x AF135162 (1-1384)

```
Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuGluLysAlaIle 20
Db 200 ATGAAGTTTCAGGCGCTTTGGAAACACAGAGATTGTCTTCTGTTGGAAAAGCGCAATC 259
Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 260 ACTAGGGAAGCACAGATGTGAAAGTGAATGTGCGAAATATGCCTTCAATCAAGATGTT 319
Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn 60
Db 320 TCTCCATCCACAGAGATGAAGTAATTCATGGCTGGCCAACTCAAGTACCAATTCAC 379
Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 380 CTTTACCAGAAAACATTTGCTCTGGCTAGCAGTCTTTTGGTAGGTTTTTACGTACCGTA 439
Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaAlaLys 100
Db 440 AAGGCTCATCCAAATACTTGGAGTGTATTGCAATCAGCTGTTTCTTCTAGCTGCCAAG 499
Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 500 ACTGTTGAGGAAGATGAGAGAATTCAGTACTAAAGGTAATTGGCAAGACAGATTCTCTGT 559
Qy 121 GlyCysSerSerGluIleLeuArgMetGluArgIleLeuLeuAspLysLeuAsnTrp 140
Db 560 GGATGTTCTCATCTGAAATTTTGGAGATGAGAGAATTTCTGGATAAGTTGAAATGG 619
Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 620 GATCTTCACACAGCCACACCACTTGGATTTCTTCATATTTCCATGCAATTCAGTGTCA 679
```

161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
 680 ACTAGGCTCAGTTACTTTTCAGTTTCCCAATGAGCCCATCTCAACATTTGGCAGTC 739
 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
 740 CTTACCAAGCAACTACTTCTACTGTATGGCTGCAACCACTTCTGCAATTCAGAGGATCC 799
 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuLeuProAspTrpLeuSer 220
 800 ATGCTTGTCTCGGCCATGTTAGTCTGAAATGAGAACTCATCTCGATTTGGCTTTCT 859
 221 LeuThrLeuGluLeuLeuGlnLeuAlaGlnMetAspSerSerGlnLeuLeuHisCysArg 240
 860 CTTACAAATGAACGTCTTCAGAAAGCAGATGATAGTCCCGAGTTGATCCATTTGTCGG 919
 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
 920 GAGCTTGTGGCACATCACCTTTCTACTCTGAGTCTTCCCTGCTCTGAAATTCGTTTAT 979
 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
 980 GTCTACCGTCCCTCAAGCACACCTGCTGACCTGTGCACAAAGGAGTTCAGATTACAT 1039
 281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
 1040 CCCCTCTGTGCCAGGCCAGACTTCTCCAAAGACACACAGCAGCAGAGTCCAGTC 1099
 301 ArgGlyThrAlaAlaPheTyrHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
 1100 AGAGTACAGCAGCGCTTTTACCATCATCTCCAGCTGCCAGTGGTGTCAGCAGACCTCT 1159
 321 ThrLysArgLysValGluGluMetGluValAspPheTyrAspGlyLysLeuValLysArgLeu 340
 1160 ACTAAACGCAAGTAGAGGAATGGAAGTGCATCTTATGATGGAATCAACAGCGCTC 1219
 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
 1220 TATAATGAAGATAATGTCTCAGAAATGTGGTGTCTGTGTGTCACCTGATTTATCAAGA 1279
 361 GlnGluGlyHisAlaSerProCysProLeuGlnProValSerValMet 377
 1280 CAAGAGGACATGCTTCCCTGTGCCACCTTTGAGCGCTGTTCTGTGCATG 1330

RESULT 8
 BC000420 1817 bp mRNA linear PRI 30-JUN-2004
 LOCUS Homo sapiens cyclin I, mRNA (cdna clone MGC:8665 IMAGE:2964432),
 DEFINITION complete cds.
 ACCESSION BC000420
 VERSION BC000420.2 GI:38197480
 KEYWORDS MGC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1817)
 Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
 Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
 Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
 Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heide, F.,
 Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
 Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
 Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
 Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
 Abramson, R.D., Mullahy, S.G., Bosak, S.A., McEwan, P.J.,
 McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
 Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, J.W.,
 Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
 Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,
 Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
 Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
 Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

TITLE
 JOURNAL
 PUBMED
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 REMARK
 COMMENT
 NIH-MGC Project URL: http://mgc.nci.nih.gov
 On Nov 6, 2003 this sequence version replaced gi:12653302.
 Contact: MGC help desk
 Email: cgabs-r@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Rubin Laboratory
 DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
 Sequencing Center (NISC),
 Gaithersburg, Maryland;
 Web site: http://www.nisc.nih.gov/
 Contact: nisc_mgc@hgrl.nih.gov
 Akhter, N., Ayale, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
 Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
 Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
 Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,
 Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
 McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,
 Teurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
 Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
 Series: IRAL Plate: 1 Row: 0 Column: 8
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA gi: 17738314.

FEATURES

source

1. .1817

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="MGC:8665 IMAGE:2964432"

/tissue type="Muscle, rhabdomyosarcoma"

/clone_lib="NIH MGC 17"

/lab_host="DH10B-R"

/notes="Vector: pOTB7"

1. .1817

/gene="CCNI"

/notes="synonyms: CYC1, CYI"

/db_xref="LocusID:10983"

544..1677

/gene="CCNI"

/product="cyclin I"

/protein_id="AAH0420.1"

/db_xref="GI:12653303"

/translation="MKPGLNQRUSFLLEKAITREAOQMKVNRKMPNQNVPSQ
RDEVIQMLAKYQFNLYPETFALASLLDRFLATVKAHPKYLSCIAISCFFLAAKTV
EEDERIPVLKVLARDSCGSSSEILMERIILDKNLDLHTATPDLDLFIHFAIAVS
TRPQLFLPKLSPOHLAVLTQKLLHMACNOLLOPRGSMALAMVSLMEKLIPOW
LSITILLQKQMSQLIHCRLVAHLSTLSSLPNSVYVYRPLKHTLVCKDKV
FRUHPSPGPDFSKONSKPEVPVGTAAFYHLLPRAAGCKQSTKKRKEMEVEDDFY
DGIKRLYNEDNSVNSVCGTDLRSQEGHSGPCPLQPVSVN"

gene

1. .1817

CDS

ORIGIN

Alignment Scores:

Pred. No.:

Score:

Percent Similarity:

2,23e-174

1962.00

100.00%

Length:

Matches:

Conservative:

1817

377

0

```
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-736-250-1 (1-377) x BC000420 (1-1817)

Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle 20
Db 544 ATGAAGTTTCAGGGCCCTTGGAAACACAGAGATTGCTTTCCTGTTGGAAAGGCAATC 603

Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 604 ACTAGGGAAGCACAGATGTCGAAAGTGAATGCGGAAAATGCGCTTCAAAATCAGATGTT 663

Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn 60
Db 664 TCTCCATCCAGAGAGATGAAGTAATCAATGGCTGGCCAAACTCAAGTACCAATTCAAC 723

Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 724 CTTTACCAGAAACATTTGCTCGTAGCAGTCTTTTGGATAGTTTGTAGCTACCGTA 783

Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPheLeuAlaAlaLys 100
Db 784 AAGGCTCATCCAAAATACTTTGAGTTGATTGCAATCAGCTGTTTTTCTAGCTGCCAAG 843

Qy 101 ThrValGluGluAspGluValIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 844 ACTGTTGAGGAAGATGAGAAATTCAGTACTAAAGGTATTGGCAAGACAGATTTCTGT 903

Qy 121 GlyCysSerSerGluIleLeuArgMetGluArgIleLeuLeuAspLysLeuAsnTrp 140
Db 904 GGATGTTCTCATCTGAAATTTTGCAGAAATGAGAGAAATTTCTGGATAAGTTCAATTGG 963

Qy 141 AspleuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 964 GATCTTCACAGACACACCATTTGATTTTCTCATATTTTCCATGTCATTTGCAAGTGTCA 1023

Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 1024 ACTAGGCTCAGTTACTTTTCAGTTTGGCCAAATGAGCCCACTCAACATTTGGCAGTC 1083

Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
Db 1084 CTTTACCAGCAACTACTTCACTGTATGCGCTGCAACCAACTTCTGCAATTCAGAGGATCC 1143

Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
Db 1144 ATGCTTGCTCTGGCCATGGTTAGTCTGGAATGGAAGAACTCAATCTCCTGATTGCTTTCT 1203

Qy 221 LeuThrIleGluLeuLeuLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
Db 1204 CTTTCAATGAACTGCTTCAGAAAGCACAGATGATAGTCTCCAGTTGATCCATTGCGG 1263

Qy 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
Db 1264 GAGCTTGTGGCACATCACTTTTCTACTCTGCAGTCTTCCCTGCTCTGAAATTCGTTTAT 1323

Qy 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db 1324 GTCTACCGTCCCTTCAAGCACACCCCTGGTGACCTGTGACAAAGGAGGTCTCAGATTACAT 1383

Qy 281 ProSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
Db 1384 CCTTCTCTGTCCAGGCCAGACTTCTCCAGGACACACAGCAGCAGCAGAGTCCAGTCC 1443

Qy 301 ArgGlyThrAlaPheTyrHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
Db 1444 AGAGGTACAGCAGCCTTTTACCATCATCTCCAGCTGCGAGTGGGTGCAAGCACACTCT 1503

Qy 321 ThrLysArgLysValGluGluMetGluValAspAspPheTyrAspGlyIleLysArgLeu 340
Db 1504 ACTAAACGCAAGTAGAGGAAATGGAAGTGGATGACTTCTATGATGGAATCAACCGGCTC 1563
```

```
Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
Db 1564 TATAATGAGATATATGCTCAGAAATGCGGTTCTGTGTGGCACTGATTTATCAAGA 1623

Qy 361 GlnGluGlyHisAlaSerProCysProProLeuGlnProValSerValMet 377
Db 1624 CAAGAGGACATGCTTCCCTTGTCCACCTTTCAGCCTGTTTCTGTGTCATG 1674

RESULT 9
CQ468129 1889 bp DNA linear PAT 30-JAN-2004
LOCUS Sequence 10907 from Patent WO0192581.
DEFINITION
ACCESSION CQ468129
VERSION CQ468129.1 GI:41433748
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
MAMMALIA; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1
AUTHORS Algate, P.A., Harlocker, S.L. and Jones, R.
TITLE Compositions and methods for the therapy and diagnosis of
JOURNAL ovariocancer
PATENT: WO 0192581-A 10907 06-DEC-2001;
CORIXA CORPORATION (US)
FEATURES
source Location/Qualifiers
1..1889
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Alignment Scores: 2,34e-174 Length: 1889
Pred. No.: 1962.00 Matches: 377
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 6

US-09-736-250-1 (1-377) x CQ468129 (1-1889)

Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuGluLysAlaIle 20
Db 544 ATGAAGTTTCAGGGCCCTTGGAAACACAGAGATTGCTTTCCTGTTGGAAAGGCAATC 603

Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 604 ACTAGGGAAGCACAGATGTCGAAAGTGAATGCGGAAAATGCGCTTCAAAATCAGATGTT 663

Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn 60
Db 664 TCTCCATCCAGAGAGATGAAGTAATCAATGGCTGGCCAAACTCAAGTACCAATTCAAC 723

Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 724 CTTTACCAGAAACATTTGCTCGTAGCAGTCTTTTGGATAGTTTGTAGCTACCGTA 783

Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPheLeuAlaAlaLys 100
Db 784 AAGGCTCATCCAAAATACTTTGAGTTGATTGCAATCAGCTGTTTTTCTAGCTGCCAAG 843

Qy 101 ThrValGluGluAspGluValIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 844 ACTGTTGAGGAAGATGAGAAATTCAGTACTAAAGGTATTGGCAAGACAGATTTCTGT 903

Qy 121 GlyCysSerSerGluIleLeuArgMetGluArgIleLeuLeuAspLysLeuAsnTrp 140
Db 904 GGATGTTCTCATCTGAAATTTTGCAGAAATGAGAGAAATTTCTGGATAAGTTCAATTGG 963

Qy 141 AspleuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
```

Db	964	GATCTTCACAGCCACACCATGGATTTCTTCATATTTTCCATGTCATGCGAGTGCA	1023
Qy	161	ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal	180
Db	1024	ACTAGGCGCTAGTTACTTTTCAGTTGTCGCAAAATGAGCCCATCTCAACATTTGGCAGTC	1083
Qy	181	LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgLysSer	200
Db	1084	CTTACCAAGCAACTACTTCTGATGTCCTGACCAACTTCTGCAATTCAGAGGATCC	1143
Qy	201	MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuLeuProAspTrpLeuSer	220
Db	1144	ATGCTTGCTCTGGCCATGTTAGTCTGGAATGAGAACTCAATCTCGATGTCCTTCT	1203
Qy	221	LeuThrLleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuLleHisCysArg	240
Db	1204	CTTACAATTAAGTCTTTCAGAAAGCAGATGATGATGTCCTCCAGTTGATCCATTTGTCG	1263
Qy	241	GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr	260
Db	1264	GAGCTTGTCGACATCACTTCTACTCTGACATCTTCCCTGCTCTGAAATTCGCTTAT	1323
Qy	261	ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis	280
Db	1324	GTCATCCCTCCCTCAACACACCTGCTGACCTGTGACAAAGGAGTTCAGATTACAT	1383
Qy	281	ProSerSerValProGlyProAspPheSerLysAspSerLysProGluValProVal	300
Db	1384	CCCTCTCTGTCGCCAGGCCAGACTTCTCCAAAGACACAGCAAGCCAGAGTGCCAGTC	1443
Qy	301	ArgGlyThrAlaAlaPheTyrHisLeuProAlaAlaSerGlyCysLysGlnThrSer	320
Db	1444	AGAGTGACAGAGCGCTTTTACCATCATCTCCAGCTGCCAGTGGTGGTCAAGCACCTCT	1503
Qy	321	ThrLysArgLysValGluGluMetGluValAspPheTyrAspGlyLleLysArgLeu	340
Db	1504	ACTAAACCAAGTAGAGAAATGGAAGTGATGACTTCTATGATGGATCAAGCGCTC	1563
Qy	341	TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg	360
Db	1564	TATAATGAAGATAATGTCTCAGAAATGTGGTCTGTGTGGCACTGATTTATCAAGA	1623
Qy	361	GlnGluGlyHisAlaSerProCysProLeuGlnProValSerValMet	377
Db	1624	CAAGAGGACATGCTTCCCTTGTCCACCTTTCAGCGCTGTTCTGTGTCATG	1674

RESULT 10

LOCUS	BC004975	1889 bp	mRNA	linear	PRI 29-JUN-2004
DEFINITION	Homo sapiens cyclin I, mRNA (cdna clone MGC:3795 IMAGE:2957878), complete cds.				
ACCESSION	BC004975				
VERSION	BC004975.1 GI:13436391				
KEYWORDS	MGC.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 1889)				
AUTHORS	Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whitling, M., Madan, A., Young, A.C., Shevchenko, Y.,				

TITLE	JOURNAL				
PUBMED	12477932				
REFERENCE	2 (bases 1 to 1889)				
AUTHORS	Strausberg, R.				
TITLE	Direct Submission				
JOURNAL	Submitted (21-MAR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA				
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov				
COMMENT	Contact: MGC help desk Email: cgapbs-r@mail.nih.gov Tissue Procurement: DCTD/DTF CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada info@bcgsc.bc.ca Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Chow, Allison Cloutier, Ruth Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao, Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prahbu, Parvaneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skaleka, Duane Smalls, Jeff Stott, Miranda Tsai, George Yang, Jackie Schein, Asim Siddiqui, Rob Holt, Marco Marra.				
FEATURES	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 9 Row: b Column: 16. Location/Qualifiers 1. .1889 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="MGC:3795 IMAGE:2957878" /tissue_type="Kidney, renal cell adenocarcinoma" /clone_lib="NIH_MGC_14" /lab_host="DH10B-R" /note="Vector: pOTB7" 1. .1889 /gene="CCNI" /note="synonyms: CYC1, CYI" /db_xref="LocusID:10983" 544. .1677 /gene="CCNI" /codon_start=1 /product="cyclin I" /protein_id="AAH04975.1" /db_xref="GI:13436392" /db_xref="LocusID:10983" /translation="MKPPGLENRQLSFLEKAITRAQMKVNVKMPNSQNVSPSQ RDEVIOVLAKLYQFNLYPETFALASSLDRLATVKAHPKLYSCIAISCFPLAAKT VEEERIPVLKVLARDSCGSSSEILRMERILDKLWDLHTATPLFLHIFHAIYS TRPQLPSLPKLSFQSLAVITKQLLHCMAQNLQPRGSLNPLNSVYVYRPLKHTLVTC DGVLSITIELLQAKMDSQSLHCRBELVAHLLTQSSLPNSVYVYRPLKHTLVTC DGV FRLHPSVPGPFDKSKNSKEPVFVRGTAFFYHPLPAASGCKQTSTKTKRKEMEVD DFEY DGIKRLYNEDNVSENVSGVCTDLDRQEGHSGPCPLPQVSM"				
source					
gene					
CDS					
ORIGIN	Alignment Scores: Pred. No.: 2,34e-174 Length: 1889 Score: 1962.00 Matches: 377 Percent Similarity: 100.00% Conservative: 0 Best Local Similarity: 100.00% Mismatches: 0 Query Match: 100.00% Indels: 0 DB: 9 Gaps: 0				

REFERENCE	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)				
AUTHORS	Strausberg, R.				
TITLE	Direct Submission				
JOURNAL	Submitted (21-MAR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA				
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov				
COMMENT	Contact: MGC help desk Email: cgapbs-r@mail.nih.gov Tissue Procurement: DCTD/DTF CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada info@bcgsc.bc.ca Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Chow, Allison Cloutier, Ruth Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao, Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prahbu, Parvaneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skaleka, Duane Smalls, Jeff Stott, Miranda Tsai, George Yang, Jackie Schein, Asim Siddiqui, Rob Holt, Marco Marra.				
FEATURES	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 9 Row: b Column: 16. Location/Qualifiers 1. .1889 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="MGC:3795 IMAGE:2957878" /tissue_type="Kidney, renal cell adenocarcinoma" /clone_lib="NIH_MGC_14" /lab_host="DH10B-R" /note="Vector: pOTB7" 1. .1889 /gene="CCNI" /note="synonyms: CYC1, CYI" /db_xref="LocusID:10983" 544. .1677 /gene="CCNI" /codon_start=1 /product="cyclin I" /protein_id="AAH04975.1" /db_xref="GI:13436392" /db_xref="LocusID:10983" /translation="MKPPGLENRQLSFLEKAITRAQMKVNVKMPNSQNVSPSQ RDEVIOVLAKLYQFNLYPETFALASSLDRLATVKAHPKLYSCIAISCFPLAAKT VEEERIPVLKVLARDSCGSSSEILRMERILDKLWDLHTATPLFLHIFHAIYS TRPQLPSLPKLSFQSLAVITKQLLHCMAQNLQPRGSLNPLNSVYVYRPLKHTLVTC DGVLSITIELLQAKMDSQSLHCRBELVAHLLTQSSLPNSVYVYRPLKHTLVTC DGV FRLHPSVPGPFDKSKNSKEPVFVRGTAFFYHPLPAASGCKQTSTKTKRKEMEVD DFEY DGIKRLYNEDNVSENVSGVCTDLDRQEGHSGPCPLPQVSM"				
source					
gene					
CDS					
ORIGIN	Alignment Scores: Pred. No.: 2,34e-174 Length: 1889 Score: 1962.00 Matches: 377 Percent Similarity: 100.00% Conservative: 0 Best Local Similarity: 100.00% Mismatches: 0 Query Match: 100.00% Indels: 0 DB: 9 Gaps: 0				

US-09-736-250-1 (1-377) x BC004975 (1-1889)

Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle 20
Db 544 ATGAAGTTTCAGGGCCCTTGGAAACACAGAGATTGCTTTCCTTGTTGGAAAAGGCAATC 603

Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 604 ACTAGGGAAGCACAGATGTGGAAGTGAATGTGGGAAAATGCCTTCAAATCAGATGTT 663

Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn 60
Db 664 TCTCCATCCAGAGAGATGAAGTAAATCAATGGCTGGCCAAACTCAAGTACCAATTCAAC 723

Qy 61 LeuTrpProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 724 CTTTACCAGAAACATTTGCTCTGGCTAGCAGTCTTTTGGATAGTGTATTTAGCTACCGTA 783

Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaAlaLys 100
Db 784 AAGGCTCATCCAAATACTTTCAGTTGTATTGCAATCAGCTGTTTTCCTAGCTGCCAAG 843

Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 844 ACTGTGTGAGGAAGATGAGAGAATTCAGTACTAAAGGTATTGGCAAGAGACAGTTCTGT 903

Qy 121 GlyCysSerSerGluLeuLeuArgMetGluArgIleLeuLeuAspLysLeuAsnTrp 140
Db 904 GGATGTTCTCATCTGAAATTTGAGAAATGAGAGAAATTTCTGGATGAATGGAATGG 963

Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 964 GATCTTCACAGCCACACCATTTGGAATTTCTTATATTTTCCATGCAATTCAGTGTCA 1023

Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 1024 ACTAGGCTCAGTTACTTTTTCAGTTGTGGCCAAATGAGCCCATCTCAACATTTGGCAGTC 1083

Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
Db 1084 CTTTACCAGCAACTACTTCACTGTATGGCTGGCAACCAACTCTGCAATTCAGAGGATCC 1143

Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
Db 1144 ATGCTTGCTCTGGCCATGTTAGTCTGGAATGAGAAACTCATCTCGATTGCTTTCT 1203

Qy 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
Db 1204 CTTACAAATTGAACCTGCTTTCAGAAAGCACAGATGATAGTCCCAAGTTGATCCATTGTCGG 1263

Qy 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
Db 1264 GAGCTTGGGACATACCTTTTACTCTGAGTCTCCCTGCTCTGAAATCCGTTAT 1323

Qy 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db 1324 GTCTACCGTCCCTCAAGCACACCTGCTGACCTGTGACAAAGAGTGTTCAGATTACAT 1383

Qy 281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
Db 1384 CCCTCTCTGTCGCCAGGCCAGACTTCTCCAAAGGACACAGCAAGCCAGAGTCCAGTC 1443

Qy 301 ArgGlyThrAlaAlaPheTyrHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
Db 1444 AGAGTACAGAGCCCTTTTACATCATCTCCAGCTGCGAGTGGTGAACAGACCTCT 1503

Qy 321 ThrLysArgLysValGluGluMetGluValAspAspPheTyrAspGlyIleLysArgLeu 340
Db 1504 ACTAAACCAAGTAGAGAAATGGAAGTGGATGATCTTCTATGATGAATCAACGGCTC 1563

Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360

Db 1564 TATAATGAAGATAATGTCTCAGAAAATGTGGTCTGTGTGTGGCACTGATTTATCAAGA 1623

Qy 361 GlnGluGlyHisAlaSerProCysProLeuGlnProValSerValMet 377
Db 1624 CAAGAGGACATGCTTCCCTTGTCCACCTTTCAGGCTGTTCTGTCATG 1674

RESULT 11

CR541783 1131 bp mRNA linear PRI 29-JUN-2004
LOCUS Homo sapiens full open reading frame cDNA clone RZPD0834E0730D for
DEFINITION gene CCNI, cyclin I; complete cds, without stopcodon.

ACCESSION CR541783
VERSION CR541783.1 GI:49456522
KEYWORDS Full ORF shuttle clone, Gateway (TM), complete cds.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1131)
AUTHORS Halleck,A., Ebert,L., Mkoondinya,M., Schick,M., Eisenstein,S.,
Neubert,P., Kstrang,K., Schatten,R., Shen,B., Henze,S., Mar,W.,
Korn,B., Zuo,D., Hu,Y. and LaBaer,J.
TITLE Cloning of human full open reading frames in Gateway (TM) system
entry vector (pDONR201)
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1131)
AUTHORS Halleck,A., Ebert,L., Mkoondinya,M., Schick,M., Eisenstein,S.,
Neubert,P., Kstrang,K., Schatten,R., Shen,B., Henze,S., Mar,W.,
Korn,B., Zuo,D., Hu,Y. and LaBaer,J.
TITLE Direct Submision
JOURNAL Submitted (28-JUN-2004) RZPD Deutsches Ressourcenzentrum fuer
Genomforschung GmbH, Im Neuenheimer Feld 580, D-69120 Heidelberg,
Germany
COMMENT RZPD: RZPD0834E0730D, ORFNo 3592
www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=RZPD0834E0730D RZPDLib;
Human Full ORF Clones Gateway(TM) - RZPD (kan-resist.) RZPD Lib No.
834
www.rzpd.de/cgi-bin/products/showLib.pl.cgi/response?libNo=834
www.rzpd.de/products/orfclones/
Contact: Inge Arlart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH,
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 100
Fax: +49 30 32639 111
www.rzpd.de
This clone is available from RZPD;
Contact RZPD (customer.service@rzpd.de) for further information.
Clone name at Harvard Institute of Proteomics
(www.hip.harvard.edu): FLH131015.01L
This CDS clone is part of a collection of human full ORF clones
jointly established and verified by the Harvard Institute of
Proteomics (HIP) and RZPD.
This CDS has been cloned without stopcodon.
The CDS has been inserted into pDONR201 via a BP Clonase(TM)
reaction. Additional sequence has been added in front of the start
codon: att. .AAAAA GCA GCC TCC ACC (ATG).
The last codon is followed by the 3' att site: GACCCAGCTTTCTT. .att
The clone is validated by full sequence check.
Compared to the reference sequence NM_006835 (GI:17738314) we found
AA exchange(s) at position (first base of changed triplet):
223 (arg->gly) 409 (lys->arg)
Clone distribution: http://www.rzpd.de/products/orfclones/
FEATURES
Location/Qualifiers
1. .1131
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/Clone="RZPD0834E0730D"
/Clone lib="Human Full ORF Clones Gateway(TM) - RZPD"
/lab host="DH5Alpha"
/note="Vector: pDONR201, Site_1: attP1; Site_2: attP2"
1. .1131
/gene="CCNI"

source
gene


```

CDS
1. >1131
/gene="CCNI"
/codon_start=1
/protein_id="CAG46582.1"
/db_xref="GI:4945623"
/translation="MKPPGPLENORLSFLLEKAITRAQMKVNVKMPNSQNVSPSQ
RDEVIOMLAKLYQFNLYPEFALASSILDDGLATVKAHPKYLSCIALSCFPLAAKT
VEDERI PVLVKVLARDSFCGSSSEILRNERIILDRNLWDLHTATPLDPLHIFHAIVS
TRPQLLSPKLSQSQUHVLUTKQLLHMACNQLQFQSGMLALAMVLENEKLIPOW
LSLTELQAKQDSSQIHLRELVHSLTQSSLPNSVYVYRPLKHTLVATCDKG
FRLHPSSVGGDFDKDMSKPEVPVGTAAFYHLPAAAGCKQTSTKRVEMEVDDFY
DGIKRLYNEDNVSENVSGVCTGDLRSQBGHSPCPPLQPVSM"

ORIGIN
Alignment Scores:
Pred. No.: 1.06e-173 Length: 1131
Score: 1952.00 Matches: 375
Percent Similarity: 99.73% Conservative: 1
Best Local Similarity: 99.47% Mismatches: 1
Query Match: 99.49% Indels: 0
DB: 9 Gaps: 0

US-09-736-250-1 (1-377) x CR541783 (1-1131)

Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle 20
Db 1 ATGAAGTTTCAGGGCCCTTGGAAACACAGAGATTGTCTTTCTCTTGGAAAGGCAATC 60

Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 61 ACTAGGGAAGCACAGATGTGAAAGTGAATGTGGGAAAGTCCCTTCAATCAGATGTT 120

Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTrpGlnPheAsn 60
Db 121 TCTCCATCCAGAGAGATGAATTCATGTGCTGGCGCAACTCAAGTACCAATTCAC 180

Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 181 CTTTACCAGAAACATTTGCTGTGGTAGCAGTCTTTTGGATGGGTTTTTACGTACCGTA 240

Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaAlaLys 100
Db 241 AAGGCTCATCAAAATACTGATGTGATTCGATTCGATTCGATTCGATTCGATTCGATTC 300

Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 301 ACTGTTGAGGAAGATGAGAGATTCCTAGTACTAAGATGATTGGCAAGACAGATTCTGT 360

Qy 121 GlyCysSerSerSerGluIleLeuArgMetGluArgIleIleLeuAspLysLeuAsnTrp 140
Db 361 GGATGTTCTCATCTGAAATTTGAGAATGGAGAGAAATTAATCTGGATAGGTTGAAATGG 420

Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 421 GATCTTCACAGCCACACCATGATGATTTCTCATATTTCCATGCCATTCGAGTGTCA 480

Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 481 ACTAGCCCTCAGTACTTTTTCAGTTTGGCCAAATGAGCCCATCTCAACATTTGGCAGTC 540

Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
Db 541 CTTACAGCAACTACTTCTCAGTGTATGCTGCAACCAACTCTGCAATTCAGAGGATCC 600

Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
Db 601 ATGCTGTCTCGGCCATGTTAGTCTGAAATGGAGAAACATTCATTCGATGCTGCTTCT 660

Qy 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
Db 661 CTTACAAATGAAGTCTCTCAGAAACACAGATGGATAGTCTCCAGTGTATCATTTGTCGG 720

Qy 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260

```

```

Db 721 GAGCTTGTGGCACATCACCTTTTCTTACTCTGAGTCTTCCCTGCTCTGAATTCGTTAT 780
Qy 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db 781 GTCTACCGTCCCTCAAGACACACCTGCTGGTACCTGTGACAAAGAGTGTTCAGATTACAT 840
Qy 281 ProSerSerValProGlyProAspPheSerLysAspLysSerLysProGluValProVal 300
Db 841 CCTCTCTCTGTCCAGGCCACAGACTTCTCCAAAGACACACAGCAAGCCAGAGTCCAGTC 900
Qy 301 ArgGlyThrAlaAlaPheTyrHisHisLeuProAlaAlaSerGlyCysValGlnThrSer 320
Db 901 AGGTACAGCAGCCTTTTACCATCTCCACTGCCAGTGGTGGCAACACACCTCT 960
Qy 321 ThrLysArgLysValGluGluMetGluValAspPheTyrAspGlyIleLysArgLeu 340
Db 961 ACTAAACGCAAGTAGAGGAAATGGAAGTGGATGACTTCTATGATGAATCAACAGGCTC 1020
Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
Db 1021 TATAATGAAGATATGTCTCAGAAATGTGGTCTCTGTGTGGCAGTGTATATCAAGA 1080
Qy 361 GlnGluGlyHisAlaSerProCysProLeuGlnProValSerValMet 377
Db 1081 CAAGAGGACATGTTCCCTTGTCCACCTTTGAGCCTGTTCTGTCTCATG 1131

RESULT 12
AF005886 1535 bp mRNA linear ROD 31-OCT-2000
LOCUS Mus musculus cyclin I mRNA, complete cds.
DEFINITION AF005886
ACCESSION AF005886
VERSION AF005886.2 GI:6850163
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus

REFERENCE
1 (bases 1 to 1535)
AUTHORS Jensen,M.R., Audolfsson,T., Factor,V.M. and Thorgeirsson,S.S.
TITLE In vivo expression and genomic organization of the mouse cyclin I
gene (Ccn1)
JOURNAL Gene 256 (1-2), 59-67 (2000)
MEDLINE 20509992
PUBMED 11054536
REFERENCE
2 (bases 1 to 1535)
AUTHORS Audolfsson,T., Jensen,M.R. and Thorgeirsson,S.S.
TITLE Direct Submission
JOURNAL Submitted (28-MAY-1997) Laboratory of Experimental Carcinogenesis, National Institutes of Health, 37 Convent Drive, Bethesda, MD 20982-4255, USA
REFERENCE
3 (bases 1 to 1535)
AUTHORS Audolfsson,T., Jensen,M.R. and Thorgeirsson,S.S.
TITLE Direct Submission
JOURNAL Submitted (01-FEB-2000) Laboratory of Experimental Carcinogenesis, National Institutes of Health, 37 Convent Drive MSC4255, Building 37, room 3C28, Bethesda, Maryland 20892-4255, USA
REMARK sequence update by submitter
COMMENT On Feb 1, 2000 this sequence version replaced gi:4101686.
FEATURES
source
1. 1535
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
279..1412
/codon_start=1
/product="cyclin I"
/protein_id="AAD01253.2"
/db_xref="GI:6850164"
/translation="MKPPGPLENORLSLLEAIRSQAQMKVNVKPIPTNONVPSQ
RDEVIOMLAKLYQFNLYPEFALASSILDDGLATVKAHPKYLSCIALSCFPLAAKT
VEDEKIPVLKVLARDSFCGSSSEILRNERIILDRNLWDLHTATPLDPLHIFHAIVS
TRPQLLSPKLSQSQUHVLUTKQLLHMACNQLQFQSGMLALAMVLENEKLIPOW

```


A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: <http://image.llnl.gov>
 Series: IRAK Plate: 9 Row: f Column: 22
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 8393062.

FEATURES

Location/Qualifiers

1..2348

/organism="Mus musculus"

/mol_type="mRNA"

/strain="FVB/N"

/db_xref="taxon:10090"

/clone="MGC:5636 IMAGE:3583418"

/tissue type="mammary tumor. Metallothionien-TGF alpha model. 10 month old virgin mouse. Taken by biopsy."

/clone.lib="NCI CGAP_Mam1"

/lab host="DH10B"

/note="Vector: pCMV-SPORT6"

1..2348

/gene="Ccni"

/db_xref="LocusID:12453"

/db_xref="MGI:1341077"

160..1293

/gene="Ccni"

/codon_start=1

/product="cyclin I"

/protein_id="AAH03290.1"

/db_xref="GI:13096997"

/db_xref="LocusID:12453"

/db_xref="MGI:1341077"

/translation="MKFPGPLENQRSLRLERASRAQMKVNVKPIPTNQVSPSQ
 DEVIOMLAKLYFNYPETFPALASLLDPLATVKAHPKYLNCIAISFPFLAAKT
 BEDSKIPVLKVLARDSFCGSSSEILRMERIIIDKLNWDHTATPLDPLHFAIAVS
 TRPLLPSLPSPSHLAVLTOLLHMCACNOLLOPKGSMALAMVSLMEKILIPW
 LPIELQLKQMSQSLIHCELVAVHLSALPLNSVTVVRPLKHTLVTCDKGA
 FKLHPSSVGGDFKSDNSKPEVRGPAAPFHLPLAASGCKQTSKAKRKBEMEVDFF
 DGIKELYNEDGNPENVSGVCGTDLRSQEGHASPFPPLQPVSM"

gene

CDS

ORIGIN

Alignment Scores:

Pred. No.: 8 35e-164 Length: 2348
 Score: 1851.00 Matches: 355
 Percent Similarity: 97.08% Conservative: 11
 Best Local Similarity: 94.16% Mismatches: 11
 Query Match: 94.34% Indels: 0
 DB: 10 Gaps: 0

US-09-736-250-1 (1-377) x BC003290 (1-2348)

Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle 20
 Db 160 ATGAAGTTTCAGGACCTTGGAAACCCAGAGATTGCTTCTCTGTTGGAAGGCGAATC 219
 Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
 Db 220 TCCAGGGAAGCCAGATGGAAGGTGAATGTGCCGAAATACCTTACAAATCAGAATGTT 279
 Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTrpGlnPheAsn 60
 Db 280 TCTCCATCCAGAGAGATGAAGTAATCAATGGTTGGCCAACTCAATACAGTTCAAC 339
 Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
 Db 340 CTCATCCAGAAACATTTGCTCTGCGACGAGCTCTTTTGGATAGGTTTTAGCTACAGTA 399
 Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaLys 100
 Db 400 AAAGCCCATCAAAATATTTGAATGTTATGCAATCAGCTGTTTTTTCTGCTGCTAAG 459
 Qy 101 ThrValGluGluAspGluArgIleProValLysValLeuAlaArgAspPheCys 120
 Db 460 ACTGTTGAGGAAGATGAGAAATATCCAGTGTAAAGGATTATGGCAAGAGACAGTTTCTGT 519

Qy 121 GlyCysSerSerSerGluIleLeuArgMetGluArgIleIleLeuAspLysLeuAsnTrp 140
 Db 520 GGAATGTTCTCATCTGAGATTTTGAGATGAGAGAAATATTCTGGATAAATGAATGG 579
 Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
 Db 580 GATCTTCACACGGCTCACCATTTGATTTCTTCCATTTTCCATGCAATGCGGTGCA 639
 Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
 Db 640 ACTAGGCTCAGTTACTTTTTCAGTTTGCCTCAAAATTGAGCCCATCTCAACATTTGGCAGTC 699
 Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
 Db 700 CTGACCAAGCAGCTGCTTCACTGTATGCGCTGCAACCAACTTCTGCGATTTCAAGGGTCC 759
 Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
 Db 760 ATGCTTCTCTGCGCATGTTAGTCTGGAATGAGAACTCATCTCTGATGCTTCTCT 819
 Qy 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
 Db 820 CTTACGATTGACTGCTTTCAGAAAGCACAGATGACAGCTCCCAAGTTGATCCACTGTGCG 879
 Qy 241 GluLeuValAlaHisHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
 Db 880 GAGCTGCTGCGCATATCACCTTTCTGCTCTGCGCTCTGCGCTCTCTCTCTCTCTCTCT 939
 Qy 261 ValTyrArgProLeuLysHisHisLeuValThrCysAspLysGlyValPheArgLeuHis 280
 Db 940 GTCTTACCGTCCCTTCAAGCACACCTGTAACCTGTGACAAAGGAGCATTCAAAATTCAT 999
 Qy 281 ProSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
 Db 1000 CCTCTCTCTCTCAGCGCCAGATTTCTCCAGGACCAACAGCAAGAGTGCACGTC 1059
 Qy 301 ArgGlyThrAlaAlaPheTyrHisHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
 Db 1060 CGAGGTCGACGAGCTTCCACCTGCATCTCTCCCTGCGCTGCGCTGCGCTGCGCTGCGCT 1119
 Qy 321 ThrLysArgLysValGluGluMetGluValAspPheTyrAspGlyIleLysArgLeu 340
 Db 1120 GCTAAACGGAAAGTGGAGAGATGAGGTGATGACTTCTACAGTGGATCAAGCGGCTC 1179
 Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
 Db 1180 TATAATGAGGACATGGTCTGAGAATGTGGTTCTGTATGTGCGCTGATTTATCAAGG 1239
 Qy 361 GlnGluGlyHisAlaSerProCysProLeuGlnProValSerValMet 377
 Db 1240 CAAGAGGCGCATGCTTCCCTGTCACCTTTGCGAGCTGTTCTCTGTCATG 1290

RESULT 14
 LOCUS CQ414515 2755 bp DNA linear PAT 23-JAN-2004
 DEFINITION Sequence 21586 from Patent WO01/70979.
 ACCESSION CQ414515
 VERSION CQ414515.1 GI:41322296
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1
 Lee, J. and Lillie, J.
 Genes, compositions, kits, and method for identification,
 assessment, prevention, and therapy of ovarian cancer
 Patent: WO 01/70979-A 21586 27-SEP-2001;
 Millennium Pharmaceuticals, Inc. (US)
 FEATURES
 Location/Qualifiers
 1..2755
 /organism="Homo sapiens"

/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Alignment Scores:

Pred. No.: 8.92e-163 Length: 2755
Score: 1841.00 Matches: 358
Percent Similarity: 94.96% Conservative: 0
Best Local Similarity: 94.96% Mismatches: 1
Query Match: 93.83% Indels: 18
DB: 6 Gaps: 1

US-09-736-250-1 (1-377) x CQ414515 (1-2755)

QY 1 MetLysPheProGluProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle 20
DB ATGAGTATTCAGGCGCCCTTGGAAACACAGAGATGTCTTTCCCTGTTGGAAAGCGCAATC 906
QY 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
DB ACTAGGGAAGACAGATGTGGAAGTGAATGTGCGAAATGCGCTTCAATCAGATGTT 966
QY 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn 60
DB TCTCCATCCAGAGAGATGAAGTAATCAATGGCTGGCCAACTCAAGTACCAATTCAAC 1026
QY 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
DB CTTTACCAGAAACATTTGCTGCTGGTAGCAGTCTTTGGATAGGTTTATAGCTACCGTA 1086
QY 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaLys 100
DB AAGGCTCATCT----- 1098
QY 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgSerPheCys 120
DB -----GAGGAAGATGAGAGAAATCCAGTACTAAAGGTATTGGCAAGAGACAGTTTCTGT 1152
QY 121 GlyCysSerSerGluIleLeuArgMetGluArgIleLeuLeuAspLysLeuAsnTrp 140
DB GGATGTTCTCATCTGAATTTTGGATGAGAGAAATTTCTGGATAGTTGAATGG 1212
QY 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
DB GATCTTCACACAGCACACACATGGATTTTCTTCATATTTTCCATGCAATTCAGTGTCA 1272
QY 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
DB ACTAGGCGTCAAGTACTTTTTCAGTTTGGCCCAAAATTTGAGCCCATCTCAACATTTGGCAGTC 1332
QY 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
DB CTTTACCAAGCACTACTTCTACTGTATGGCTGCAACCACTTCTGCAATTCAGAGGATCC 1392
QY 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
DB ATGCTGCTCTGGCCATGTTAGTCTGGAATGAGAAACTCAATCTCGATTGGCTTTCT 1452
QY 221 LeuThrIleGluLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
DB CTTTCAATTAAGTGTCTTCAAGAGCAGATGATAGTCTCCCAAGTTCATGTCGTTGCGG 1512
QY 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
DB GAGCTTGTGGACATCACCCTTCTACTCTGAGTCTTCCCTGCTCTGAAATTCGTTAT 1572
QY 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
DB GTCTACCGTCCCTCAAGCACACCCCTGCTGACAAAGAGGTTCAGATTACAT 1632
QY 281 ProSerValProGlyProAspPheSerLysAsnSerLysProGluValProVal 300
DB CCCTCTCTGTGCCGCCAGCTTCTTCAAGAGCAACAGCAAGCCAGAGTGCAGTC 1692

QY 301 ArgGlyThrAlaAlaPheTyrHisHisLeuProAlaHisSerGlyCysLysGlnThrSer 320
DB AGAGGTACAGCAGCCCTTTTACCATCATCTCCAGTCCGAGTGGTCCAGACACTCT 1752
QY 321 ThrLysArgLysValGluGluMetGluValAspPheTyrAspGlyIleLysArgLeu 340
DB ACTAAGCCAAAGTAGAGGAATGGAAGTGGATGACTTCTATGATGAATCAACGGCTC 1812
QY 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
DB TATAATGAAGATAATGTCTCAGAAAATGTGGTCTGTGTGGCACTGATTTATCAAGA 1872
QY 361 GluGluGlyHisAlaSerProCysProProLeuGlnProValSerValMet 377
DB CAAGAGGAGCATGCTTCCCTTGTGTACCTTTGAGCCTGTTTCTGTGTCATG 1923
RESULT 15
AC101881/c
LOCUS
DEFINITION Mus musculus chromosome 14 clone RP23-387F19 map 14, *** SEQUENCING
IN PROGRESS ***, 6 unordered pieces.
AC101881
VERSION HTG1881.4 GI:42628095
KEYWORDS HTG; HTGS PHASE1; HTGS FULLTOP; HTGS_ACTIVEFIN.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Birren,B., Nusbaum,C. and Lander,E.
1 (bases 1 to 200850)
Mus musculus chromosome 14, clone RP23-387F19
Unpublished
2 (bases 1 to 200850)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Boguslavsky,L., Boukhgalter,B.,
Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
Choepel,Y., Collangelo,M., Collins,S., Collymore,A., Cook,A.,
Cooper,P., DeArrellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S.,
Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,
Jones,C., Kamat,A., Karatas,A., Kells,C., LaRocque,K.,
Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Liu,G.,
Maclean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,
McCarthy,M., McEwan,P., McKernan,K., McPheeters,R., Meldrum,J.,
Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C.,
Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D.,
Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R.,
Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliou,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 200850)
Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,
Boguslavsky,L., Boukhgalter,B., Camarata,J., Chang,J., Choepel,Y.,
Collymore,A., Cook,A., Cooke,P., Corum,B., DeArrellano,K.,
Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S.,
Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J., Gardyna,S.,
Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B.,
Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R.,
Lindblad-Toh,K., Liu,X., Lui,A., Mabbitt,R., Maclean,C.,
Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M.,
Meldrum,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J.,
Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P.,

O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schuback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Testaye, S., Theodore, J., Topham, K., Travers, M., Vassiliou, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
 Direct Submission
 Submitted (19-FEB-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>
 ----- Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: <http://www-seq.wi.mit.edu>
 Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information
 Center project name: L17690
 Center clone name: 387_F_19

NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 13662: contig of 13662 bp in length
 * 13663 13762: gap of 100 bp
 * 13763 111127: contig of 97365 bp in length
 * 111128 111227: gap of 100 bp
 * 111228 134282: contig of 23055 bp in length
 * 134283 134382: gap of 100 bp
 * 134383 157520: contig of 23138 bp in length
 * 157521 157620: gap of 100 bp
 * 157621 172448: contig of 14828 bp in length
 * 172449 172548: gap of 100 bp
 * 172549 200850: contig of 28302 bp in length.

Location/Qualifiers
 1. .200850
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10090"
 /chromosome="14"
 /map="14"
 /clones="RP23-387F19"
 /clone_lib="RPCI-23 Female Mouse BAC"

Alignment Scores:
 Pred. No.: 5.32e-144 Length: 200850
 Score: 1666.50 Matches: 332
 Percent Similarity: 91.82% Conservative: 16
 Best Local Similarity: 87.60% Mismatches: 21
 Query Match: 84.94% Indels: 11
 DB: 2 Gaps: 2

US-09-736-250-1 (1-377) x AC101881 (1-200850)

Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuLysAlaIle 20
 Db 155593 ATGAAGTTTCAGGACCTTTGGAAACACAGAGATTGCTTCTCTGTGGAAAGGGCAATC 155534
 Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
 Db 155533 TCCAGGAGAGCCAGATGCTGGAAGGTGAATGTGCGGAATAATACCTACAAATCAGAAATGTT 155474
 Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn 60

Db 155473 TCTCCATCCAGAGAGATGAAGTAATTAATGTTGGCCAACTCAATACCAGTTCAAC 155414
 Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
 Db 155413 CTCTATCCAGAAACATTTGCTCTATCAAGCAGCTCTTTGGATAGTGTATTTAGCTACAGTA 155354
 Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCys---PhePheLeuAlaAla 99
 Db 155353 AAAGCCCATCAAAATATTTGAATTTGTAATCGAATCAGCTGTTTTTTTTTCTGGCTGCT 155294
 Qy 100 LysThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPhe 119
 Db 155293 AAGACTGTTGAGGAGAGATGAGAAATTCAGTGTCTAAGGTATTTGGCAGAGACAGTTTC 155234
 Qy 120 CysGlyCysSerSerGluIleLeuArgMetGluArgIleLeuLeuAspLysLeuAsn 139
 Db 155233 TGTGGATGTTCTCATCTGAGATTTTGAAGATGGAGAGAAATTTATCTGGATAAATTTGAAT 155174
 Qy 140 TrpAspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaVal 159
 Db 155173 TGGGATCTTCACACGGCCACCATCTGGATTTTCTTCACATTTTTCATGTCATTTCCGTG 155114
 Qy 160 SerThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAla 179
 Db 155113 TCACTAGGCTCAGTTACTTTTCAGTTTCCCAATTTGAGCCATCTCAACATTTGGCA 155054
 Qy 180 ValLeuThrLysGln-LeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgG 199
 Db 155053 GTCTGACTAAGCAGCATGCTTCACTGTATGGAGTCAACCACTTCTGCAGTTCAAAGG 154994
 Qy 199 YSerMetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuLeuProAspTrpLe 219
 Db 154993 GTCCATGCTGGCTCTGGCCATGTTAGTCTGGAAATGGAGAAATCTATCTCGATTGGCT 154934
 Qy 219 uSerLeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCy 239
 Db 154933 TCCTCTTAAGATTGAACCTGCTCAGGAGCAGAGATGGGAGCTCCCGATTGATCCACTG 154874
 Qy 239 sArgGluLeuValAlaHisHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerVa 259
 Db 154873 TCGGAGCTGGTGGCATATCACCGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 154814
 Qy 259 lTyrValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLe 279
 Db 154813 TTTTGTCTACCGTCCCTCAAGCACACCTGTGAACCTGTGACAAAGGAGCAGCTCAAAAT 154754
 Qy 279 uHisProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValPr 299
 Db 154753 ACATCCCTCTCTGCTCTCAGGCCAGATTTCTCAAGGACAAACAGCAAGTCAAGTACC 154694
 Qy 299 oValArgGlyThrAlaAlaPheTyrHisHisLeuProAlaAlaSerGlyCysLysGlnTh 319
 Db 154693 AGTCCGAGGTCAGAGAGCTTCCACCTGCATCTCCCGCAGCC----- 154651
 Qy 319 rSerThrLysArgLysValGluGluMetGluValAspAspPheTyrAspGlyLysAr 339
 Db 154650 -----AAACCGAAAGTGAGGAGATGGAGTGGATGACTTCTCCGATGGATCAAGTG 154598
 Qy 339 gLeuTyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSe 359
 Db 154597 GCTCTATAATGAGGACAAATCTCTGAGAATGTGGGTCTGTATGTGGCAGTGAATTC 154538
 Qy 359 rArgGlnGluGlyHisAlaSerProCysProProLeuGlnProValSerValMet 377
 Db 154537 AAGGCAAGAGGGCAGTGGCTTC-CCCTGTCCACCTTTTGACGCTGTTTCTGTCTATA 154484

Search completed: February 11, 2005, 05:55:25
 Job time : 7743.41 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 11, 2005, 03:05:24 ; Search time 86.7775 Seconds
(without alignments)
1419.543 Million cell updates/sec

Title: US-09-736-250-1
Perfect score: 1962
Sequence: 1 MKFPGPLENQLSFLLEKAL.....LSRQGHASCPPLQPVSVVM 377

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1376875 seqs, 326749119 residues

Total number of hits satisfying chosen parameters: 1376875

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1962	100.0	377	12 US-09-736-250-1	Sequence 1, Appli
2	1309	66.7	254	9 US-09-796-149-4	Sequence 4, Appli
3	326.5	16.6	344	15 US-10-170-385-321	Sequence 321, App
4	271.5	13.8	249	9 US-09-796-149-3	Sequence 3, Appli
5	234	11.9	238	14 US-10-218-542-2	Sequence 2, Appli
6	218	11.1	88	14 US-10-029-386-30305	Sequence 30305, A
7	204	10.4	404	14 US-10-265-062-3	Sequence 3, Appli
8	202	10.3	403	14 US-10-265-062-4	Sequence 4, Appli
9	192	9.8	357	15 US-10-388-269-10	Sequence 10, Appli
10	188.5	9.6	373	15 US-10-388-269-4	Sequence 4, Appli
11	187.5	9.6	395	14 US-10-245-618-32	Sequence 32, Appli
12	187.5	9.6	395	14 US-10-245-618-46	Sequence 46, Appli
13	187.5	9.6	395	14 US-10-245-618-47	Sequence 47, Appli

14	187.5	9.6	395	14	US-10-245-618-48	Sequence 48, Appli
15	187.5	9.6	410	14	US-10-245-618-31	Sequence 31, Appli
16	187.5	9.6	451	9	US-09-964-899-31	Sequence 31, Appli
17	177.5	9.0	289	13	US-10-024-066-2	Sequence 2, Appli
18	177.5	9.0	420	15	US-10-310-154-414	Sequence 414, App
19	177.5	9.0	424	10	US-09-496-444-2	Sequence 2, Appli
20	177	9.0	371	15	US-10-424-599-160823	Sequence 160823, A
21	177	9.0	394	15	US-10-425-114-48711	Sequence 48711, A
22	176.5	9.0	419	15	US-10-310-154-412	Sequence 412, App
23	176	9.0	471	15	US-10-369-493-21977	Sequence 21977, A
24	175.5	8.9	359	15	US-10-369-493-22561	Sequence 22561, A
25	175.5	8.9	424	15	US-10-310-154-418	Sequence 418, App
26	170.5	8.7	383	15	US-10-424-599-160824	Sequence 160824, A
27	170.5	8.7	427	15	US-10-425-114-38905	Sequence 38905, A
28	170	8.7	506	15	US-10-389-566-734	Sequence 734, App
29	170	8.7	532	15	US-10-389-566-1352	Sequence 1352, Ap
30	169.5	8.6	441	15	US-10-389-566-2182	Sequence 2182, Ap
31	169.5	8.6	469	15	US-10-424-599-238352	Sequence 238352, A
32	169	8.6	289	9	US-09-919-497-54	Sequence 54, Appli
33	169	8.6	289	13	US-10-024-066-4	Sequence 4, Appli
34	169	8.6	480	15	US-10-425-114-63937	Sequence 63937, A
35	169	8.6	508	15	US-10-310-154-415	Sequence 415, App
36	169	8.6	508	15	US-10-389-566-749	Sequence 749, App
37	169	8.6	508	15	US-10-389-566-2399	Sequence 2399, App
38	168.5	8.6	424	15	US-10-310-154-429	Sequence 429, App
39	168	8.6	276	15	US-10-369-493-22562	Sequence 22562, A
40	167.5	8.5	479	15	US-10-310-154-419	Sequence 419, App
41	167	8.5	84	9	US-09-864-761-46425	Sequence 46425, A
42	167	8.5	305	15	US-10-424-599-169546	Sequence 169546, A
43	167	8.5	450	15	US-10-389-566-745	Sequence 745, App
44	167	8.5	491	9	US-09-801-368-78	Sequence 78, Appli
45	167	8.5	491	15	US-10-369-493-22530	Sequence 22530, A

ALIGNMENTS

RESULT 1
US-09-736-250-1
; Sequence 1, Application US/09736250
; Publication No. US20050014139A1
; GENERAL INFORMATION:
; APPLICANT: SUMITOMO ELECTRIC INDUSTRIES, LTD.
; APPLICANT: NAKAMURA, Takeshi
; TITLE OF INVENTION: HUMAN CYCLIN I AND GENES ENCODING THE SAME
; FILE REFERENCE: 050212-0278
; CURRENT APPLICATION NUMBER: US/09/736,250
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 09/054,492
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: PCT/JF96/02905
; PRIOR FILING DATE: 1996-10-07
; PRIOR APPLICATION NUMBER: 284663/1995
; PRIOR FILING DATE: 1995-10-05
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 377
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-736-250-1

Query Match	100.0%	Score 1962;	DB 12;	Length 377;
Best Local Similarity	100.0%	Pred. No. 2e-184;		
Matches 377;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MKFPGLLENQLSFLLEKAITREAWKVNVRKPNQNVSPSORDEVIQWLAKLKYQFN	60	
Db	1	MKFPGLLENQLSFLLEKAITREAWKVNVRKPNQNVSPSORDEVIQWLAKLKYQFN	60	
Qy	61	LYPTFALASSLLDRFLATVKAHPKYLSCIAISCFFLAAKTVBEDRIPVLKVLARSFC	120	
Db	61	LYPTFALASSLLDRFLATVKAHPKYLSCIAISCFFLAAKTVBEDRIPVLKVLARSFC	120	

Qy 121 GCSSEILRMERIIIDKLNWDLHTATPLDPLHIFHAIIVSTRPQLLSPLKSPSOHLAV 180
Db 121 GCSSEILRMERIIIDKLNWDLHTATPLDPLHIFHAIIVSTRPQLLSPLKSPSOHLAV 180
Qy 181 LTKQLLHMACNQLLOFRGSMALAMVLEMEKLPDWLSLTIELLQKQWMDSSQLIHR 240
Db 181 LTKQLLHMACNQLLOFRGSMALAMVLEMEKLPDWLSLTIELLQKQWMDSSQLIHR 240
Qy 241 ELVAHHLSTLQSSLPNSVYVRPLKHTLVTCDKGVFRLHPSVPGPDFSKDNKPEVPV 300
Db 241 ELVAHHLSTLQSSLPNSVYVRPLKHTLVTCDKGVFRLHPSVPGPDFSKDNKPEVPV 300
Qy 301 RGTAAFYHHLPAASCKOTSTKRKYEMEVDYDYGIKRLYNEDNVSENVGSGCTDLR 360
Db 301 RGTAAFYHHLPAASCKOTSTKRKYEMEVDYDYGIKRLYNEDNVSENVGSGCTDLR 360
Qy 361 QEGHASPCCPPLQPVSV 377
Db 361 QEGHASPCCPPLQPVSV 377

RESULT 2

US-09-796-149-4

; Sequence 4, Application US/09796149

; Patent No. US20020035079A1

; GENERAL INFORMATION:

; APPLICANT: Univ. of Southern California

; TITLE OF INVENTION: Mutated cyclin G1 protein

; FILE REFERENCE: 4-31342A/USC

; CURRENT APPLICATION NUMBER: US/09/796,149

; PRIOR FILING DATE: 2001-02-28

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: Patent in version 3.1

; SEQ ID NO 4

; LENGTH: 254

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-796-149-4

Query Match 66.7%; Score 1309; DB 9; Length 254;

Best Local Similarity 100.0%; Pred. No. 2.7e-120; Mismatches 0; Indels 0; Gaps 0;

Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 40 VPSQRDEVIQWLAKLYQFNLYPETFALASSLLDRFLATVKAHPKYLSCIAISCFFLAA 99
Db 1 VPSQRDEVIQWLAKLYQFNLYPETFALASSLLDRFLATVKAHPKYLSCIAISCFFLAA 60
Qy 100 KTVEEDERIPVLKVLARDSFCGSSSEILRMERIIIDKLNWDLHTATPLDPLHIFHAIIV 159
Db 61 KTVEEDERIPVLKVLARDSFCGSSSEILRMERIIIDKLNWDLHTATPLDPLHIFHAIIV 120
Qy 160 STRPQLLSPLKSPSOHLAVLTKQLLHMACNQLLOFRGSMALAMVLEMEKLPDWL 219
Db 121 STRPQLLSPLKSPSOHLAVLTKQLLHMACNQLLOFRGSMALAMVLEMEKLPDWL 180
Qy 220 SLTIELLQKQWMDSSQLIHRCLVAHLSTLQSSLPNSVYVRPLKHTLVTCDKGVFRL 279
Db 181 SLTIELLQKQWMDSSQLIHRCLVAHLSTLQSSLPNSVYVRPLKHTLVTCDKGVFRL 240
Qy 280 HPSSVPGPDFSKDN 293
Db 241 HPSSVPGPDFSKDN 254

RESULT 3

US-10-170-385-321

; Sequence 321, Application US/10170385

; Publication No. US2003020372A1

; GENERAL INFORMATION:

; APPLICANT: Ward, Neil Raymond

; APPLICANT: Mundy, Christopher Robert

; APPLICANT: Kan, On

; APPLICANT: Harris, Robert Alan
; APPLICANT: White, Jonathan
; APPLICANT: Binley, Katie Mary
; APPLICANT: Rayner, William Nigel
; APPLICANT: Naylor, Stuart
; APPLICANT: Kingsman, Susan Mary
; APPLICANT: Krige, David
; TITLE OF INVENTION: ANALYSIS METHOD
; FILE REFERENCE: 532682000100
; CURRENT APPLICATION NUMBER: US/10/170,385
; CURRENT FILING DATE: 2002-06-12
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: PCT/GB02/01662
; PRIOR FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 549
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 321
; LENGTH: 344
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-170-385-321

Query Match 16.6%; Score 326.5; DB 15; Length 344;

Best Local Similarity 36.4%; Pred. No. 3.1e-23;

Matches 86; Conservative 44; Mismatches 73; Indels 33; Gaps 7;

Qy 31 VRKMPNSON-VSPQRDEVIQWLAKLYQFNLYPETFALASSLLDRFLATVKAHPKYLSC 89
Db 41 IEATPENDNTLCPLGRNAKVEDLRSLNFFGSCSTETFLAVNLDRFLALMKVQPKHLSC 100
Qy 90 IAISCFFLAAKTVEEDERIPVLKVLARDSFCGSSSEILRMERIIIDKLNWDLHTATPLD 149
Db 101 IGVCSPFLAARIVEEDCNIPSTHDVIRISQCKTASDIKRMEXIISEKLHVELEATTALN 160
Qy 150 FLHIFHAIIV---STRPQLLSPLKSPSOHLAVLTKQLLHMACNQLLOP---RGSMLA 203
Db 161 FLHLYHTIILCHTSEKEL-SLDKLE-----AQLKACNCRLLIFSKAKPSVLA 207
Qy 204 LAMVLEMEKLPDWLSLTIELLQ-----KAQMDSSQLIHRCLVAHLSTLQSS 252
Db 208 LCLLNLEVEYL-----KSVLELLEILLVVKHSHKINDTEFFYRWELVSKCLAEYSS 257

RESULT 4

US-09-796-149-3

; Sequence 3, Application US/09796149

; Patent No. US20020035079A1

; GENERAL INFORMATION:

; APPLICANT: Univ. of Southern California

; TITLE OF INVENTION: Mutated cyclin G1 protein

; FILE REFERENCE: 4-31342A/USC

; CURRENT APPLICATION NUMBER: US/09/796,149

; CURRENT FILING DATE: 2001-02-28

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: Patent in version 3.1

; SEQ ID NO 3

; LENGTH: 249

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-796-149-3

Query Match 13.8%; Score 271.5; DB 9; Length 249;

Best Local Similarity 32.6%; Pred. No. 5e-18;

Matches 77; Conservative 51; Mismatches 89; Indels 19; Gaps 5;

Qy 45 RDEVIQWLAKLYQFNLYPETFALASSLLDRFLATVKAHPKYLSCIAISCFFLAAKTVEE 104
Db 6 RDEVEKDLLSLTQTFGFGDTETFLAVNLDRFLSKMKVQPKHLGCVGLSCFYLAVKISIE 65
Qy 105 DERIPVLKVLARDSFCGSSSEILRMERIIIDKLNWDLHTATPLDPLHIFHAIIVSTRPQ 164
Db 66 ERNVPLATDLIRISQYRFTVSDLRMEKIVLEKVCWKVATTAFQFLQLYSL----- 118


```

RESULT 6
US-10-029-386-30305
; Sequence 30305, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
; SEQ ID NO 30305
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Homo sapiens

```

Query Match	10.4%;	Score 204;	DB 14;	Length 404;
Best Local Similarity	27.7%;	Pred. No. 4.7e-11;		
Matches	75;	Conservative 54;	Mismatches 96;	Indels 46; Gaps 12;

Qy	4	PGPLENQRISFLLEKAITREAOQWKVNRKMP	-----NQNVSPSQRDEVIQWL	52
		:::	:::	
Db	99	PSPLPD--LSWGCK	-----EYV-LNMLCKESRYVHDKHFEVLHSDLEPQMSILLDWL	149
		:::	:::	
Qy	53	AKLKYONLYPEFALASSILLDRFLATVK-AHPKYLSCIAISCFEAAKTVBDERIPVL	111	
		:::	:::	
Db	150	LEVCEVYTHRETFYLAQOFFDFRMLTQDKINMLQLIGITSLFIASKL--BEIYAPKL	207	
		:::	:::	
Qy	112	KVLARDSFCGCSSEILRMERIILDKLNMDLHTATPLDFLHIEPAH-AVSTRQLQLFSLP	170	
		:::	:::	
Db	208	QEFAYVTDGACSEEDILRMELIILKALKWEELCPVTIISWNLFLQVDALKDAPKVL--LP	265	
		:::	:::	
Qy	171	KLSPYSQHLAVLTQKLLHMACNOLLOFRGSMILAMVSLMEKLIIPDWLSL----	226	
		:::	:::	
Db	266	QY--SQETFTQIAQLL-----DLCILATDSLEFQVRIILTAALCHFTSI	310	
		:::	:::	
Qy	227	QKAQ-WDSQQLIHCRELVAAHLSTLOSSPL	256	
		:::	:::	
Db	311	KKASGLEWDSISRCVDWMPFVFNWVKSTSPV	341	
		:::	:::	

Db 338 TSSVF-----PVFKSRVQEQM-KLASSISRVF-----VEAVGS 371

RESULT 11

US-10-245-618-32
; Sequence 32, Application US/10245618
; Publication No. US20030143582A1

GENERAL INFORMATION:

APPLICANT: Reed, Steven

APPLICANT: Strohmaier, Heimo

APPLICANT: Spruck, Charles

APPLICANT: Sangfelt, Olle

FILE OF INVENTION: HCDC4 MODULATES CYCLIN E DEGRADATION

CURRENT APPLICATION NUMBER: US/10/245,618

PRIOR FILING DATE: 2002-09-16

PRIOR APPLICATION NUMBER: US 60/404,116

PRIOR FILING DATE: 2002-08-15

PRIOR APPLICATION NUMBER: US 60/322,947

PRIOR FILING DATE: 2001-09-14

NUMBER OF SEQ ID NOS: 48

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 32

LENGTH: 395

TYPE: PRT

ORGANISM: Homo sapien

US-10-245-618-32

Query Match 9.6%; Score 187.5; DB 14; Length 395;

Best Local Similarity 27.0%; Pred. No. 1.9e-09;

Matches 71; Conservative 48; Mismatches 105; Indels 39; Gaps 11;

QY 25 QMKVNVVRK-----MPSNQVSPSQRDEVIQWLAKLYQFNLYPETFALASSLLD 74

Db 100 EVWKIMLNKENTYLRDQHFLQHPQLQPKRAILLDMLMEVCEVVKLHRETFYLAQDFD 159

QY 75 RFLATVKAHPK-YLSCIAISCFEFLAAKTVEDEIRPVLKVLARDSFCGSSSEILRMERI 133

Db 160 RYMATQENVVKTLLQLIGISLFLAAKL--BEIYPPKHLQFAYVTDGACSGDEILTMELM 217

QY 134 ILDKLNWDLHTATPLDPLHIF-----HAIAVSTRPQLLFLSLPKLSPSHLAVLTQ 184

Db 218 IMKALKWRLSPLTIVSWLVNVMQVAYLNDLHEVLLPQVPOQIFI--QIAELLDCVLVD 275

QY 185 LLH-----CMACNQLQFRGSMALAMVS-----LEMEXLIPDWLSLITIELLOKAQMDSSQL 236

Db 276 CLEPPYGILAAALYHFSSSEL-MQKVSQYQWCDIENCV-KWMVPFAMVIR--ETGSSKL 331

QY 237 IHCRELV---AHLSTLOSSLPL 256

Db 332 KHFRGVADEAHNIQTHRDSLDL 354

RESULT 12

US-10-245-618-46

; Sequence 46, Application US/10245618

; Publication No. US20030143582A1

GENERAL INFORMATION:

APPLICANT: Reed, Steven

APPLICANT: Strohmaier, Heimo

APPLICANT: Spruck, Charles

APPLICANT: Sangfelt, Olle

FILE OF INVENTION: HCDC4 MODULATES CYCLIN E DEGRADATION

CURRENT APPLICATION NUMBER: US/10/245,618

PRIOR FILING DATE: 2002-09-16

PRIOR APPLICATION NUMBER: US 60/404,116

PRIOR FILING DATE: 2002-08-15

PRIOR APPLICATION NUMBER: US 60/322,947

PRIOR FILING DATE: 2001-09-14

NUMBER OF SEQ ID NOS: 48

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 46

; LENGTH: 395

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthesized

; FEATURE:

; NAME/KEY: VARIANT

; LOCATION: 62

; OTHER INFORMATION: Xaa = Any Amino Acid or none

US-10-245-618-46

Query Match 9.6%; Score 187.5; DB 14; Length 395;

Best Local Similarity 27.0%; Pred. No. 1.9e-09;

Matches 71; Conservative 48; Mismatches 105; Indels 39; Gaps 11;

QY 25 QMKVNVVRK-----MPSNQVSPSQRDEVIQWLAKLYQFNLYPETFALASSLLD 74

Db 100 EVWKIMLNKENTYLRDQHFLQHPQLQPKRAILLDMLMEVCEVVKLHRETFYLAQDFD 159

QY 75 RFLATVKAHPK-YLSCIAISCFEFLAAKTVEDEIRPVLKVLARDSFCGSSSEILRMERI 133

Db 160 RYMATQENVVKTLLQLIGISLFLAAKL--BEIYPPKHLQFAYVTDGACSGDEILTMELM 217

QY 134 ILDKLNWDLHTATPLDPLHIF-----HAIAVSTRPQLLFLSLPKLSPSHLAVLTQ 184

Db 218 IMKALKWRLSPLTIVSWLVNVMQVAYLNDLHEVLLPQVPOQIFI--QIAELLDCVLVD 275

QY 185 LLH-----CMACNQLQFRGSMALAMVS-----LEMEXLIPDWLSLITIELLOKAQMDSSQL 236

Db 276 CLEPPYGILAAALYHFSSSEL-MQKVSQYQWCDIENCV-KWMVPFAMVIR--ETGSSKL 331

QY 237 IHCRELV---AHLSTLOSSLPL 256

Db 332 KHFRGVADEAHNIQTHRDSLDL 354

RESULT 13

US-10-245-618-47

; Sequence 47, Application US/10245618

; Publication No. US20030143582A1

GENERAL INFORMATION:

APPLICANT: Reed, Steven

APPLICANT: Strohmaier, Heimo

APPLICANT: Spruck, Charles

APPLICANT: Sangfelt, Olle

FILE OF INVENTION: HCDC4 MODULATES CYCLIN E DEGRADATION

CURRENT APPLICATION NUMBER: US/10/245,618

PRIOR FILING DATE: 2002-09-16

PRIOR APPLICATION NUMBER: US 60/404,116

PRIOR FILING DATE: 2002-08-15

PRIOR APPLICATION NUMBER: US 60/322,947

PRIOR FILING DATE: 2001-09-14

NUMBER OF SEQ ID NOS: 48

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 47

LENGTH: 395

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Synthesized

NAME/KEY: VARIANT

LOCATION: 380

OTHER INFORMATION: Xaa = Any Amino Acid or none

US-10-245-618-47

Query Match 9.6%; Score 187.5; DB 14; Length 395;

Best Local Similarity 27.0%; Pred. No. 1.9e-09;

Matches 71; Conservative 48; Mismatches 105; Indels 39; Gaps 11;

QY 25 QMKVNVVRK-----MPSNQVSPSQRDEVIQWLAKLYQFNLYPETFALASSLLD 74

Db 100 EVWKIMLNKENTYLRDQHFLQHPQLQPKRAILLDMLMEVCEVVKLHRETFYLAQDFD 159

QY 75 RFLATVKAHPK-YLSCIAISCFEFLAAKTVEDEIRPVLKVLARDSFCGSSSEILRMERI 133

Db 160 RYMATQENVVKTLLQLIGISLFLAAKL--BEIYPPKHLQFAYVTDGACSGDEILTMELM 217

QY 134 ILDKLNWDLHTATPLDPLHIF-----HAIAVSTRPQLLFLSLPKLSPSHLAVLTQ 184

Db 218 IMKALKWRLSPLTIVSWLVNVMQVAYLNDLHEVLLPQVPOQIFI--QIAELLDCVLVD 275

QY 185 LLH-----CMACNQLQFRGSMALAMVS-----LEMEXLIPDWLSLITIELLOKAQMDSSQL 236

Db 276 CLEPPYGILAAALYHFSSSEL-MQKVSQYQWCDIENCV-KWMVPFAMVIR--ETGSSKL 331

QY 237 IHCRELV---AHLSTLOSSLPL 256

Db 332 KHFRGVADEAHNIQTHRDSLDL 354

RESULT 14

US-10-245-618-48

; Sequence 48, Application US/10245618

; Publication No. US20030143582A1

GENERAL INFORMATION:

APPLICANT: Reed, Steven

APPLICANT: Strohmaier, Heimo

APPLICANT: Spruck, Charles

APPLICANT: Sangfelt, Olle

FILE OF INVENTION: HCDC4 MODULATES CYCLIN E DEGRADATION

CURRENT APPLICATION NUMBER: US/10/245,618

PRIOR FILING DATE: 2002-09-16

PRIOR APPLICATION NUMBER: US 60/404,116

PRIOR FILING DATE: 2002-08-15

PRIOR APPLICATION NUMBER: US 60/322,947

PRIOR FILING DATE: 2001-09-14

NUMBER OF SEQ ID NOS: 48

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 48

Db 100 EVKIMLNKEXTYLRDQHLEQHPLOPKMRAILLDMLMEVCEVYKHLHRETFYLAQDFD 159
Qy 75 RFLATVKAHPK-YLSCIAISCFPLAAKTVEDERIPVLKVLARDSFCGCSSESILRMERI 133
Db 160 RYMATQENVVKTLLQLIGISLFAAKL--EEIYPPKHLQFAYVTDGACSGDEILTMELM 217
Qy 134 ILDKLNWDLHTATPLDPLHIF-----HAIIVSTRPQLLFLSLPKLSPSOHLAVLTQ 184
Db 218 IMKALKWRLSPLTIVSWLVNVMQVAYLNDLHEVLLPQYPOQIFI--QIAELLDLCVLVD 275
Qy 185 LLH-----CMACNQLQFRGSMALAMVS-----LEMEKLPDWLSLTIELLOKQAMDSSQL 236
Db 276 CLEPPYGILAAALYHFSSEL-MQKVSQYQWCDIENCV-KMWVPFAMVIR--ETGSSKL 331
Qy 237 IHCRELV---AHLSTLQSSLP 256
Db 332 KHFRGVADEDAHNIQTHRDSLDL 354

RESULT 14

US-10-245-618-48
; Sequence 48, Application US/10245618
; Publication No. US20030143582A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven
; APPLICANT: Strohmaier, Heimo
; APPLICANT: Spruck, Charles
; APPLICANT: Sangfelt, Olle
; TITLE OF INVENTION: HCD4 MODULATES CYCLIN E DEGRADATION
; FILE REFERENCE: TSRI 779.2
; CURRENT APPLICATION NUMBER: US/10/245,618
; PRIOR FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 60/404,116
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: US 60/322,947
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 395
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized
; NAME/KEY: VARIANT
; LOCATION: 62, 380
; OTHER INFORMATION: xaa = Any Amino Acid or none
US-10-245-618-48

Query Match 9.6%; Score 187.5; DB 14; Length 395;
Best Local Similarity 27.0%; Pred. No. 1.9e-09;
Matches 71; Conservative 48; Mismatches 105; Indels 39; Gaps 11;
Qy 25 QMKVNVK-----MPSNQNVSPQRDEVIOWLAKLYQFNLYPETFALASSLLD 74
Db 100 EVKIMLNKEXTYLRDQHLEQHPLOPKMRAILLDMLMEVCEVYKHLHRETFYLAQDFD 159
Qy 75 RFLATVKAHPK-YLSCIAISCFPLAAKTVEDERIPVLKVLARDSFCGCSSESILRMERI 133
Db 160 RYMATQENVVKTLLQLIGISLFAAKL--EEIYPPKHLQFAYVTDGACSGDEILTMELM 217
Qy 134 ILDKLNWDLHTATPLDPLHIF-----HAIIVSTRPQLLFLSLPKLSPSOHLAVLTQ 184
Db 218 IMKALKWRLSPLTIVSWLVNVMQVAYLNDLHEVLLPQYPOQIFI--QIAELLDLCVLVD 275
Qy 185 LLH-----CMACNQLQFRGSMALAMVS-----LEMEKLPDWLSLTIELLOKQAMDSSQL 236
Db 276 CLEPPYGILAAALYHFSSEL-MQKVSQYQWCDIENCV-KMWVPFAMVIR--ETGSSKL 331
Qy 237 IHCRELV---AHLSTLQSSLP 256
Db 332 KHFRGVADEDAHNIQTHRDSLDL 354

RESULT 15

US-10-245-618-31
; Sequence 31, Application US/10245618
; Publication No. US20030143582A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven
; APPLICANT: Strohmaier, Heimo
; APPLICANT: Spruck, Charles
; APPLICANT: Sangfelt, Olle
; TITLE OF INVENTION: HCD4 MODULATES CYCLIN E DEGRADATION
; FILE REFERENCE: TSRI 779.2
; CURRENT APPLICATION NUMBER: US/10/245,618
; PRIOR FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 60/404,116
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: US 60/322,947
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 410
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-245-618-31

Query Match 9.6%; Score 187.5; DB 14; Length 410;
Best Local Similarity 27.0%; Pred. No. 2e-09;
Matches 71; Conservative 48; Mismatches 105; Indels 39; Gaps 11;
Qy 25 QMKVNVK-----MPSNQNVSPQRDEVIOWLAKLYQFNLYPETFALASSLLD 74
Db 115 EVKIMLNKEXTYLRDQHLEQHPLOPKMRAILLDMLMEVCEVYKHLHRETFYLAQDFD 174
Qy 75 RFLATVKAHPK-YLSCIAISCFPLAAKTVEDERIPVLKVLARDSFCGCSSESILRMERI 133
Db 175 RYMATQENVVKTLLQLIGISLFAAKL--EEIYPPKHLQFAYVTDGACSGDEILTMELM 232
Qy 134 ILDKLNWDLHTATPLDPLHIF-----HAIIVSTRPQLLFLSLPKLSPSOHLAVLTQ 184
Db 233 IMKALKWRLSPLTIVSWLVNVMQVAYLNDLHEVLLPQYPOQIFI--QIAELLDLCVLVD 290
Qy 185 LLH-----CMACNQLQFRGSMALAMVS-----LEMEKLPDWLSLTIELLOKQAMDSSQL 236
Db 291 CLEPPYGILAAALYHFSSEL-MQKVSQYQWCDIENCV-KMWVPFAMVIR--ETGSSKL 346
Qy 237 IHCRELV---AHLSTLQSSLP 256
Db 347 KHFRGVADEDAHNIQTHRDSLDL 369

Search completed: February 11, 2005, 03:13:12
Job time : 87.7775 secs

GenCore version 5.1.6

Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 11, 2005, 02:59:54 ; Search time 28.9258 Seconds
(without alignments)
1254.025 Million cell updates/sec

Title: US-09-736-250-1

Perfect score: 162

Sequence: 1 MKFPGPLENQLSFLEKAI.....LSRQEGHASPFPQPVSVM 377

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	902	46.0	178	2	JE0264
2	271.5	13.8	249	2	cyclin G - rat
3	271.5	13.8	295	2	cyclin G1 - human
4	269.5	13.7	256	2	cyclin G - human
5	263.5	13.4	249	2	cyclin G - mouse
6	201.5	10.3	410	2	cyclin E - zebra f
7	196	10.0	361	2	cyclin D3-like prot
8	187.5	9.6	395	2	cyclin E - human
9	187	9.5	309	2	T16660
10	181.5	9.3	449	2	hypothetical prote
11	177.5	9.0	289	2	cyclin - common to
12	176.5	9.0	419	2	cyclin D2 - mouse
13	176	9.0	291	2	cyclin 2 - rice
14	176	9.0	471	2	cyclin D1 - Africa
15	175.5	8.9	359	2	cyclin B1 - yeast
16	175.5	8.9	601	2	cyclin - fission y
17	175	8.9	386	2	cyclin E type I -
18	174.5	8.9	372	2	cyclin 4, D-type -
19	174	8.9	288	2	cyclin D-like prot
20	174	8.9	291	2	cyclin D2 - rat
21	173.5	8.8	502	2	cyclin D1 - zebra
22	171.5	8.7	359	2	cyclin A-like prot
23	171.5	8.7	456	2	cyclin pucl - fiss
24	171	8.7	327	2	cyclin II - maize
25	170.5	8.7	242	2	probable cyclin, 2
26	170.5	8.7	460	2	cyclin - rice
27	169.5	8.6	441	2	protein F2D10.10 [
28	169.5	8.6	469	2	mitosis-specific c
29	169	8.6	289	2	cyclin a2-type, mi
					cyclin D2 - human

30 168.5 8.6 428 2 T04743 cyclin cycl1 - Arab
31 168 8.6 291 2 S57925 cyclin D2 - Africa
32 168 8.6 440 2 T07676 cyclin b1-type, mi
33 167.5 8.5 424 2 D57742 cyclin III - maize
34 167 8.5 473 2 T03611 cyclin, B-type - c
35 167 8.5 491 2 S14166 cyclin B2 - Yeast
36 166.5 8.5 479 2 T04104 B-type cyclin homo
37 166.5 8.5 491 2 JC2497 cyclin E - mouse
38 164.5 8.4 262 2 T42986 v-cyclin - ateline
39 164.5 8.4 291 2 JC4579 cyclin D2 - chicke
40 164.5 8.4 371 2 T02963 cyclin A-type (C10
41 163.5 8.3 492 2 JC4828 cyclin B - yeast (c
42 162.5 8.3 498 2 D86298 hypothetical prote
43 162 8.3 443 2 T14916 mitosis-specific c
44 161.5 8.2 376 2 T05420 cyclin delta-3 - A
45 161.5 8.2 408 2 A56186 cyclin E - African

ALIGNMENTS

RESULT 1

JE0264

cyclin I - human

C;Species: Homo sapiens (man)

C;Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 09-Jul-2004

C;Accession: JE0264

R;Zhu, X.; Naz, R.K.

Biochem. Biophys. Res. Commun. 249, 56-60, 1998

A;Title: Expressin of a novel isoform of cyclin I in human testis.

A;Reference number: JE0264; MUID:98381026; PMID:9705831

A;Accession: JE0264

A;Molecule type: mRNA

A;Residues: 1-178 <ZHU>

A;Cross-references: UNIPROT:Q14094

C;Comment: This protein may have a physiological role in spermatogenesis and/or human sp

Query Match 46.0%; Score 902; DB 2; Length 178;

Best Local Similarity 98.3%; Pred. No. 1.8e-70;

Matches 175; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy

1 MKFPGPLENQLSFLEKAITREAQMKVKNVRKMPNSQNVSPORDEVIOMLKLYQFN 60

Db 1 MKFPGPLEDQKLSFLEKAITREAQMKVKNVRKMPNSQNVSPORDEVIOMLKLYRFN 60

Qy

61 LYPETFALASSLLDRFLATVKAHPKYLSCIAISCFFLAAKTVEEDERIPVLKVLARDSFC 120

Db 61 LYPETFALASSLLDGFLATVKAHPKYLSCIAISCFFLAAKTVEEDERIPVLKVLARDSFC 120

Qy

121 GCSSEILRMERIILDKLNWDLHTATPLDFLHIFHAIAVSTRPQLLSPLKSPSOHL 178

Db 121 GCSSEILRMERIILDKLNWDLHTATPLDFLHIFHAIAVSTRPQLLSPLKSPSOHL 178

RESULT 2

S37693

cyclin G - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Jan-1995

C;Accession: S37693

R;Tamura, K.; Kansoka, Y.; Jinno, S.; Nagata, A.; Ogiso, Y.; Shimizu, K.; Hayakawa, T.;

Oncogene 8, 2113-2118, 1993

A;Title: Cyclin G: a new mammalian cyclin with homology to fission yeast Cig1.

A;Reference number: S37693; MUID:93330551; PMID:8336937

A;Accession: S37693

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-249 <TAM>

A;Cross-references: EMBL:X70871

Query Match 13.8%; Score 271.5; DB 2; Length 249;

Best Local Similarity 31.8%; Pred. No. 7.9e-16;

Matches 77; Conservative 49; Mismatches 85; Indels 31; Gaps 7;

RESULT 6
S52288
C:Species: Brachydanio rerio (zebra fish)
C:Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 12-Jul-2004
C:Accession: S52288
R:Yarden, A.; Geiger, B.
submitted to the EMBL Data Library, December 1994
A:Reference number: S52288
A:Accession: S52288
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-410 <YAR>
A:Cross-references: UNIPROT:P47794; EMBL:X83594; NID:G643111; PIDN:CAA58574.1; PID:G64311
C:Superfamily: cyclin, A/B/D/E type
C:Keywords: cell cycle control

Query Match 10.3%; Score 201.5; DB 2; Length 410;
Best Local Similarity 27.1%; Pred. No. 1.7e-09;
Matches 80; Conservative 51; Mismatches 117; Indels 47; Gaps 10;

Qy 30 NVRKPNQNVSPQRDEVIQWLAKLYQFNLYPETFALASSLLDRFLATVKAHPK-VLS 88
Db 132 DTRVWRHPNLPKQRAILLDNLMEVCEVYKLRHETFLGQDYFDRPWAQENVLKTQLQ 191
Qy 89 CIAISCFFLAAKTVEEDERIPVLKVLARDSPCGSSSEILRMERIIIDKLNWDLHTATPL 148
Db 192 LIGISCLFIAAKM--EETYPKQHVQFAVVDGACTEDDILSWEIIIMKELNWSLSPLTPV 249
Qy 149 DFLHIFHAIIV--STRPOLLESPLKLSQSHLAVLTQQLHCHMACNQQLQPRGSMALAM 206
Db 250 AMLNIYQMAYLKETAEVLTQAQYQATFVQ----IAELLDLCLDVRSLFSYSLAASA 305
Qy 207 V-----SLEM-----EKLIIPDWLSLTIELLQKQMDSSSLIHCRELVAAH 246
Db 306 LFHSSLELVKIVGSLKWCLEECVRMVPFAMSI-----REAGSALKTFKGIADD 358
Qy 247 LSTLQSSLP-----LNSVVVYRPLKHTLVCTDKGVFLRHPSSVPQDFSKNSKPE 297
Db 359 MHNITQHPVLEWLGKHSYQ-----LVDISSQSRSPVTCGLTPPSSS--KPE 406

RESULT 7
T45860
cyclin D3-like protein - Arabidopsis thaliana
N:Alternate names: protein F3A4.150
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C:Accession: T45860
R:Bargues, M.; Collado, M.C.; Navarro, P.; Terol, J.; Perez-Alonso, M.; Mewes, H.W.; May
submitted to the Protein Sequence Database, December 1999
A:Reference number: 223007
A:Accession: T45860
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-361 <BAR>
A:Cross-references: UNIPROT:Q9SN11; EMBL:AL132978
A:Experimental source: cultivar Columbia; BAC clone F3A4
C:Genetics:
A:Map position: 3
A:Introns: 157/3; 225/1; 268/3
A:Note: F3A4.150

Query Match 10.0%; Score 196; DB 2; Length 361;
Best Local Similarity 25.8%; Pred. No. 4.3e-09;
Matches 76; Conservative 53; Mismatches 120; Indels 46; Gaps 11;

Qy 45 RDEVIQWLAKLYQFNLYPETFALASSLLDRFLATVKAH---PKYLSIAISCFFLAAKT 101
Db 86 REKALDWIFKVKSHVGFNSLTALLAVNYFDRFITSRKFTQDKPWNQSQTALACLALAAKV 145
Qy 102 VEEDERIPVLKVL-----ARDSPCGSSSEILRMERIIIDKLNWDLHTATPLDFL-HIFHA 156

Db 146 --BEIRVPFLDFQVEEARYVF---EAKTQRMELLVLSTLDMRMHPVTPISFFDHIIR 200
Qy 157 IAVSTRPQLLFSLPKLSQSHLAVLTQQLHCHMACNQQLQPRGSMALALA-MVSLMEBKLI 215
Db 201 YSPKSHHQLF-----LSRCESL-----LLSIIPDSRFLSPSVLATAMVSVIRDLKM 250
Qy 216 PDWLSLTIELLQKQMDSSSLIHCRELVAAHLSLTQSSSLPLNSVYVVRPLKHTLVCTDKG 275
Db 251 CDEAVYQSLMTLLKVDSEKVNKCYELVDHDSFKKMMN-----WMOQPAS----- 297
Qy 276 VFRLLHPSVPGPDPSKDNKPEVPVRCGTAAFYHHLPAASGCKQTSTKRKVEEMEV 330
Db 298 -----PIGVFDASFSSDSNESWVVSASAS-----VSSSPSEPLKRRRVQEQQM 343

RESULT 8
A40270
cyclin E - human
C:Species: Homo sapiens (man)
C:Date: 17-Jan-1992 #sequence_revision 17-Jan-1992 #text_change 12-Jul-2004
C:Accession: A40270; C40268
R:Koff, A.; Cross, F.; Fisher, A.; Schumacher, J.; Leguellec, K.; Philippe, M.; Roberts
Cell 66, 1217-1228, 1991
A:Title: Human cyclin E, a new cyclin that interacts with two members of the CDC2 gene f
A:Reference number: A40270; MUID:92005673; PMID:1833068
A:Accession: A40270
A:Molecule type: mRNA
A:Residues: 1-395 <KOF>
A:Cross-references: UNIPROT:P24864; GB:M73812
R:Lew, D.J.; Dulic, V.; Reed, S.I.
Cell 66, 1197-1206, 1991
A:Title: Isolation of three novel human cyclins by rescue of G1 cyclin (Cln) function in
A:Reference number: A40268; MUID:92005671; PMID:1833065
A:Accession: C40268
A:Molecule type: mRNA
A:Residues: 1-395 <LEW>
A:Cross-references: GB:M74093
C:Comment: This protein is one of the G1 type cyclins; it forms a complex with both prot
C:Genetics:
A:Gene: GDB:CCNE
A:Cross-references: GDB:128967; OMIM:123837
A:Map position: 19q12-19q12
C:Superfamily: cyclin, A/B/D/E type
C:Keywords: cell cycle control

Query Match 9.6%; Score 187.5; DB 2; Length 395;
Best Local Similarity 27.0%; Pred. No. 2.6e-08;
Matches 71; Conservative 48; Mismatches 105; Indels 39; Gaps 11;

Qy 25 QMKVNVVRK-----MPSNQNVSPQRDEVIQWLAKLYQFNLYPETFALASSLLD 74
Db 100 EVKIMLNKEKTYLRDQHFLEQHPLQPKRAILLDNLMEVCEVYKLRHETFLYAQDFD 159
Qy 75 RFLATVKAHPK-YLSCIAISCFFLAAKTVEEDERIPVLKVLARDSPCGSSSEILRMERI 133
Db 160 RYMATQENVVKTLLQLIGISLSFLAAKL--BEIYPPKLPQYVYTDGACSGDEILTMELM 217
Qy 134 ILDKLNWDLHTATPLDPLHIF-----HAIIVSTRPQLLFSLPKLSQSHLAVLTQK 184
Db 218 IMKALKWRSLPFLTIVSWINVMQVAYLNDLHEVLLPQYPOQIFI--QIAELLDLCLVDVD 275
Qy 185 LLH-----CMACNQQLQPRGSMALAMVS-----LEMEKLIPDWLSLTIELLQKQMDSSQL 236
Db 276 CLEFPYGIILAAALYHFSSSEL-MQKSYGVQWCDIENCV-KMWVPFAMVIR--ETGSSKL 331
Qy 237 IHCRELV---AHLSTLQSSLP 256
Db 332 KHFRGVADEAHNIQTHRDSLDL 354

RESULT 9
T16660

[illegible]

T03675
cyclin_2 - rice
C;Species: Oryza sativa (rice)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 12-Jul-2004
C;Accession: T03675
R;Sauter, M.; Mekhedov, S.L.; Kende, H.
Plant J. 7, 623-632, 1995
A;Title: Gibberellin promotes histone H1 kinase activity and the expression of cdc2 and A;Status: preliminary;
A;Reference number: Z14999; MUID:95261415; PMID:7742859 translated from GB/EMBL/DDBB
A;Molecule type: mRNA
A;Residues: 1-419 <SAU>
A;Cross-references: UNIPROT:Q04671; EMBL:X82036; NID:g1694891; PIDN:CAA57556.1; PID:g1694891
A;Experimental source: cv. Pingaw53
C;Genetics:
A;Gene: cyc2
C;Superfamily: cyclin, A/B/D/E type

Query Match 9.0%; Score 176.5; DB 2; Length 419;
Best Local Similarity 24.6%; Pred. No. 2.5e-07;
Matches 62; Conservative 45; Mismatches 100; Indels 45; Gaps 5;

QY 29 VNVKMPNSNQVSPSQDEVIQWLAKLYQNLYPETFALASSLLDRLATVKAHPKYLS 88
DB :
179 VSPNYMLUSDINEKMGILDLWIEVHYKLELDDELFTLVNIIDRFARENVRKKLQ 238
CY 89 CIAISCFPLAAKTVEEDERIPVLKVLRDSFCGSSSEILLRMERIILDKNWDLHTATPL 148
DB :
239 LVGVMTALLACK--YEVSVPVEDLLICDRAYTRDILEMERIVNTLFQDMSVPTPY 296
QY 149 DFLHIFHAIAVSTRPQLL--FSLPKPSOHLAVLTQKLHHCMACNOLLQFRGSMLALAM 206
DB :
297 CFMRRTLKAAQSDKKLEMSFFIETSLVEY-----EMLXFQPSMLAAAA 341
QY 207 V-----SLEMKLIIDWLSLTIELLQKQMDSSLIHCEELVAHH 246
DB :
342 IYTAQCTINGFKSNWKCELHTKYSEQLMECSMMVVELHQKHGKLTGVH-----RK 395
CY 247 LSTLQSSLPLNS 258
DB 396 YSTFRYGCPPAKS 407

RESULT 13
S57922
cyclin D1 - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 12-Jul-2004
C;Accession: S57922
R;Cockerill, M.J.; Hunt, T.
submitted to the EMBL Data Library, July 1995
A;Description: D-type cyclins in Xenopus laevis.
A;Reference number: S57922
A;Accession: S57922
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-291 <COC>
A;Cross-references: UNIPROT:P50755; EMBL:X89475; NID:g897818; PIDN:CAG51664.1; PID:g897818
C;Superfamily: cyclin, A/B/D/E type
C;Keywords: cell cycle control

Query Match 9.0%; Score 176; DB 2; Length 291;
Best Local Similarity 26.5%; Pred. No. 1.7e-07;
Matches 68; Conservative 33; Mismatches 100; Indels 56; Gaps 9;

QY 26 MWKVNVRKMPS-----NNQVGPSORDEVIOWLAKLYQNLYPETFALASSLLDRFLA 78
DB :
29 MLRAEETSCFPSMSYFKVCQEILLPNMKIVATWMLEVCEEQKCBEVFPLANNYLDRFLS 88
QY 79 TVXAHPKYLSIAISCFFLAAKTVEEDERIPVLKVLRDSFC-----GCCSSELLRMERI 133
DB 89 VEPLRKSWSLQLLGATNCMFASKM---KETIP----LTAELKCIYTDSNIRPDILLINMELR 141

Search completed: February 11, 2005, 03:05:48
Job time : 29.9258 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 11, 2005, 03:18:45 ; Search time 948.767 Seconds
(without alignments)
2352.255 Million cell updates/sec

Title: US-09-736-250-1

Perfect score: 1962

Sequence: 1 MKFPGPLENORLSFLEKAI.....LSRQGHASPCPPLPQVSVM 377

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Deiop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/usPTO_spool/US09736250/runat_07022005_154923_20396/app_query.fasta_1.718
-DB=N Geneseq 16Dec04 -QFMT=fastap -SUFFIX=ring -MINMATCH=0.1 -LOPCL=0
-LOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsum2 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09736250@cgn 1 586 @runat_07022005_154923_20396 -NCPU=6 -ICPU=3
-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq 16Dec04: *
1: Geneseqn1980s: *
2: Geneseqn1990s: *
3: Geneseqn2000s: *
4: Geneseqn2001as: *
5: Geneseqn2001bs: *
6: Geneseqn2002as: *
7: Geneseqn2002bs: *
8: Geneseqn2003as: *
9: Geneseqn2003bs: *
10: Geneseqn2003cs: *
11: Geneseqn2003ds: *
12: Geneseqn2004as: *
13: Geneseqn2004bs: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1962	100.0	1260	3	Aaz37836 Human cyc
2	1962	100.0	1260	6	Abk83672 Human cDN
3	1962	100.0	1260	10	Adk61064 Ovarian c
4	1962	100.0	1260	11	Adi31573 Human cDN
5	1962	100.0	1260	13	Adr25465 Breast ca

6	1962	100.0	1328	2	AAT73937	Aat73937 DNA encod	
7	1962	100.0	1384	8	ACC47339	Acc47339 Human pro	
8	1962	100.0	1889	6	ABL87929	AbL87929 Human ova	
9	1962	100.0	1890	12	ADP10653	Adp10653 Reference	
10	1962	100.0	1890	13	ACN38124	Acn38124 Tumour-as	
11	1841	93.8	2755	5	ADL63374	AdL63374 Human ova	
12	1713.5	87.3	1651	9	AAD57247	Aad57247 Human CGD	
13	1529.5	78.0	903	12	ADNO1156	Adno1156 Human cel	
14	770.5	39.3	2146	5	ADL63082	AdL63082 Human ova	
c	15	763	38.9	804	2	AAX40003	Aax40003 Prostate
	16	748	38.1	444	3	AAC01909	Aac01909 Human sec
	17	647	33.0	392	2	AAQ61358	Aaq61358 Human bra
c	18	633	32.3	417	2	AAT26236	Aat26236 Human gen
c	19	621	31.7	516	5	ADL44155	AdL44155 Human ova
	20	550	28.0	389	10	ADK61066	Adk61066 Ovarian c
	21	540	27.5	1493	2	AAZ41284	Aaz41284 Human nor
	22	517	26.4	329	2	AAT23729	Aat23729 Human gen
	23	502.5	25.6	1110	5	AAS82590	Aas82590 DNA encod
	24	502.5	25.6	2356	13	ADR10427	Adr10427 Full leng
	25	486	24.8	348	6	ABS69603	AbS69603 Novel mur
c	26	466	23.8	536	10	ADF82253	Adf82253 Leukaemia
c	27	465	23.7	597	10	ADK61065	Adk61065 Ovarian c
c	28	433	22.1	409	10	ADF80870	Adf80870 Leukaemia
c	29	408	20.8	486	5	ADL43407	AdL43407 Human ova
c	30	377.5	19.2	426	5	ADL37023	AdL37023 Human ova
c	31	377.5	19.2	426	5	ADI71872	Adi71872 Human ova
	32	346	17.6	447	4	AAS25071	Aas25071 Human ova
	33	346	17.6	447	5	AAH83716	Aah83716 Human ova
	34	326.5	16.6	1410	11	ADI31587	Adi31587 Human cDN
	35	326.5	16.6	2044	6	ABL61909	AbL61909 Colon ade
	36	326.5	16.6	2044	6	ABK84346	Abk84346 Human cDN
	37	326.5	16.6	2044	6	ABV78034	Abv78034 Hypoxia-r
	38	326.5	16.6	2044	10	ADH28975	Adh28975 Human chr
	39	326.5	16.6	2044	12	ADO19807	Ado19807 Human PRO
	40	326.5	16.6	2044	12	ADO19316	Ado19316 Human PRO
	41	326.5	16.6	2044	13	ADR25164	Adr25164 Breast ca
	42	326.5	16.6	2044	13	ADP54949	Adp54949 Human PRO
	43	326.5	16.6	2044	13	ADP23417	Adp23417 PRO polyP
	44	326.5	16.6	2044	13	ADR65826	Adr65826 Human pro
	45	326.5	16.6	2044	13	ADR66510	Adr66510 Human pro

ALIGNMENTS

RESULT 1	
AAZ37836	
ID	AAZ37836 standard; DNA; 1260 BP.
XX	
AC	AAZ37836;
XX	
DT	09-FEB-2000 (first entry)
XX	
DE	Human cyclin I nucleotide sequence.
XX	
KW	Cyclin-dependent kinase 2; CDK2; hsReq; hsReq*-1; hsReq*-2; cyclin I;
KW	ERH; cell cycle; proliferation; cancer; hyperproliferative disorder;
KW	atherosclerosis; tumour; ss.
XX	
OS	Homo sapiens.
XX	
PH	Key
CDS	Location/Qualifiers
FT	1..1134
FT	/*tag= a
XX	/product= "Cyclin_I"
XX	
DN	WO9925829-A2.
XX	
PD	27-MAY-1999.
XX	
PF	12-NOV-1998; 98WO-US024095.
XX	
PR	13-NOV-1997; 97US-00969106.
XX	

(CURA-) CURAGEN CORP.

PI Yang M, Nandabalan K, Schulz VP;

XX WPI; 2000-061923/05.

DR P-PSDB; AAY52185.

XX New complexes of the cyclin-dependent kinase 2 protein with its
PT interacting proteins, used to treat, e.g. atherosclerosis.

XX Example; Fig 2; 90pp; English.

XX This sequence is the human Cyclin I nucleotide sequence. Cyclin I is
CC expressed at almost constant levels throughout the cell cycle, and is
CC implicated in controlling cell cycle progression and transcriptional
CC control. Cyclins form complexes with cyclin-dependent kinases. CDK2,
CC cyclin-dependent kinase 2, is used in the invention which relates to
CC complexes of the CDK2 protein with other proteins, selected from cyclin
CC I, ERH, hReg, hReg-1 and hReg-2 (AAY52185-Y52188). CDK2 is expressed
CC late in G1 or early in S phase of the cell cycle, and is pivotal for G1/S
CC transition. Compositions containing a CDK2 complex, an antibody targeting
CC the complex, and nucleotide sequences encoding CDK2 or its derivatives
CC can be used therapeutically. The complexes and their nucleotide sequences
CC can be used to treat diseases or disorders associated with increased or
CC decreased levels of the complex. Screening the complex, or a derivative
CC or a modulator of the complex for neoplastic activity by measuring the
CC survival or proliferation of cells from a malignant cell line when in
CC contact with the complex can be used to indicate if the complex has
CC anti-neoplastic activity. Screening for molecules that modulate the
CC formation of the complexes can be used for treating or preventing
CC atherosclerosis or atherosclerosis-associated disease by contacting cells
CC or using a test animal, in which tumour growth or regression is measured
CC to test whether anti-neoplastic activity is displayed. Diseases which can
CC be treated or prevented by molecule/s which modulate the function of the
CC complex include cancer, hyperproliferative disorders and atherosclerosis

XX SQ Sequence 1260 BP; 352 A; 283 C; 274 G; 351 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.92e-205	Length:	1260
Score:	1962.00	Matches:	377
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	3	Gaps:	0

US-09-736-250-1 (1-377) x AAZ37836 (1-1260)

Qy	1	MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle	20
Db	1	ATGAAGTTTCCAGGCGCTTTCGAAACCCAGAGATTGCTTTCTCTGTTGGAAAGGCAATC	60
Qy	21	ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGluAsnVal	40
Db	61	ACTAGGGAAGCACAGATGTGAAGTGAATGTGGGAAATAGTTCCTTCAATCAGAGTTT	120
Qy	41	SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTrpGlnPheAsn	60
Db	121	TCTCATCCAGAGATGAAGTAATTCATGGCTGGCCAACTCAAGTACCAATTCAC	160
Qy	61	LeuTrpProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal	80
Db	181	CTTTACCCAGAAACATTTGCTCTGGCTAGCAGTCTTTTGGATAGTGTTCCTAGCTACCGTA	240
Qy	81	LysAlaHisProLysTrpLeuSerCysIleAlaIleSerCysPhePheLeuAlaLys	100
Db	241	AAGGCTCATCAATACTTGAGTTGATTGCAATCAGCTGTTCCTAGCTGCCAAG	300
Qy	101	ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys	120
Db	301	ACTGTTGAGGAAGATGACAGAAATCCAGTACTAAGAGTATTGGCAAGACAGATTTCTGT	360
Qy	121	GlyCysSerSerSerGluIleLeuArgMetGluArgIleLeuLeuAspLysLeuAsnTrp	140

Db	361	GGATGTTCTCTCATCTGAAATTTTGAGAAATGAGAGAAATATTCTGGATAAGTTCAATTGG	420
Qy	141	AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer	160
Db	421	GATCTTCACACAGCCACACCAATTTGGATTTCTTCATATTTTCCATGTCATTCAGTGTCA	480
Qy	161	ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal	180
Db	481	ACTAGGCTCAGTTACTTTTCAGTTTGGCCCAATTTGAGCCCACTCAACATTTGGCAGTC	540
Qy	181	LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer	200
Db	541	CTTACCAGCAACTACTTCTGATGGCTGCAACCACTCTGCAATTCAGAGGATCC	600
Qy	201	MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuLeuProAspTrpLeuSer	220
Db	601	ATGCTTGTCTCTGGCCATGTTAGTCTGGAATGAGAACTCATTTCTGATGGCTTTCT	660
Qy	221	LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuLeuHisCysArg	240
Db	661	CTTACAATTGAAGTCTTTCAGAAAGCACAGATGATAGTCTCCAGTTGATCCATTTGTCG	720
Qy	241	GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTrp	260
Db	721	GAGCTTGTGGCACATCACCTTTCTACTCTGCAGTCTTCCCTGCTCTGAATTCGGTTAT	780
Qy	261	ValTrpArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis	280
Db	781	GTCTACCGTCCCTTCAGACACACCTGTGTGACCTGTGACAAAGAGTTCAGATTACAT	840
Qy	281	ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal	300
Db	841	CCCTCTCTCTGCCAGGCCAGACTTCTCCAGGACAAACAGAGCCAGAGTSCCAGTC	900
Qy	301	ArgGlyThrAlaPheTrpHisLeuProAlaHisLeuProAlaSerGlyCysLysGlnThrSer	320
Db	901	AGAGGTACAGACGCTTTTACCATCATCTCCAGCTGCCAGTGGTGGTCAAGACACCTCT	960
Qy	321	ThrLysArgLysValGluGluMetGluValAspAspPheTrpAspGlyLysArgLeu	340
Db	961	ACTAAACGCAAGTAGAGGAATGGAAGTGGATGACTTCTATGATGGAATCAACAGGCTC	1020
Qy	341	TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg	360
Db	1021	TATAATGAGATAATGTCTCAGAAATGTGGTTCTGTGTGGCACTGATTTATCAAGA	1080
Qy	361	GlnGluGlyHisAlaSerProCysProProLeuGlnProValSerValMet	377
Db	1081	CAAGAGGAGCATGCTCCCTTTGTCACCTTTGTCAGCTGTTCCTGTGTCATG	1131
RESULT 2			
ID	ABK83672	standard; cDNA; 1260 BP.	
XX	AC	ABK83672;	
XX	DT	14-AUG-2002 (first entry)	
XX	DE	Human cDNA differentially expressed in granulocytic cells #243.	
XX	KW	Human; ss; granulocytic cell; DNA chip; bacterial infection;	
XX	KW	viral infection; parasitic infection; protozoal infection;	
XX	KW	fungal infection; sterile inflammatory disease; psoriasis;	
XX	KW	rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;	
XX	KW	cardiac reperfusion injury; renal reperfusion injury; ARDS;	
XX	KW	adult respiratory distress syndrome; inflammatory bowel disease;	
XX	KW	Crohn's disease; ulcerative colitis; periodontal disease;	
XX	OS	granulocyte activation; chronic inflammation; allergy.	
XX	OS	Homo sapiens.	
XX	PN	WO2002028999-A2.	

XX PD 11-APR-2002.

XX PF 03-OCT-2001; 2001WO-US030821.

XX PR 03-OCT-2000; 2000US-0237189P.

XX PA (GENE-) GENE LOGIC INC.

XX PI Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;

XX DR WPI; 2002-435328/46.

XX DR

XX PT Detecting granulocyte activation by detecting differential expression of

PT genes associated with granulocyte activation, which serves as diagnostic

PT markers that is useful for monitoring disease states and drug toxicity.

XX

PS Claim 1; SEQ ID NO 243; 114pp; English.

XX

CC The invention relates to detecting (M1) granulocyte (GC) activation

CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by

CC DNA chip analysis as given in the specification, and comparing the

CC expression level to an expression level in an unactivated GC, where

CC differential expression of Gs is indicative of GCA. Also included are

CC modulating (M2) GCA by contacting GC with an agent that alters the

CC expression of at least one gene in Gs; (2) screening (M3) for an agent

CC capable of modulating GCA or an inflammation (especially chronic) in a

CC tissue, an allergic response in a subject, exposure of a subject to a

CC pathogen or sterile inflammatory disease using the gene expression

CC profile; (3) detecting (M4) an inflammation (especially chronic) in a

CC tissue, an allergic response in a subject, exposure of a subject to a

CC pathogen or sterile inflammatory disease, by detecting the level of

CC expression in a sample of the tissue of gene(s) from Gs, where the level

CC of expression of the gene is indicative of inflammation; (4) treating

CC (M5) an inflammation (especially chronic) or in a tissue, an allergic

CC response in a subject, exposure of a subject to a pathogen or sterile

CC inflammatory disease, by contacting a tissue having inflammation with an

CC agent that modulates the expression of gene(s) from Gs in the tissue. M1

CC is useful for detecting GCA; M2 is useful for modulating GCA; M3 is useful

CC for screening an agent capable of modulating GCA preferably in an

CC inflammation in a tissue; M4 is useful for detecting an inflammation

CC (especially chronic) in a tissue, an allergic response in a subject,

CC exposure of a subject to a pathogen or sterile inflammatory disease (e.g.

CC psoriasis, rheumatoid arthritis, glomerulonephritis, asthma, thrombosis,

CC cardiac reperfusion injury, renal reperfusion injury, ARDS, adult

CC respiratory distress syndrome, inflammatory bowel disease, Crohn's

CC disease, ulcerative colitis, periodontal disease; also bacterial

CC infection, viral infection, parasitic infection, protozoal infection,

CC fungal infection and M5 is useful for treating one of the above

CC conditions. The present sequence represents a gene differentially

CC expressed in granulocytes. Note: The sequence data for this patent did

CC not form part of the printed specification, but was obtained in

CC electronic format directly from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences

XX

SQ Sequence 1260 BP; 352 A; 283 C; 274 G; 351 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.92e-205	Length:	1260
Score:	1962.00	Matches:	377
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-09-736-250-1 (1-377) x ABK83672 (1-1260)

Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle 20

Db 1 ATGAAGTTTCAGGGCCCTTGGAAACACAGAGATTGCTTTCTCTGTTGGAAAGGCAATC 60

Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40

Db 1

RESULT 3
ADK61064
ID ADK61064 standard; DNA; 1260 BP.

XX ADK61064;
AC 06-MAY-2004 (first entry)
DT Ovarian cancer-related DNA #219 with altered ovarian cancer expression.
DE ds; Gene; ovarian tumor; BRCA-1-like; BRCA-2-like; non-BRCA-like;
KW gene expression; primer; cancer.
KW Homo sapiens.
OS WO2003068054-A2.
XX 21-AUG-2003.
XX 13-FEB-2003; 2003WO-US004688.
XX 13-FEB-2002; 2002US-0357031P.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX (SLOK) SLOAN KETTERING INST CANCER RES.
XX Jazaeri AA, Boyd J, Liu ET;
XX WPI; 2003-689589/65.
XX Classifying an ovarian tumor as a BRCA-1-like or BRCA-2-like or non-BRCA-
PT like tumor by determining a pattern of expression in the ovarian tumor of
PT several markers.
XX Disclosure; SEQ ID NO 234; 137pp; English.
XX The invention relates to a method of classifying an ovarian tumor as a
CC BRCA-1-like or BRCA-2-like or non-BRCA-like tumor by: (1) determining a
CC pattern of expression in the ovarian tumor of several markers given in
CC the specification; and (2) comparing a similarity of the pattern of
CC expression of the markers in the ovarian tumor to a pattern of expression
CC of the markers in a comparison tissue of a known BRCA-1-like or BRCA-2-
CC like or non-BRCA-like tumor. The method is useful for classifying an
CC ovarian tumor as a BRCA-1-like or BRCA-2-like or non-BRCA-like tumor.
CC This sequence corresponds to an ovarian cancer -related gene having an
CC altered pattern of expression in ovarian cancer. (Note: The sequence data
CC for this patent did not form part of the printed specification but was
CC obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences).
XX Sequence 1260 BP; 352 A; 283 C; 274 G; 351 T; 0 U; 0 Other;
SQ

Alignment Scores:
Pred. No.: 1,92e-205 Length: 1260
Score: 1962.00 Matches: 377
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-736-250-1 (1-377) x ADK61064 (1-1260)

QY 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle 20
DB 1 ATGAAGTTTCAGGGCCCTTGGAAACCCAGAGATTGCTTTCCCTGTTGGAAAGGCAATC 60
QY 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
DB 61 ACTAGGGAAGCACAGATGTGGAAGTGAATGTGGGAAATGGCTTCAATCAGATGTT 120
QY 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyTrpGlnPheAsn 60
DB 121 TCTCCATCCACAGAGATGAAGTAATCAATGGCTGGCCAAACTCAAGTACCAATTC AAC 180
QY 61 LeuTyTrpProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80

DB 181 CTTTACCAGAAACATTTGCTCTGGCTAGCAGCTTTTGGATAGGTTTTTGTAGTACCATA 240
QY 81 LysAlaHisProLysTyTrpLeuSerCysAlaIleAspPheCysPheLeuAlaAlaLys 100
DB 241 AAGGCTCATCAAAATACTTGGATTGATTGCAATCAGCTGTTTTTCTTCTAGTCCAG 300
QY 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
DB 301 ACTGTTGAGGAAGATGAGAGAAATCCAGTAGTACTAAAGGTATTGGCAGAGACAGTTTCTGT 360
QY 121 GlyCysSerSerSerGluIleLeuArgMetGluArgIleIleLeuAspLysLeuAsnTrp 140
DB 361 GGATGTTCTCATCTGAATTTTGGAAATGGAGAAATATTCTGGTAAGTGAATGG 420
QY 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
DB 421 GAICTTCACAGCCACCATTTGGATTTCTTCATATTTTCCATGTCATGTCAGTGTCA 480
QY 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
DB 481 ACTAGGCTCAGTTACTTTTCAGTTTGGCCAAATTTAGCCCATCTCAACATTTGGCAGTC 540
QY 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
DB 541 CTTACCAAGCAACTACTTCTGATGGCTGCAACCACTTCTGCAATTCAGAGGATCC 600
QY 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
DB 601 ATGCTTGCTCTGGCCATGGTTAGTCTGGAATGGAGAACTCATCTCTGATGGCTTCT 660
QY 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
DB 661 CTTACAAATTCAGCTTTCAGAAAGCACAGATGATGATGATGATGATGATGATGATGATG 720
QY 241 GluLeuValAlaHisIleLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTy 260
DB 721 GAGCTTGTGGCAGATCATCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
QY 261 ValTyArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
DB 781 GTCTACCGTCCCTCAAGCACACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
QY 281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
DB 841 CCTCTCTCTCTCCAGGCCAGACTTCTCCAGGACAAACAGCAGCAGCAGCAGCAGCAGC 900
QY 301 ArgGlyThrAlaAlaPheTyTrpHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
DB 901 AGAGGTACAGAGCTTTTACCATCATCTCCAGCTGCCAGTGGGTGGTGGTGGTGGTGGTGG 960
QY 321 ThrLysArgLysValGluGluMetGluValAspAspPheTyTrpAspGlyIleLysArgLeu 340
DB 961 ACTAAACGCAAGATAGAGGAAATGGAAATGGAGTGGATGCTTCTATGATGGAATCAAAACGGCTC 1020
QY 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
DB 1021 TATAATGAAGATAATGTCTCAGAAATGTGGTGTCTGTGTGGTGGTGGTGGTGGTGGTGG 1080
QY 361 GlnGluGlyHisAlaSerProCysProLeuGlnProValSerValMet 377
DB 1081 CAAGAGGAGCATGCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCT 1131

RESULT 4
ADI31573
ID ADI31573 standard; cDNA; 1260 BP.
XX
XX ADI31573;
AC
XX 17-JUN-2004 (first entry)
DT
XX Human cDNA #899.
DE
XX Human; gene; ss; immunological response; immunopathological condition;
KW

KW Crohn's disease; asthma; ulcerative colitis; hypereosinophilia;
KW irritable bowel syndrome; osteoarthritis; rheumatoid arthritis;
KW acute monocytic leukaemia; antiinflammatory; antiasthmatic; antiulcer;
KW osteopathic; antiarthritic; antirheumatic; cytostatic.
XX Homo sapiens.
XX US6607879-B1.
XX 19-AUG-2003.
XX 09-FEB-1998; 98US-00023655.
XX 09-FEB-1998; 98US-00023655.
XX (INCY-) INCYTE CORP.
XX Cocks BG, Stuart SG, Seilhamer JJ;
XX WPI; 2003-895307/82.
XX A composition comprising a plurality of cDNAs, useful for detecting
XX altered expression of genes in an immunological response or for
XX diagnosing and treating an immunopathology, e.g. Crohn's disease, asthma
XX or osteoarthritis.
XX Claim 1; SEQ ID NO 899; 50pp; English.
XX The invention relates to a composition comprising a plurality of cDNAs
XX for detecting the altered expression of genes in an immunological
XX response. The invention also relates to a method of diagnosing or
XX monitoring the treatment of an immunopathological condition in a sample,
XX comprising obtaining nucleic acids from a sample, contacting the nucleic
XX acids of the sample with an array comprising the plurality of cDNAs under
XX conditions to form one or more hybridisation complexes, detecting the
XX hybridisation complexes and comparing the levels of the detected
XX hybridisation complexes with the level of hybridisation complexes
XX detected in a non-diseased sample, where an altered level of the detected
XX hybridisation complexes correlates with the presence of an
XX immunopathological condition. Also disclosed are an expression profile
XX comprising a microarray and a plurality of detectable complexes and a
XX method for identifying a plurality of polynucleotide probes. The cDNAs
XX are useful as hybridisable array elements in a microarray for monitoring
XX the expression of target polynucleotides. The microarray can be used in
XX the diagnosis of an immunopathology, such as Crohn's disease, asthma,
XX ulcerative colitis, hypereosinophilia, irritable bowel syndrome,
XX osteoarthritis, rheumatoid arthritis or acute monocytic leukaemia, and in
XX identifying agents for the treatment of the diseases. The microarray may
XX also be used in drug discovery and development, toxicological and
XX carcinogenicity studies, forensics or pharmacogenomics. The composition
XX may also be used in purification of a subpopulation of mRNAs, cDNAs or
XX genomic fragments. This sequence represents a human cDNA of the
XX invention. Note: The sequence data for this patent did not form part of
XX the printed specification but was obtained in electronic format directly
XX from USPTO at seqdata.uspto.gov/sequence.html.
SQ Sequence 1260 BP; 352 A; 283 C; 274 G; 351 T; 0 U; 0 Other;
Alignment Scores:
Pred No.: 1-92e-205 Length: 1260
Score: 1962.00 Matches: 377
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 11 Gaps: 0
US-09-736-250-1 (1-377) x ADI31573 (1-1260)
Qy 1 MetlysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle 20
Db 1 ATGAAGTTTCAGGCGCTTGGAAACACAGAGATTGCTTCTCTGTTGGAAAGGCAATC 60
Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40

Db 61 ACTAGGAAGCACAGATGTGAAAGTGAATGTGCGAAATGCCTTCAATCAGAATGTT 120
Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn 60
Db 121 TCTCCATCCAGAGAGATGAAGTAATTCATGGCTGGCCAAACTCAAGTACCAATTCAC 180
Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 181 CTTTACCAGAAAACATTTGCTCTGGCTAGCAGTCTTTTGGATAGTGTTTTACGTACCGTA 240
Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaAlaLys 100
Db 241 AGGCTCATCAAAATACTTGGATTGATTGCAATCAGCTGTTTTTCTTACGTGCCAAG 300
Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgSerPheCys 120
Db 301 ACTGTTGAGGAAGATGAGAGAATTCAGTAGTAAAGGTATTGGCAGAGACAGATTTCTGT 360
Qy 121 GlyCysSerSerSerGluIleLeuArgMetGluArgIleLeuLeuAspLysLeuAsnTrp 140
Db 361 GGATGTTCTCTCATCTGAAATTTTGGAGATGGAGAGAAATTATTCTGGATAAGTTGAATGG 420
Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 421 GATCTTCACAGCACCAACCATTTGATTTCTCATATTTCATGCAATTCAGTGTGCA 480
Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 481 ACTAGGCTCAGTTACTTTTTCAGTTTGCCTCCAAATTAAGCCATCTCAACATTTGGCAGTC 540
Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
Db 541 CTTTACCAAGCAACTACTTCTCTGATGGCTGCAACCAACTTCTGCAATTCAGAGGATCC 600
Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
Db 601 ATGCTTCTCTGCGCATGTTGTTAGTCTGGAATGGAAACTCATCTCTGATGGCTTTCT 660
Qy 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
Db 661 CTTTACATTCAGCTCTTCAGAAAGCACAGATGATAGTCCCAAGTTGATTCATTCGCG 720
Qy 241 GluLeuValAlaHisHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
Db 721 GAGCTTGTGGCACATCATCTCTTCTACTCTGCAGTCTTCCCTGCCTCTGAAATTCGTTAT 780
Qy 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db 781 GTCTACCGTCCCTCAAGCACACCTGCTGACCTGTGACAAAGGAGTGTTCAGATTACAT 840
Qy 281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
Db 841 CCTCTCTCTGCCAGCCCGACAGCTTCTCCAGGACAAACAGCAAGCCAGAAAGTCCAGTC 900
Qy 301 ArgGlyThrAlaAlaPheTyrHisHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
Db 901 AGAGGTACAGCAGCCTTTTACCATCATCTCCAGCTGCCAGTGGGTGGCAGCAGCTCT 960
Qy 321 ThrLysArgLysValGluGluMetGluValAspAspPheTyrAspGlyLysLeuArgLeu 340
Db 961 ACTAAACGCAAGATAGAGGAAATGGAAAGTGATGATGATGATGATGATGATGATGATGAT 1020
Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
Db 1021 TATTAATCAAGATAATGTCTCAGAAATGTGGTCTCTGTGTGTGGCAGCTGATTTATCA 1080
Qy 361 GlnGluGlyHisAlaSerProCysProLeuGlnProValSerValMet 377
Db 1081 CAAGAGGAGCATGCTTCCCTTGTCCACCTTTTGACGCTGTTTCTGTCTCATG 1131
RESULT 5
ADR25465

ID ADR25465 standard; DNA; 1260 BP.
 AC ADR25465;
 XX 21-OCT-2004 (first entry)
 DT Breast cancer prognosis marker #1326.
 DE ds; breast cancer; prognosis; gene expression; diagnosis.
 XX Homo sapiens.
 OS WO2004065545-A2.
 PN 05-AUG-2004.
 PD 15-JAN-2004; 2004WO-US0001100.
 XX 15-JAN-2003; 2003US-00342887.
 XX (ROSE-) ROSETTA INPHARMATICS LLC.
 PA (NECA-) NETHERLANDS CANCER INST.
 XX Van't Veer LJ, He Y;
 PI WPI; 2004-593473/57.
 DR Classifying a breast cancer patient according to prognosis comprises
 PT determining the similarity between the level of expression of each of
 PT five genes in a cell sample taken from patient, to control levels.
 XX Disclosure; SEQ ID NO 1326; 226pp; English.
 PS The invention relates to a method of classifying a breast cancer patient
 CC according to prognosis by determining the similarity between the level of
 CC expression of each of five genes for which markers are listed in the
 CC specification, in a cell sample taken from the breast cancer patient, to
 CC control levels of expression for each respective five genes to obtain a
 CC patient similarity value. The methods are useful for classifying a breast
 CC cancer patient according to prognosis. Kits and computer program products
 CC are useful for data analysis using the diagnostic, prognostic and
 CC statistical methods of the invention. This sequence corresponds to a
 XX marker used in the method of the invention.
 SQ Sequence 1260 BP; 352 A; 283 C; 274 G; 351 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 1.92e-205 Length: 1260
 Score: 1962.00 Matches: 377
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 13 Gaps: 0
 US-09-736-250-1 (1-377) x ADR25465 (1-1260)
 Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle 20
 Db 1 ATGAAGTTTCAGGGCCCTTGGAAACACAGAGATTGCTTCTCTGGTGGAAAGCCAAATC 60
 Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
 Db 61 ACTAGGGAAGCACAGATGCTGGAAGTGAATGTGGGAAATGCCCTTCAAAATCAGATGTT 120
 Qy 41 SerProSerGlnArgAsnGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn 60
 Db 121 TCTCCATCCCAGAGAGATGAAGTAATCAATGGCTGGCCAAACTCAAGTACCAATCAAC 180
 Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
 Db 181 CTTTACCAGAAACATTGCTCTGGCTAGCAGTCTTTTGGATAGATTTTGTAGTACCGTA 240
 Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaLys 100

Db 241 AAGGCTCATCAAAATACTTGAGTTGATTGCAATCAGCTGTTTTTCTTCTAGTCCCAAG 300
 Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
 Db 301 ACTGTTGAGGAAGATGAGAGAAATTCAGTAGTAAAGGTATTGGCAAGAGACAGATTTCTGT 360
 Qy 121 GlyCysSerSerSerGluIleLeuArgMetGluArgIleIleLeuAspLysLeuAsnTrp 140
 Db 361 GGATGTTCTCATCTGAAATTTTGAAGATGAGAGAAATTTCTGGTAAGATTGAATGG 420
 Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
 Db 421 GATCTTCACACAGCCACACCATTTGATTTTCTCATATTTTCCATGTCATTCAGTGTCA 480
 Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
 Db 481 ACTAGGCTCAGTTACTTTTTCAGTTTGCCTTGCCTGCAACCACTTCTGCAATTCAGAGGATCC 540
 Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuPheArgGlySer 200
 Db 541 CTTACCAAGCAACTACTTCTGATGGCTTGCCTGCAACCACTTCTGCAATTCAGAGGATCC 600
 Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
 Db 601 ATGCTTGCTCTGGCCATGGTTAGTCTGGAATGGAGAACTCATTTCTGATGGCTTTCT 660
 Qy 221 LeuThrIleGlnLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
 Db 661 CTTTACCAATGCACTGCTTTCAGAAAGCACAGATGATAGTCCCGATGATCCATTTGCGG 720
 Qy 241 GluLeuValAlaHisIleLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
 Db 721 GAGCTTGTCACATACCTTTTCTACTCTGAGTCTTCTCTGCTCTGAAATTCGGTTAT 780
 Qy 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
 Db 781 GTCTACCGTCCCTCAAGCACACCCCTGGTGACCTGTGACAAAGAGAGTGTTCAGATTACAT 840
 Qy 281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
 Db 841 CCTCTCTCTGTCAGGCCAGACTTCTCCAAAGCAACAGCAAGGAGGAGGAGTCCAGTCC 900
 Qy 301 ArgGlyThrAlaAlaPheTyrHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
 Db 901 AGAGGTACAGCAGCCCTTTTACCAATCATCTCCAGCTGCCAGTGGGTGGCAAGACCTCT 960
 Qy 321 ThrLysArgLysValGluGluMetGluValAspAspPheTyrAspGlyIleLysArgLeu 340
 Db 961 ACTAAACGCCAAAGTAGAGGAAATGGAAGTGGATGACTTCTTATGATGGAATCAAACGGCTC 1020
 Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
 Db 1021 TATAATCAAGATAATGTCTCAGAAATGTGGGTCTGTGTGTGGCTGCTGATTTATCAAGA 1080
 Qy 361 GlnGluGlyHisAlaSerProCysProProLeuGlnProValSerValMet 377
 Db 1081 CAAGAGGGACATGCTTCCCTTGTCCACCTTTCAGCCCTGTTTCTGTCTCATG 1131
 RESULT 6
 AAT73937
 ID AAT73937 standard; DNA; 1328 BP.
 XX
 AC AAT73937;
 DT 02-DEC-1997 (first entry)
 XX
 DE DNA encoding human cyclin I.
 XX human; cyclin I; antisense; probe; neurone; cancer; antibody; ds.
 XX Homo sapiens.
 XX

PR 03-AUG-2001; 2001US-0309470P.
 XX 30-OCT-2001; 2001US-0330747P.
 PA (ORIG-) ORIGENE TECHNOLOGIES INC.
 XX Sun Z, Li X, Jay G, Kovacs KF, Shu Y, Fan W;
 DR WPI; 2003-256562/25.
 XX P-PSDB; ABR39934.
 PT New polynucleotide, useful for preparing a composition for treating
 PT prostate disease, e.g., cancer.
 XX Claim 1; Page 147-149; 212pp; English.
 PS The invention relates to prostate selective polynucleotides and
 CC polypeptides. The polynucleotides are expressed in prostate and are
 CC useful as molecular markers, as drug targets, and for detecting,
 CC monitoring, preventing or treating diseases and conditions related to
 CC prostate, such as prostate cancers. Sequences ACC47325-356 represent
 CC specific examples of prostate specific polynucleotides
 XX
 SQ Sequence 1384 BP; 364 A; 329 C; 324 G; 367 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 2.23e-205 Length: 1384
 Score: 1962.00 Matches: 377
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 8 Gaps: 0

US-09-736-250-1 (1-377) x ACC47339 (1-1384)

QY 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle 20
 DB 200 ATGAAGTTTCAGGGCCCTTTGGAAACACAGAGATTGCTTTTCCTGTGGAAAGGCCAATC 259

QY 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
 DB 260 ACTAGGGAAGCACAGATGCTGGAAGTGAATCTGGGAAATGCCCTTCAATCAGAAATGTT 319

QY 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn 60
 DB 320 TCTCCATCCAGAGAGATGAAGTAAATCAATGGCTGGCCAACTCAAGTACCAATTCAAC 379

QY 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
 DB 380 CTTTACCAGAAACATTTGCTCTGGTAGCAGTCTTTTGGATAGGTTTTTGTAGCTACCGTA 439

QY 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaAlaLys 100
 DB 440 AAGGCTCATCAAAATACTTGTAGTTGATTGCAATCAGCTGTTTTTTCCTAGCTGCCAAG 499

QY 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
 DB 500 ACTGTTGAGGAAGATGAGAAATTCAGTACTAAAGGTATTGGCAAGACAGATTTCTGT 559

QY 121 GlyCysSerSerSerGluIleLeuArgMetGluArgIleIleLeuAspLysLeuAsnTrp 140
 DB 560 GGAATGCTCATCTGAATTTTGGAAATTTGAGAAATGAGAGAAATTTCTGGATAAGTTGAAATGG 619

QY 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
 DB 620 GATCTTCACAGCCACACCATGGAATTTTCTCATATTTTCCATGTCATGTCAGTGTCA 679

QY 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
 DB 680 ACTAGGCTCAGTACTTTTTCAGTTTGCCTCAAAATTTGAGCCCATCTCAACATTTTGGCAGTC 739

QY 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
 DB 740 CTTTACCAAGCACTACTTCTACTGTATGGCTGCAACCACTTCTGCAATTCAGAGGATCC 799

QY 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
 DB 800 ATGCTTGCTCTGGCCATGGTTAGTCTGAAATGAGAAACTCATTTCTGATGGCTTTCT 859

QY 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
 DB 860 CTTTACAATTGAACTGCTTTCAGAAAGCACAGATGATAGTCTCCAGTTGATCCATTTGTCGG 919

QY 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
 DB 920 GAGCTTGTGGCACATCACCTTTCTACTCTGAGTCTTCCCTGCTCTGAATTCGGTTTAT 979

QY 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
 DB 980 GTCTACCGTCCCTTCAGCACACCTTGTGTGACCTGTGACAAAGAGTGTTCAGATTACAT 1039

QY 281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
 DB 1040 CCCTCTCTGTCCAGGCCAGACTTCTCCAGGACAAACAGCAAGCCAGAGTGCAGTC 1099

QY 301 ArgGlyThrAlaAlaPheTyrHisLeuProAlaHisLeuProAlaHisLeuGlnThrSer 320
 DB 1100 AGAGGTACAGCAGCCTTTTACCATCATCTCCAGCTGCCAGTGGTGTGCAAGCAGACTCT 1159

QY 321 ThrLysArgLysValGluGluMetGluValAspAspPheTyrAspGlyIleLysArgLeu 340
 DB 1160 ACTAAGCCAAAGTAGGAAATGGAGTGGATGACTTCTATGATGGAATCAACGGCTC 1219

QY 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
 DB 1220 TATAATGAAGATAATGTCTCAGAAATGTGGTCTGTGTGTGGCACTGATTTATCAAGA 1279

QY 361 GlnGluGlyHisAlaSerProCysProLeuGlnProValSerValMet 377
 DB 1280 CAAGAGGAGCATGCTTCCCTTGTCCACCTTTGAGCCTGTTTCTGTGTCATG 1330

RESULT 8
 ABL87929
 ID ABL87929 standard; DNA; 1889 BP.
 AC ABL87929;
 XX
 XX 17-MAY-2002 (first entry)
 DT
 XX Human ovarian cancer related DNA clone SEQ ID NO:10907.
 DE
 XX Human; ovarian cancer; ovarian tumour; cytostatic; gene; ds.
 XX Homo sapiens.
 OS
 XX WO200192581-A2.
 PN
 XX
 PD 06-DEC-2001.
 XX
 XX 29-MAY-2001; 2001WO-US017756.
 PF
 XX
 XX 26-MAY-2000; 2000US-0207484P.
 PR
 XX (CORI-) CORIXA CORP.
 PA
 XX
 XX Algate PA, Harlocker SL, Jones R;
 PI
 XX WPI; 2002-122075/16.
 DR
 XX
 XX Composition for therapy and diagnosis of ovarian cancer comprising
 PT polypeptide of a ovarian tumor polypeptide, polynucleotide encoding
 PT polypeptide, antibody specific to polypeptide or T cell expressing
 PT polypeptide.
 XX
 PS Claim 1; SEQ ID NO 10907; 489pp; English.
 XX
 CC The present invention describes a composition (I) comprising: carriers

CC and immunostimulants; and a polypeptide (II) of a ovarian tumour
 CC polypeptide encoded by a polynucleotide (III) having a cDNA sequence (S1)
 CC from the 10912 nucleotide sequences as given in ABL77023 to ABL87934,
 CC (III) encoding (II) having a sequence (S2), a T cell population of (II),
 CC or antigen presenting cells that express (II). (I) has cytostatic
 CC activity. An oligonucleotide (IV) that hybridises to (S1) can be used for
 CC detecting ovarian cancer in a patient's biological sample preferably
 CC serum or ovarian tissue. The method comprises contacting a biological
 CC sample from a patient with (IV), detecting the amount of polynucleotide
 CC hybridising to (IV) and comparing the amount to a predetermined cutoff
 CC value and thereby detecting ovarian cancer in the patient, where the
 CC amount of polynucleotide hybridising to (IV) is detected preferably by
 CC polymerase chain reaction (PCR). (I) comprising (III) and/or (II) is
 CC useful for stimulating and/or expanding T cells specific for an ovarian
 CC tumour protein comprising contacting T cells with (III) or (II). (III) is
 CC useful in design and preparation of ribozyme molecules for inhibiting
 CC expression of the tumour polypeptides and proteins in tumour cells; and
 CC to isolate a full length gene from a suitable library e.g., a tumour cDNA
 CC library using well known techniques

XX
 SQ Sequence 1889 BP; 473 A; 501 C; 436 G; 479 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 3,62e-205 Length: 1889
 Score: 1962.00 Matches: 377
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-09-736-250-1 (1-377) x ABL87929 (1-1889)

Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle 20
 Db 544 ATGAAGTTTCAGGCGCTTCGAAACCCAGAGATTGCTTTCTCTGTGGAAAGGCAATC 603
 Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
 Db 604 ACTAGGGAAGCACAGATGTGAAAGTGAATGTGGGAAATGCGCTTCAATCAAGATGTT 663
 Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn 60
 Db 664 TCTCATCCAGAGAGATGAAGTAATTCATGCTGGCCAACTCAAGTACCAATTCAC 723
 Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
 Db 724 CTTTACCAGAAACATTGCTCTGCTAGCAGTCTTTTGGATAGGTTTTAGCTACCGTA 783
 Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaLys 100
 Db 784 AAGGCTCATCCAAATATCTGAGTTGTATTGCAATCAGCTGTTTTTCTAGCTGCCAAG 843
 Qy 101 ThrValGluAspGluArgGluProValLeuLysValLeuAlaArgAspSerPheCys 120
 Db 844 ACTGTTGAGGAAGATGAGAGAAATCCAGTACTAAGGTATTGGCAAGACAGATTTCTGT 903
 Qy 121 GlyCysSerSerGluIleLeuArgMetGluArgIleLeuLeuAspLysLeuAsnTrp 140
 Db 904 GGATGTTCTCATCTGAAATTTTGAAGATGAGAGAAATATTCTGGATGAATGGAATTGG 963
 Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
 Db 964 GATCTTCACAGGCACACCACTGGATTTCTTCATATTTTCCATGTCATGCGAGTGCA 1023
 Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
 Db 1024 ACTAGGCTCAGTACTTTTCAGTTTGGCCAAATGAGCCCACTCAACATTTGGCAGTC 1083
 Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
 Db 1084 CTTACCAAGCAACTACTTCACTGTATGCGCTGCAACCAACTTCTGCAATTCAGAGGATCC 1143
 Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuLeuProAspTrpLeuSer 220

Db 1144 ATGCTTCTCTGGCCATGGTTAGTCTGGAATGGAGAACTCATTTCTGATGGCTTTCT 1203
 Qy 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
 Db 1204 CTTACAAATGCACTGCTTCAGAAAGCACAGATGGATAGCTCCCGATGATCCATTGCGG 1263
 Qy 241 GluLeuValAlaHisHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
 Db 1264 GAGCTTGTGGCACATCACCTTTTACTCTGCAAGTCTTCCCTGCTGCTGAAATTCGGTTAT 1323
 Qy 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
 Db 1324 GTCTACCGTCCCTCAAGCACACCTGCTGACCTGTGCAAAAGAGGTTCAGATTACAT 1383
 Qy 281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
 Db 1384 CCCTCTCTCTCCAGGCCCCAGACTTCTCCAGGACAAACAGCAAGCCAGAGTCCAGTC 1443
 Qy 301 ArgGlyThrAlaAlaPheTyrHisHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
 Db 1444 AGAGGTACAGCAGCCTTTTACCATCATCTCCAGCTGCCAGTGGGTGCAAGCAGACCTCT 1503
 Qy 321 ThrLysArgLysValGluGluMetGluValAspAspPheTyrAspGlyIleLysArgLeu 340
 Db 1504 ACTAAACGCAAGTAGAGGAAATGGAAAGTGAGTACTTCTATGATGGAATCAAAACGGCTC 1563
 Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
 Db 1564 TATAATGAAGATAATGTCTCAGAAATGTGGTTCTGTGTGGCACTGATTATCAAGA 1623
 Qy 361 GlnGluGlyHisAlaSerProCysProLeuGlnProValSerValMet 377
 Db 1624 CAAGAGGAGCATGCTTCCCTTGTCCACCTTTGCGCCTGTTCTGTGTCTGTCATG 1674
 RESULT 9
 ADP10653
 ID ADP10653 standard; DNA; 1890 BP.
 XX
 AC ADP10653;
 XX
 DT 12-AUG-2004 (first entry)
 XX
 DE Reference mRNA sequences for marker probe #330.
 XX
 KW transplant rejection; immune system; rheumatoid arthritis; lupus;
 KW inflammatory bowel disease; multiple sclerosis; HIV; AIDS; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO2004042346-A2.
 XX
 XX 21-MAY-2004.
 XX
 PF 24-APR-2003; 2003WO-US012946.
 XX
 XX 24-APR-2002; 2002US-00131831.
 PR 20-DEC-2002; 2002US-00325899.
 XX
 XX (EXPR-) EXPRESSION DIAGNOSTICS INC.
 XX
 XX Wohlgenuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;
 PI Rosenberg S;
 PI
 XX WPI; 2004-400724/37.
 DR
 XX
 PT Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,
 PT pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
 PT rejection, in an individual, comprises detecting the expression level of
 PT the genes.
 XX
 PS Claim 80; SEQ ID NO 662; 1762pp; English.
 XX

CC The present invention relates to diagnosing or monitoring transplant
 CC rejection, e.g. cardiac or kidney transplant rejection, in an individual
 CC comprises detecting the expression level of one or more genes. The
 CC methods, system and kits are useful in diagnosing or monitoring
 CC transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
 CC islet, lung, bone marrow or stem cell transplant rejection,
 CC xenotransplant rejection or mechanical organ replacement rejection, in an
 CC individual. The method is also useful in assessing the immune status of
 CC an individual. The methods are also useful in diagnosing and monitoring
 CC diseases that involve the immune system, e.g. rheumatoid arthritis,
 CC lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
 CC viral, bacterial or fungal infection. The present sequence represents a
 CC mRNA reference sequence for a 50 mer oligonucleotide marker for diagnosis
 CC and monitoring of allograft rejection and other disorders.

XX
 SQ Sequence 1890 BP; 473 A; 501 C; 436 G; 480 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 3.62e-205 Length: 1890
 Score: 1962.00 Matches: 377
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 12 Gaps: 0

US-09-736-250-1 (1-377) x ADP10653 (1-1890)

Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle 20
 Db 545 ATGAAGTTTCAGGGCCCTTGGAAACACAGAGATTGCTTTTCCTGTTGGAAAGGCAATC 604
 Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
 Db 605 ACTAGGGAAGCACAGATGCGAAGTGAATGTCGGAAATGCTTCAATCAGATGTT 664
 Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn 60
 Db 665 TCTCCATCCAGAGAGATGAAGTAATTCATGCGTGGCCAACTCAAGTACCAATTCAAC 724
 Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
 Db 725 CTTTACCAGAAACATTTGCTGCTGGTAGCAGTCTTTTGGATAGATTTTATGCTACCGTA 784
 Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaAlaLys 100
 Db 785 AAGGCTCATCCAAATACTTTCAGTTGATTGCAATCAGCTGTTTTCCTAGCTGCCAAG 844
 Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
 Db 845 ACTGTTGAGGAAGATGAGAGAATTCAGTACTAAAGGTATTGGCAAGACAGATTCTGT 904
 Qy 121 GlyCysSerSerGluIleLeuArgMetGluArgIleLeuLeuAspLysLeuAsnTrp 140
 Db 905 GGATGTTCTCATCTGAATTTTGAAGATGAGAGAATTTCTGGATAAGTTGAAATGG 964
 Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
 Db 965 GATCTTCACAGCCACACACCATTTGATTTTCTTATATTTTCCATGCAATTCAGTGTCA 1024
 Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
 Db 1025 ACTAGGCTCAGTTACTTTTTCAGTTTGGCCAAATTTGAGCCCATCTCAACATTTGGCAGTC 1084
 Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
 Db 1085 CTTACCAAGCAACTACTTCACTGATGCTGCGCCGCAACCACTTCTGCAATTCAGAGATCC 1144
 Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
 Db 1145 ATGCTTGCTCTGGCCATGGTTAGTCTGGAATGAGAACTCAATTCCTGATTGCTTTCT 1204
 Qy 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuLeuIleHisCysArg 240

Db 1205 CTTACAATTGAACGTGCTTCAGAAAGACAGATGATGATGCTCCAGTTGATCCATTGTGG 1264
 Qy 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
 Db 1265 GAGCTTGTGGACATACCTTTTCTACCTGAGTCTTCCCTGCTCTGAAATCCGTTAT 1324
 Qy 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
 Db 1325 GTCTACCGTCCCTCAAGCACACCTGCTGACCTGTGCACAAAGGAGTGTTCAGATTACAT 1384
 Qy 281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
 Db 1385 CCTCTCTCTGTCAGGCGCCAGACTTCTCCAAAGACACACAGCAGCAGAGTGCAGTC 1444
 Qy 301 ArgGlyThrAlaAlaPheTyrHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
 Db 1445 AGAGTACAGAGCCTTTTACCATCATCTCCAGCTCCAGTGGGTGGTGCAGACACCTCT 1504
 Qy 321 ThrLysArgLysValGluGluMetGluValAspAspPheTyrAspGlyIleLysArgLeu 340
 Db 1505 ACTAAACGCAAGTAGAGGAAATGGAAGTGGATGACTTCTATGATGAATCAAACGGCTC 1564
 Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
 Db 1565 TATAATGAAGATAATGTCTCAGAAAATGTGGTTCGTGTGGCACTGATTATCAAGA 1624
 Qy 361 GlnGluGlyHisAlaSerProCysProLeuGlnProValSerValMet 377
 Db 1625 CAAGAGGACATGCTTCCCTTGTCCACCTTTCAGAGCTGTTCTCTGTCATG 1675

RESULT 10
 ACN38124
 ID ACN38124 standard; cdna; 1890 BP.
 XX
 AC ACN38124;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE Tumour-associated antigenic target (TAT) CDNA DNA324488, SEQ ID NO:1449.
 XX
 KW Tumour-associated antigenic target; TAT; human; overexpression; cancer;
 KW tumour; diagnosis; cell proliferative disorder; breast cancer;
 KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;
 KW central nervous system cancer; bladder cancer; pancreatic cancer;
 KW cervical cancer; melanoma; leukaemia; hybridisation probe;
 KW chromosome identification; chromosome mapping; gene mapping;
 KW gene therapy; cytostatic; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO2004030615-A2.
 XX
 PD 15-APR-2004.
 XX
 PF 29-SEP-2003; 2003WO-US028547.
 XX
 PR 02-OCT-2002; 2002US-0414971P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Wu TD, Zhang Z, Zhou Y;
 XX
 DR WPI; 2004-347921/32.
 XX
 DR P-PSDB; ABM80569.
 XX
 PT New tumor-associated antigenic target polypeptides and nucleic acids,
 PT useful in preparing a medicament for treating or detecting a
 PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or
 PT prostate cancer or tumor.
 XX
 PS Claim 1; SEQ ID NO 1449; 7273pp; English.
 XX
 CC The invention relates to human tumour-associated antigenic target (TAT)

polypeptides, and their related nucleic acids. The TAT polypeptides are overexpressed in cancer tissues compared to normal tissues, and may thus serve as effective targets for the diagnosis and treatment of cancer in mammals. The invention also relates to nucleic acid and polypeptide sequences at least 80% identical to the TAT nucleic acids and polypeptides; expression vectors and host cells comprising a TAT nucleic acid; an antibody specific for a TAT polypeptide; a peptide or organic molecule which binds to a TAT polypeptide; fusion proteins comprising a TAT polypeptide; and methods and compositions for the treatment or diagnosis of cancer in mammals. TAT polypeptides, nucleic acids, antibodies, antagonists, binding molecules and compositions are useful for diagnosing or treating a cell proliferative disorder associated with increased TAT expression, particularly cancers such as breast cancer, colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder cancer, pancreatic cancer, cervical cancer, cancers of the central nervous system, melanoma and leukemia. TAT nucleic acids may further be used as hybridisation probes, in chromosome and gene mapping, in chromosome identification and in gene therapy. The present sequence represents a TAT nucleic acid of the invention

XX SQ Sequence 1890 BP; 473 A; 501 C; 436 G; 480 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	3,62e-205	Length:	1890
Score:	1962.00	Matches:	377
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	13	Gaps:	0

US-09-736-250-1 (1-377) x ACN38124 (1-1890)

Qy	1	MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle	20
Db	545	ATGAAGTTTCAGGGCCCTTGGAAACACAGAGATTGCTTCTCTGTTGGAAAGCGCAATC	604
Qy	21	ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGluAsnVal	40
Db	605	ACTAGGGAAGCACAGATGCGAAAGTGAATGTGGGAAATGCCTTCAAAATCAGATGTT	664
Qy	41	SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyTrpGlnPheAsn	60
Db	665	TCCTCATCCAGAGATGAAGTAAATTCATGGCTGGCCAAACTCAAGTACCAATTCAAC	724
Qy	61	LeuTyTrpGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal	80
Db	725	CTTTACCCAGAAACATTTGCTCTGGTAGCAGTCTTTTGGATAGTATTAGCTACCGTA	784
Qy	81	LysAlaHisProLysTyTrpLeuSerCysIleAlaIleSerCysPhePheLeuAlaAlaLys	100
Db	785	AAGGCTCATCCAAAATATCTGAGTTGTATTGCAATCAGCTGTTTTTCTAGCTGCCAAG	844
Qy	101	ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys	120
Db	845	ACTGTGTAGGAAGATGAGAGAATTCAGTACTAAAGTATTGGCAAGACAGATTTCTGT	904
Qy	121	GlyCysSerSerGluIleLeuArgMetGluArgIleLeuAspLysLeuAsnTrp	140
Db	905	GGATGTTCTCATCTGAATTTTGGAAATGAGAGAATATTCTGGATGAATTTGAATGG	964
Qy	141	AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer	160
Db	965	GATCTTCACAGCCACACCATTTGATTTTCTCATATTTTCCATGTCATTCAGTGTCA	1024
Qy	161	ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal	180
Db	1025	ACTAGGCTCATGTTACTTTTCAAGTTGGCCCAAAATGAGCCCATCTCAACATTTGGCAGTC	1084
Qy	181	LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer	200
Db	1085	CTTACCAAGCAACTCTTCACTGTATGTCCTGCAACCAACTCTGCAATTCAGAGATCC	1144
Qy	201	MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer	220

Db	1145	ATGCTTCTCTGGCCATGGTTAGTCTGGAATGGAGAACTCATTTCTGATTGCTTTCT	1204
Qy	221	LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg	240
Db	1205	CTTACATTTGAACATGCTTTCAGAAAGCACAGATGATAGTCCCGATTGATTCATTCGCG	1264
Qy	241	GluLeuValAlaHisHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTy	260
Db	1265	GAGCTTGTGGCACATCACCTTTCTACTCTGCAGTCTTCCCTGCTCTGAAATTCGGTTAT	1324
Qy	261	ValTyArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis	280
Db	1325	GTCTACCGTCCCTTCAAGCACACCTGCTGACCTGTGACAAAGAGTGTTCAGATTACAT	1384
Qy	281	ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal	300
Db	1385	CCCTCTCTGTCGCCAGCCCGACAGCTTCTCCAGGACAAACAGCAGAGTCCAGTC	1444
Qy	301	ArgGlyThrAlaAlaPheTyTrpHisHisLeuProAlaAlaSerGlyCysLysGlnThrSer	320
Db	1445	AGAGGTACAGCAGCCTTTTACCATCATCTCCAGCTGCCAGTGGGTGCAAGCAGACCTCT	1504
Qy	321	ThrLysArgLysValGluGluMetGluValAspAspPheTyTrpAspGlyIleLysArgLeu	340
Db	1505	ACTAAACGCAAGTAGAGAAATGGAAATGGAGTGGATGACTTCTATGATGGAATCAAACGGCTC	1564
Qy	341	TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg	360
Db	1565	TATATGAAGTAAATGCTCAGAAATGTGGTCTGTGTGGCACTGATTATCAAGA	1624
Qy	361	GlnGlyHisAlaSerProCysProLeuGlnProValSerValMet	377
Db	1625	CAAGAGGACATGCTTCCCTTGTCCACCTTTGCGCTGTTCTGTCTGTCATG	1675

RESULT 11
ADL63374
ID ADL63374 standard; DNA; 2755 BP.
XX AC ADL63374;
XX AC ADL63374;
DT 20-MAY-2004 (first entry)
XX Human ovarian cancer DNA marker #21586.
DE Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
XX Homo sapiens.
OS WO200170979-A2.
XX PD 27-SEP-2001.
XX PF 21-MAR-2001; 2001WO-US009126.
XX PR 21-MAR-2000; 2000US-0191031P.
XX PR 25-MAY-2000; 2000US-0207124P.
XX PR 15-JUN-2000; 2000US-0211940P.
XX PR 07-JUL-2000; 2000US-0216820P.
XX PR 25-JUL-2000; 2000US-0220661P.
XX PR 21-DEC-2000; 2000US-0257672P.
XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX PI Lee J, Lillie J;
XX WPI; 2001-611502/70.
XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian cancer cells as compared to their normal non-cancerous ovarian cells are used to characterize stage, grade, histological type of ovarian cancer.
XX Disclosure; SEQ ID NO 21586; 106pp; English.
PS

XX The invention relates to nucleic acid markers which are overexpressed in
 CC ovarian cancer cells as compared to their expression in normal (i.e. non-
 CC cancerous) ovarian cells. The invention also relates to polypeptides
 CC encoded by the markers, antibodies that selectively bind to the
 CC polypeptides, a method of inhibiting ovarian cancer in a patient at risk
 CC of developing ovarian cancer involving inhibiting expression of a gene
 CC corresponding to a marker of the invention and a method of treating a
 CC patient afflicted with ovarian cancer comprising providing to cells of
 CC the patient an antisense oligonucleotide complementary to a marker of the
 CC invention. The markers are useful for assessing if a patient is afflicted
 CC with ovarian cancer, which involves comparing the level of expression of
 CC a marker in a patient sample and a normal level of expression of the
 CC marker in a control non-ovarian cancer sample. A difference between the
 CC expression levels indicates ovarian cancer. The level of expression of a
 CC marker corresponds to a secreted protein or to a transcribed
 CC polynucleotide or its portion. The level of expression of the marker is
 CC assessed by detecting the presence in the sample, a protein or protein
 CC fragment corresponding to the marker. The presence of protein or protein
 CC fragment is detected using an antibody that specifically binds with the
 CC protein or protein fragment. Alternatively, the level of expression of
 CC the marker is assessed by detecting the presence of a transcribed
 CC polynucleotide which anneals with the marker or anneals with a portion of
 CC the polynucleotide comprising the marker, under stringent conditions. The
 CC marker is also used for monitoring the progression of ovarian cancer in a
 CC patient which involves detecting expression of the marker in a patient
 CC sample at a first point in time, repeating the method at a subsequent
 CC time and comparing the level of expression. The method is carried out
 CC using an ovarian tissue sample. A composition comprising a marker,
 CC polypeptide or antibody of the invention is used to treat ovarian cancer.
 CC This sequence represents a human ovarian cancer DNA marker of the
 CC invention.

XX SQ Sequence 2755 BP; 749 A; 673 C; 606 G; 727 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.36e-191 Length: 2755
 Score: 1841.00 Matches: 358
 Percent Similarity: 94.96% Conservative: 0
 Best Local Similarity: 94.96% Mismatches: 1
 Query Match: 93.83% Indels: 18
 DB: 5 Gaps: 1

US-09-736-250-1 (1-377) x ADL63374 (1-2755)

Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuGluLysAlaIle 20
 Db 847 ATGAAGTTTCCAGGCGCTTTGGAAACCAGAGATTGCTTTCTCTGGTGGAAAGGCAATC 906
 Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
 Db 907 ACTAGGGAAGCACAGATGTGGAAAGTGAATGTGGGAAATGCCCTTCAATCAGATGTT 966
 Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn 60
 Db 967 TCTCCATCCAGAGAGATGAAGTAATTCATATGGCTGGCCAACTCAAGTACCAATTCAC 1026
 Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
 Db 1027 CTTTACCAGAAACATTTGCTCTGGCTAGCAGTCTTTGGATAGGTTTATAGCTACCGTA 1086
 Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaLys 100
 Db 1087 AAGGCTCATCT----- 1098
 Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
 Db 1099 -----GAGGAAGATGAGAGATTCAGTACTAAAGGATTATGGCAAGAGACAGTTTCTGT 1152
 Qy 121 GlyCysSerSerGluLeuArgMetGluArgIleLeuLeuAspLysLeuAsnTrp 140
 Db 1153 GGATGTTCTCATCTGAAATTTGAGAAATGAGAGAAATTTCTGGATAAGTTGAATGG 1212

Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
 Db 1213 GATCTTCACAGCCACACCATTTGGATTTTCTTCATATTTCCATGCAATGCAGTGCA 1272
 Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
 Db 1273 ACTAGGCTCAGTTACTTTTCAGTTTGGCCAAATAGAGCCACTCTCAACATTTGGCAGTC 1332
 Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
 Db 1333 CTTACCAAGCACTACTTCACTGTATGGCTGCAACCACTTCTGCAATTCAGAGGATCC 1392
 Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
 Db 1393 ATGCTTGTCTGGCCATGGTTAGTCTGGAATGGAGAACTCATCTCTGATGGCTTTCT 1452
 Qy 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuLeuHisCysArg 240
 Db 1453 CTTTACCAATTCAGTCTTCAGAAAGCACAGATGATAGCTCCAGATTTGATCCATTTGTCGG 1512
 Qy 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
 Db 1513 GAGCTTGTGGCAGCATCACCTTTCTACTCTCAGTCTTCCCTGCTCTGAATTCGGTTAT 1572
 Qy 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
 Db 1573 GTCTACCGTCCCTCAAGCACACCTGGTGACCTGTGACAAAGAGAGTGTTCAGATTACAT 1632
 Qy 281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
 Db 1633 CCCTCTCTCTGCCAGGCCAGACTTCTCCAGGACAAACAGCAAGCCAGAGTGCACAGTC 1692
 Qy 301 ArgGlyThrAlaAlaPheTyrHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
 Db 1693 AGAGGTACAGAGCGCTTTTACCATCATCTCCAGCTGCCAGTGGGTGCAAGCAGACCTCT 1752
 Qy 321 ThrLysArgLysValGluGluMetGluValAspAspPheTyrAspGlyIleLysArgLeu 340
 Db 1753 ACTAAAGCAAGATAGAGGAAATGGAATGGATGATGACTTCTATGATGGAATCAACGGCTC 1812
 Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
 Db 1813 TATAATGAGATAATGTCTCAGAAATGTGGGTCTGTGTGTGGCACTGATTTATCAAGA 1872
 Qy 361 GlnGluGlyHisAlaSerProCysProProLeuGlnProValSerValMet 377
 Db 1873 CAAGAGGAGATGCTTCCCTTGTCTACCTTTCAGCGCTGTTTCTGTCAAG 1923
 RESULT 12
 AAD57247
 ID AAD57247 standard; cDNA; 1651 BP.
 XX
 AC AAD57247;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DE Human CGDD-27 cDNA.
 XX
 KW Human; cell growth, differentiation and death protein; CGDD; leukaemia;
 KW neurodegenerative disorder; Parkinson's disease; Alzheimer's disease;
 KW muscular disorder; myotonic dystrophy; catatonia; endocrine disorder;
 KW diabetes; Grave's disease; cancer; immunological disorder; scleroderma;
 KW systemic lupus erythematosus; allergy; Crohn's disease; renal disorder;
 KW gastrointestinal disorder; Goodpasture's syndrome; infection; cirrhosis;
 KW cardiovascular disorder; atherosclerosis; hepatic disease; transgenic;
 KW transgenic animal; gene therapy; neuroprotective; relaxant; cytosolic;
 KW dermatological; immunosuppressive; cerebroprotective; anticonvulsant;
 KW antibacterial; antiparasitic; fungicide; virucide; uropathic; cardiant;
 KW protozoacide; nootropic; gene; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers

FT CDS 184. .1188
 FT /*tag= a
 FT /product= "Human CGDD-27 protein"
 XX
 XX
 PN WO2003050253-A2.
 XX
 XX 19-JUN-2003.
 XX
 XX 04-DEC-2002; 2002WO-US039133.
 XX
 XX 07-DEC-2001; 2001US-0340747P.
 PR 20-DEC-2001; 2001US-0342761P.
 PR 15-JAN-2002; 2002US-0349705P.
 PR 06-FEB-2002; 2002US-0354764P.
 PR 12-FEB-2002; 2002US-0356216P.
 XX
 XX (INCY-) INCYTE GENOMICS INC.
 XX
 XX Griffin JA, Ramkumar J, Emerling BM, Kable AE, Elliott VS;
 PI Marquis JP, Baughn MR, Gorvad AE, Yue H, Lee EA, Becha SD, Tang YT;
 PI Tran UK, Swarnakar A, Lee S, Ison CH, Hafalia AJA, Tran B;
 PI Sprague WM, Lee SY, Khare R, Gandhi AR, Gietzen KJ, Bhatia U;
 PI Burrill JD, Blake JJ, Ho A, Zheng W;
 XX
 XX WPI; 2003-532903/50.
 DR P-PSDB; AAE37938.
 XX
 XX New CGDD polypeptides, useful for diagnosing, preventing, and treating
 PT disorders associated with an abnormal expression or activity of CGDD,
 PT e.g. neuromuscular, immunological, cardiovascular disorders, cancer
 PT and/or infections.
 XX
 XX Claim 5; Page 291; 299pp; English.
 XX
 XX The present invention relates to novel cell growth, differentiation and
 CC death (CGDD) proteins and polynucleotides encoding them. The sequences of
 CC the invention are useful in diagnosing, preventing and treating disorders
 CC associated with an abnormal expression or activity of CGDD such as
 CC neurodegenerative disorders (e.g. Parkinson's disease, Alzheimer's
 CC disease), muscular disorders (e.g. myotonic dystrophy, catatonial),
 CC endocrine disorders (e.g. diabetes, Grave's disease), cancers (e.g.
 CC leukaemia, cervical or breast cancers), immunological disorders (e.g.
 CC scleroderma, systemic lupus erythematosus, allergies), gastrointestinal
 CC disorders (e.g. Crohn's disease), renal disorders (e.g. Goodpasture's
 CC syndrome), infections (e.g. viral, bacterial, fungal, parasitic,
 CC protozoal, helminthic), cardiovascular disorders (e.g. atherosclerosis)
 CC and hepatic diseases (e.g. cirrhosis). The polynucleotides can be used to
 CC create humanised animals or transgenic animals to model human diseases.
 CC The invention is also used in gene therapy. The present sequence is human
 CC CGDD-27 cDNA
 XX
 XX SQ Sequence 1651 BP; 447 A; 370 C; 373 G; 431 T; 0 U; 30 Other;
 Alignment Scores:
 Pred. No.: 6.64e-178 Length: 1651
 Score: 1713.50 Matches: 334
 Percent Similarity: 88.59% Conservative: 0
 Best Local Similarity: 88.59% Mismatches: 0
 Query Match: 87.33% Indels: 43
 DB: 9 Gaps: 1
 US-09-736-250-1 (1-377) x AAD57247 (1-1651)
 QY 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle 20
 DB 184 ATGAGTTTCACGGCCCTTGGAAAACAGAGATTGCTTCTTCCTGTTGGAAAAGCCATC 243
 QY 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
 DB 244 ACTAGGGAAGCACAGATGTGGAAGTGAATGTGCGAAAATGCGCTTCAATCAG----- 297
 QY 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn 60
 297 ----- 297
 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
 297 ----- 297
 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaLys 100
 298 ---GCTCATCAAAATACCTTGAGTTGATTGCAATCAGCTGTTTTTCTAGTCGCAAG 354
 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
 355 ACTGTTGAGGAGAGATGAGAGATTCAGTACTAAAGGTATTGGCAAGACAGACAGTTCTGT 414
 121 GlyCysSerSerGluIleLeuArgMetGluArgIleLeuLeuAspLysLeuAsnTrp 140
 415 GGATGTTCTCTCATCTGAAATTTTGAGAAATGAGAGAAATATTCTGGATAAGTTGAAATTGG 474
 141 AspLeuHisThrAlaThrProLeuAspPheIleHisIlePheHisAlaIleAlaValSer 160
 475 GATCTTCACACAGCCACCATTTGGATTTTCTTCATATTTTCCATGCAATTCAGAGTGTCA 534
 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
 535 ACTAGGCTCAGTTACTTTTTCAGTTTCCCAATTTGAGCCCATCTCAACATTTGGCAGTC 594
 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgLys 200
 595 CTTACCAAGCAACTACTTCACTGTATGCGCTGCAACCAACTTCTGCAATTCAGAGGATCC 654
 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
 655 ATGCTTGTCTCTGGCCATGGTTAGTCTGGAATGGAGAACTCATCTCTGATTTGCTTTCT 714
 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
 715 CTTACAATTGACTGCTTCAGAAAGCACAGATGGATAGTCTCCAGTGTATTCATTTGCGG 774
 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
 775 GAGCTTGTGGCACATCACTTTTCTACTCTGCAGTCTTCCCTGCTCTGAAATTCGTTTAT 834
 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
 835 GTCTACCGTCCCTCAAGCACACCTGCTGACCTGTGCAAAAGAGAGTGTTCAGATTACAT 894
 281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
 895 CCTCTCTGTCCAGGCCCCAGACTTCTCCAGGACCAACAGCAAGCCAGAAAGTCCAGTC 954
 301 ArgGlyThrAlaPheTyrHisHisLeuProAlaLeuAlaSerGlyCysLysGlnThrSer 320
 955 AGAGGTACAGCAGCCTTTTACCATCATCTCCAGCTGCCAGTGGGTGGCAAGCAGACCTCT 1014
 321 ThrLysArgLysValGluGluMetGluValAspAspPheTyrAspGlyIleLysArgLeu 340
 1015 ACTAAACGCAAGTAGAGGAAATGGAAGTGGATGACTTCTATGATGGAATCAAAAGCGCTC 1074
 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
 1075 TATATGAGATATATGCTCAGAAAATGTGGTCTGTGTGTGGCATGATTTATCAAGA 1134
 361 GlnGluGlyHisAlaSerProCysProLeuGlnProValSerValMet 377
 1135 CAAGAGGAGCATGCTTCCCTTGTCCACCTTTGAGCCTGTTTCTGTCTCATG 1185
 RESULT 13
 ADN01156
 ID ADN01156 standard; DNA; 903 BP.
 XX
 AC ADN01156;
 XX DT 01-JUL-2004 (first entry)

XX DE Human cell growth, differentiation, and death-associated coding seq #15.
 XX KW human; cell growth; cell differentiation; cell death; CGDD;
 KW cell proliferative disorder; arteriosclerosis; atherosclerosis; bursitis;
 KW cirrhosis; hepatitis; polycythaemia vera; psoriasis; cancer;
 KW neurological disorder; Cushing's syndrome; hypothyroidism;
 KW Pick's disease; Huntington's disease; Parkinson's disease;
 KW multiple sclerosis; autoimmune disorder; inflammatory disorder; AIDS;
 KW allergy; anaemia; asthma; contact dermatitis; diabetes mellitus;
 KW reproductive disorder; infertility; endometriosis; uterine fibroid; gene;
 XX OS ds.
 XX OS Homo sapiens.
 XX PN WO2004031364-A2.
 XX PD 15-APR-2004.
 XX PF 03-OCT-2003; 2003WO-US031441.
 XX PR 03-OCT-2002; 2002US-0416205P.
 XX PR 25-OCT-2002; 2002US-0421521P.
 XX PR 21-NOV-2002; 2002US-0428376P.
 XX PR 23-DEC-2002; 2002US-0436258P.
 XX PR 10-JAN-2003; 2003US-0439292P.
 XX PR 13-FEB-2003; 2003US-0447578P.
 XX PA (INCY-) INCYTE CORP.
 XX PA (BURL) BURLILL J D.
 XX PI Elliott VS, Swarnakar A, Tang YT, Yue H, Lu DAM, Khare R;
 PI Chawla NK, Richardson TW, Marquis JP, Lal PG, Nguyen DB, Lee SY;
 PI Tran UK, Bhatia UG, Lee S, Blake JJ, Ho A, Zheng W, Gao J, Tran B;
 PI Yang YG, Gietzen KJ, Hatfield AJA;
 XX WPI, 2004-330172/30.
 XX P-PSDB; ADN01131.
 XX New isolated polypeptides associated with cell growth, differentiation
 PT and death, useful for diagnosing, treating or preventing e.g.
 PT atherosclerosis, psoriasis, cancers, Alzheimer's disease, AIDS, anaemia,
 PT diabetes mellitus or infertility.
 XX Claim 5; SEQ ID NO 40; 213pp; English.
 XX The invention comprises the amino acid and coding sequences of human
 CC proteins that are associated with cell growth, differentiation, and death
 CC (CGDD). The DNA and protein sequences of the invention are useful for
 CC diagnosing, treating or preventing disorders associated with aberrant
 CC expression of CGDD, such as: cell proliferative disorders (e.g.
 CC arteriosclerosis, atherosclerosis, bursitis, cirrhosis, hepatitis,
 CC polycythaemia vera, psoriasis and cancers), developmental disorders (e.g.
 CC Cushing's syndrome and hypothyroidism), neurological disorders (e.g.
 CC epilepsy, stroke, Alzheimer's disease, Pick's disease, Huntington's
 CC disease, Parkinson's disease and multiple sclerosis),
 CC autoimmune/inflammatory disorders (e.g. AIDS, allergies, anaemia, asthma,
 CC contact dermatitis and diabetes mellitus), and reproductive disorders
 CC (e.g. infertility, endometriosis and uterine fibroid). The present DNA
 CC sequence encodes a human CGDD-associated protein of the invention.
 XX SQ Sequence 903 BP; 247 A; 202 C; 201 G; 253 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 4,64e-158 Length: 903
 Score: 1529.50 Matches: 300
 Percent Similarity: 79.58% Conservative: 0
 Best Local Similarity: 79.58% Mismatches: 0
 Query Match: 77.96% Indels: 77
 DB: 12 Gaps: 1

US-09-736-250-1 (1-377) x ADN01156 (1-903)

QY 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle 20
 DB 2 ATGAAGTTCCTCCAGGCGCTTTGGAAACACAGAGATTGCTTCTCTCTGTTGGAAGGCAATC 61
 QY 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
 DB 62 ACTAGGGAAGCACAGATGTGGAAGTGAATGTGCGGAAATGCTTCAATCAAGATGTT 121
 QY 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn 60
 DB 122 TCTCCATCCAGAGAGATGAAGTAATCAATGGCTGCCAACTCAAGTACCAATCAAC 181
 QY 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
 DB 182 CTTTACCCAGAAACATTGCTCTGGCTAGCAGCTTTTGGATAGGTTTTTAGCTACCGTA 241
 QY 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaLys 100
 DB 242 AAGGCTCATCCAAATACTTGAATTTGAGATGAGAGAAATTATTCTGGATAGTGAATTGG 301
 QY 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
 DB 302 ACTGTTGAGGAAGATGAGAGAAATCCAGTACTTAAGTATTGCAAGACACAGTTCGT 361
 QY 121 GlyCysSerSerGluIleLeuArgMetGluArgIleIleLeuAspLysLeuAsnTrp 140
 DB 362 GGATGTTCTCACTGAAATTTTGAATGAGAGAAATTATTCTGGATAGTGAATTGG 421
 QY 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
 DB 422 GATCTTACACAGACACACCAATTTGGATTTCTTCATATT----- 460
 QY 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
 DB 460 ----- 460
 QY 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
 DB 460 ----- 460
 QY 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
 DB 460 ----- 460
 QY 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
 DB 461 -----ATGGATAGCTCCAGTTCCTGATCCATTGTCGG 490
 QY 241 GluLeuValAlaHisHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
 DB 491 GAGCTTGTGGCACATCACCTTTCTACTCTGCAGTCTTCCCTGCTCTGAATTCGGTTAT 550
 QY 261 ValTyrArgProLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
 DB 551 GTCTACCGTCCCTCAAGCACACCTGGTACCTGTGACAAAGAGAGTTCAGATTACAT 610
 QY 281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
 DB 611 CCTCTCTCTGTCAGAGCCAGACTTCTCCAGGACAAACAGCAGAGTCCAGTC 670
 QY 301 ArgGlyThrAlaAlaPheTyrHisHisLeuProAlaIleSerGlyCysLysGlnThrSer 320
 DB 671 AGAGGTACAGCAGCCTTTTACCATCATCTCCAGCTGCCAGTGGGTGCCAGCACCTCT 730
 QY 321 ThrLysArgLysValGluGluMetGluValAspAspPheTyrAspGlyValLeuArgLeu 340
 DB 731 ACTAACGCAAGATGAGGAAATGGAAGTGGATGAGTCTTATGATGTAATCAACAGCGTC 790
 QY 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
 DB 791 TATAATGAAGATATGCTCAGAAAATGTGGTCTCTGTGTGGCACTGATTTATCAAGA 850

Qy 361 GlnGluGlyHisAlaSerProCysProLeuGlnProValSerValMet 377
Db 851 CAAGAGGACATGCTCCCTTGTCCACCTTTGCGAGCTGTTCTGTCATG 901

RESULT 14

ADL63082
ID ADL63082 standard; DNA; 2146 BP.

AC ADL63082;

XX 20-MAY-2004 (first entry)

XX Human ovarian cancer DNA marker #21294.

XX Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.

XX Homo sapiens.

XX WO200170979-A2.

XX 27-SEP-2001.

XX 21-MAR-2001; 2001WO-US009126.

XX 21-MAR-2000; 2000US-0191031P.

XX 25-MAY-2000; 2000US-0207124P.

XX 15-JUN-2000; 2000US-0211940P.

XX 07-JUL-2000; 2000US-0216820P.

XX 25-JUL-2000; 2000US-0220661P.

XX 21-DEC-2000; 2000US-0257672P.

XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX Lee J, Lillie J;

XX WPI; 2001-611502/70.

XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian cancer cells as compared to their normal non-cancerous ovarian cells are used to characterize stage, grade, histological type of ovarian cancer.

XX Disclosure; SEQ ID NO 21294; 106pp; English.

XX The invention relates to nucleic acid markers which are overexpressed in ovarian cancer cells as compared to their expression in normal (i.e. non-cancerous) ovarian cells. The invention also relates to polypeptides encoded by the markers, antibodies that selectively bind to the polypeptides, a method of inhibiting ovarian cancer in a patient at risk of developing ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a patient afflicted with ovarian cancer comprising providing to cells of the patient an antisense oligonucleotide complementary to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer, which involves comparing the level of expression of a marker in a patient sample and a normal level of expression of the marker in a control non-ovarian cancer sample. A difference between the expression levels indicates ovarian cancer. The level of expression of a marker corresponds to a secreted protein or to a transcribed polynucleotide or its portion. The level of expression of the marker is assessed by detecting the presence in the sample, a protein or protein fragment corresponding to the marker. The presence of protein or protein fragment is detected using an antibody that specifically binds with the protein or protein fragment. Alternatively, the level of expression of the marker is assessed by detecting the presence of a transcribed polynucleotide which anneals with the marker or anneals with a portion of the polynucleotide comprising the marker, under stringent conditions. The marker is also used for monitoring the progression of ovarian cancer in a patient which involves detecting expression of the marker in a patient sample at a first point in time, repeating the method at a subsequent time and comparing the level of expression. The method is carried out using an ovarian tissue sample. A composition comprising a marker, polypeptide or antibody of the invention is used to treat ovarian cancer. This sequence represents a human ovarian cancer DNA marker of the

CC invention.
XX
SQ Sequence 2146 BP; 662 A; 392 C; 432 G; 660 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6.38e-74 Length: 2146
Score: 770.50 Matches: 154
Percent Similarity: 91.18% Conservative: 1
Best Local Similarity: 90.59% Mismatches: 12
Query Match: 39.27% Indels: 3
DB: 5 Gaps: 1

US-09-736-250-1 (1-377) x ADL63082 (1-2146)

Qy 210 GluMetGlnLysLeuIleProAspTrpLeuSerLeuThrIleGluLeuLysGlnLysAla 229
Db 815 GAGCAGCCTATGTTAAATTAATGATCAACTGTGTGGCTTTT---TTTTTTTCTCGCC 871
Qy 230 GlnMetAspSerSerGlnLeuIleHisCysArgGluLeuValAlaHisLeuSerThr 249
Db 872 CAGATGGATAGCTCCCGAGTTGATCCATTGTGCGGAGCTTGTGGCAGCATCCTTTCTACT 931
Qy 250 LeuGlnSerSerLeuProLeuAsnSerValTyArgProLeuLysHisThrLeu 269
Db 932 CTGCAGTCTTCCCTGCCCTCTGAATTCGTTTATGTCTACCTCCCTCAAGCACACCTG 991
Qy 270 ValThrCysAspLysGlyValPheArgLeuHisProSerSerValProGlyProAspPhe 289
Db 992 GTGACCTGTGACAAAGGAGTGTTCAGATTACATCCCTCTCTGTCCAGGCCAGACTTC 1051
Qy 290 SerLysAspAsnSerLysProGluValProValArgGlyThrAlaAlaPheTyHisHis 309
Db 1052 TCCAAGGACAAACAGCAAGCCAGAGTGCAGAGTACAGCAGCTTTTATACCATCAT 1111
Qy 310 LeuProAlaAla-SerGlyCysLysGlnThrSer-ThrLysArgLysValGluGluMetG 329
Db 1112 CTCCAGCTCCAGTGGGGTGCAGAGCCTCTTACTAAACGCAAGTAGAGGAATGG 1171
Qy 329 luValAspAspPheTyArgGlyIleLysArgLeuTyArgGluAsnValSerGluA 349
Db 1172 AAGTGGATGACTTCTATGATGGAATCAACGGCTCTATATAGATAATGTCTCAGAA 1231
Qy 349 snValGlySerValCysGlyThrAspLeuSerArgGlnGluGlyHisAlaSerProCysP 369
Db 1232 ATGTGGGTTCTGTGTGGCAGCTGATTATCAAGACAAGAGGAGCATGCTTCCCTTTGTC 1291
Qy 369 roProLeuGlnProValSerValMet 377
Db 1292 CACCTTTGAGCCTGTTTCTGTGTCATG 1317

RESULT 15
AAAX4003/c
ID AAAX4003 standard; DNA; 804 BP.
XX
AC AAAX4003;
XX
DT 02-JUL-1999 (first entry)
XX
DE Prostate cancer associated gene.
XX
KW Cancer associated antigen; diagnosis; research; treatment; human;
KW breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer;
KW prostate cancer; ss.
XX
OS Homo sapiens.
XX
PN WO9904265-A2.
XX
PD 28-JAN-1999.
XX
PF 15-JUL-1998; 98WO-US014679.
XX
PR 17-JUL-1997; 97US-00896164.

```
PR 10-OCT-1997; 97US-0061599P.
PR 10-OCT-1997; 97US-0061765P.
PR 10-OCT-1997; 97US-00948705.
PR 11-OCT-1997; 97GB-00021697.
PR 22-JUN-1998; 98US-00102322.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
XX
XX Old LJ, Scanlan MJ, Stockert E, Gure A, Chen Y, Gout I;
XX O'hare M, Obata Y, Pfreundschuh M, Tureci O, Sahin U;
XX WPI; 1999-132448/11.
XX
XX New isolated cancer associated nucleic acids and polypeptides - isolated
XX using sera from cancer patients, used to develop products for the
XX diagnosis, monitoring or treatment of cancers.
XX
XX Claim 67; Page 630; 787pp; English.
XX
XX The invention relates to a method for diagnosing a disorder characterised
XX by expression of a human cancer associated antigen precursor coded for by
XX a nucleic acid molecule (NAM). The method comprises: (a) contacting a
XX biological sample isolated from a subject with an agent that specifically
XX binds to the NAM, an expression product or a fragment of an expression
XX product complexed with an HLA molecule; and (b) determining the
XX interaction between the agent and the NAM or the expression product as a
XX determination of the disorder. The products and methods can be used in
XX the diagnosis, monitoring, research, or treatment of conditions
XX characterised by the expression of various cancer associated antigens.
XX The invention provides nucleic acid sequences and encoded polypeptides
XX which are cancer associated antigen precursors expressed in human breast
XX cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and
XX lung cancer
XX
XX SQ Sequence 804 BP; 208 A; 172 C; 188 G; 222 T; 0 U; 14 Other;
```

Alignment Scores:

```
Pred. No.: 9.18e-74 Length: 804
Score: 763.00 Matches: 161
Percent Similarity: 94.25% Conservative: 3
Best Local Similarity: 92.53% Mismatches: 7
Query Match: 38.89% Indels: 5
DB: 2 Gaps: 0
```

US-09-736-250-1 (1-377) x AAX40003 (1-804)

```
Qy 207 ValSerLeuGluMetGluLeu-1lePro-AspTpo-LeuSerLeuThrIleGluLeu 225
Db 710 GTTAGCTGAAAATGGANGAACTCCATTCCNGGATGGGCTTCTCTTACAAATTGANCTG 651
Qy 226 LeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArgGluLeuValAlaHis 245
Db 650 CTTCAGAAAGC-CAGATGNATAGTCCAGTTGATCCATGTCGGAAGCTTGG-GCACAT 593
Qy 246 HisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyrValTyrArgProLeu 265
Db 592 CACCTTTNTACTCTGCAGCTCTCCCTGCTGCTGAATTCGGTTATGTCTACCGTCCGCTC 533
Qy 266 LysHisThrLeuValThrCysAspLysGlyValPheArgLeuHisProSerSerValPro 285
Db 532 AAGCACACCCCTGGTGACCTGTGCAAAAGGAGTGTTTCAGATTACATCCCTCTCTGTCCCA 473
Qy 286 GlyProAspPheSerLysAspAsnSerLysProGluValProValArgGlyThrAlaAla 305
Db 472 GGCCACAGACTTCTCCAGGACAACAGCAAGCCAGAGTGCCAGTCAGAGGTACAGCAGCC 413
Qy 306 PheTyrHisHisLeuProAlaAlaSerGlyCysLysGlnThrSerThrLysArgLysVal 325
Db 412 TTTTACCATCATCTCCAGCTGCCAGTGGGTGCAAGCAGACCTCTACTAAACGCAAAAGTA 353
Qy 326 GluGluMetGluValAspAspPheTyrAspGlyIleLysArgLeuTyrAsnGluAspAsn 345
Db 352 GAGGAATGGGAATGGATGACTTTCTATGATGAATCAACCGCTCTATATGAAGATAAT 293
```

```
Qy 346 ValSerGluAsnValGlySerValCysGlyThrAspLeuSerArgGlnGluGlyHisAla 365
Db 292 GTCTCAGAAAATGTGGGTTCTGTGTGTGGCACTGATTTATCAAGACAAGAGGACATGCT 233
Qy 366 SerProCysProProLeuGlnProValSerValMet 377
Db 232 TCCCCCTTGTCCACCTTTGCAGCCCTGTTTCTGTGTCATG 197
```

Search completed: February 11, 2005, 03:41:45
Job time : 964.767 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 11, 2005, 03:24:00 ; Search time 301.793 Seconds
(without alignments)
2044.039 Million cell updates/sec

Title: US-09-736-250-1
Perfect score: 1962
Sequence: 1 MKPFGPLENQLRSLLEKAI.....LSRQGHASCPPLQPVSM 377

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO.spool/US09736250/runat 07022005 154924 20422/app query.fasta_1.718
-DB=Issued Patents NA -QWTF=fastap -SUFFIX=rni -MINMATCH=0.1 -LOEPCI=0
-LOEPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pco -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09736250.cgn 1 1 93 @runat 07022005 154924 20422 -NCPU=6 -ICPU=3
-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/ina/FACTUS.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				
Result No.	Score	Query Match	Length DB ID	Description
1	1962	100.0	1133	3 US-09-054-492B-2
2	1962	100.0	1260	2 US-08-969-106-5
3	1962	100.0	1260	4 US-09-338-125-5
4	1962	100.0	1260	4 US-09-023-655-899
5	748	38.1	444	4 US-09-513-998C-1907
6	326.5	16.6	1410	4 US-09-023-655-913
7	326.5	16.6	2039	4 US-09-949-016-1852
8	271.5	13.8	1576	4 US-09-949-016-4342
9	271.5	13.8	1578	4 US-09-949-016-578
10	271.5	13.8	1602	4 US-09-023-655-912
11	269.5	13.7	2212	4 US-09-023-655-948
12	204	10.4	1214	2 US-09-092-770-7

13	204	10.4	1214	3	US-09-222-851-7	Sequence 7, Appli
14	204	10.4	1215	2	US-09-092-770-1	Sequence 1, Appli
15	204	10.4	1215	3	US-09-222-851-1	Sequence 1, Appli
16	204	10.4	2637	4	US-09-949-016-5313	Sequence 5313, Ap
17	202	10.3	1212	2	US-09-092-770-2	Sequence 2, Appli
18	202	10.3	1212	2	US-09-092-770-17	Sequence 17, Appli
19	202	10.3	1212	3	US-09-222-851-2	Sequence 17, Appli
20	202	10.3	1212	3	US-09-222-851-17	Sequence 17, Appli
21	196	10.0	13424	4	US-09-949-016-13594	Sequence 13594, A
22	193	9.8	1414	4	US-09-404-296B-9	Sequence 9, Appli
23	188.5	9.6	1679	4	US-09-404-296B-3	Sequence 3, Appli
24	188	9.6	1680	1	US-08-706-539-1	Sequence 1, Appli
25	188	9.6	1680	1	US-08-522-166-1	Sequence 1, Appli
26	188	9.6	1680	1	US-08-488-382A-1	Sequence 1, Appli
27	188	9.6	1680	1	US-08-385-142-1	Sequence 1, Appli
28	188	9.6	1680	2	US-08-480-912-1	Sequence 1, Appli
29	188	9.6	1680	3	US-09-027-007-1	Sequence 1, Appli
30	188	9.6	1680	4	US-09-023-655-1049	Sequence 1049, Ap
31	188	9.6	1692	1	US-08-485-859-1	Sequence 1, Appli
32	187.5	9.6	1101	3	US-08-895-707-5	Sequence 5, Appli
33	187.5	9.6	1158	3	US-08-895-707-8	Sequence 8, Appli
34	187.5	9.6	1179	1	US-08-706-539-3	Sequence 3, Appli
35	187.5	9.6	1179	3	US-09-027-007-3	Sequence 3, Appli
36	187.5	9.6	1188	1	US-08-706-539-2	Sequence 2, Appli
37	187.5	9.6	1188	3	US-09-027-007-2	Sequence 2, Appli
38	183	9.3	304	4	US-09-513-998C-29894	Sequence 29894, A
39	176	9.0	1951	3	US-08-895-707-1	Sequence 1, Appli
40	171.5	8.7	1311	1	US-08-706-539-4	Sequence 4, Appli
41	171.5	8.7	1311	3	US-09-027-007-4	Sequence 4, Appli
42	170.5	8.7	1632	4	US-09-404-296B-31	Sequence 31, Appli
43	169	8.6	1129	4	US-09-920-760-3	Sequence 3, Appli
44	169	8.6	1911	2	US-08-246-361A-3	Sequence 3, Appli
45	169	8.6	1911	4	US-09-023-655-1022	Sequence 1022, Ap

ALIGNMENTS

RESULT 1
US-09-054-492B-2
; Sequence 2, Application US/09054492B
; Patent No. 6218115
; GENERAL INFORMATION:
; APPLICANT: TAKESHI NAKAMURA
; TITLE OF INVENTION: HUMAN CYCLIN I AND GENES ENCODING SAME
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY, MADISON & SUTRO
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/054,492B
; FILING DATE: APRIL 3, 1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: PAUL E. WHITE, JR.
; REGISTRATION NUMBER: 32,011
; REFERENCE/DOCKET NUMBER: 7898/252159
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1133
; TYPE: nucleic acid

STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-054-492B-2

Alignment Scores:

Pred. No.: 1.52e-236 Length: 1133
Score: 1962.00 Matches: 377
Percent Similarity: 100.00% Conservativity: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-09-736-250-1 (1-377) x US-09-054-492B-2 (1-1133)

Qy 1 MetLysPheProGluProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle 20
Db 1 ATGAAGTTTCCAGGGCCCTTGGAAACCCAGAGATTGTTTCTCTGTTGGAAAGGCCAATC 60
Qy 21 ThrArgGluAlaGlnMetTyrLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 61 ACTAGGGAAGCACAGATGTGAAAGTGAATGTGGGAAATGCCCTTCAATCAGATGTT 120
Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn 60
Db 121 TCTCCATCCAGAGAGATGAAGTAATTCATGGCTGGCCAACTCAAGTACCAATTCAAC 180
Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 181 CTTTACCAGAAACATTTGCTGTGGCTAGCAGTCTTTTGGATAGGTTTTAGCTACCGTA 240
Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaAlaLys 100
Db 241 AAGGCTCATCAAAATATCTGATGTGATTTGCAATCAGCTGTTTCTAGCTGCCAAG 300
Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 301 ACTGTGAGGAAGATGAGAGAAATCCAGTAAAGGTATTTGGCAAGACAGATTTCTGT 360
Qy 121 GlyCysSerSerSerGluIleuArgMetGluArgIleLeuLeuAspLysLeuAsnTrp 140
Db 361 GGATGTTCTCATCTGGAATTTTGAAGATGGAGAGAAATTTCTGGATPAAGTTGAATGG 420
Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 421 GATCTTCACAGCCACACCATTTGATTTCTTCATATTTTCCATGCTCCATTCAGTGTC 480
Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 481 ACTAGGCTCAGTTACTTTTTCAGTTTGGCCAAATTTGAGCCCATCTCAACATTTGGCAGTC 540
Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
Db 541 CTTACAGCAACTACTTCTACGTATGGCTGCACCAACTTCTGCAATTCAGAGATCC 600
Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
Db 601 ATGCTTGCTCTGCGCATGTTAGTCTGGAATGGAGAACTCATCTCGATTGGCTTTCT 660
Qy 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
Db 661 CTTACAATTTGAATGCTCTCAGAAACACAGATGGATAGCTCCAGTTGATTCATTTGTCGG 720
Qy 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
Db 721 GAGCTTGTGGCAGATCACCTTTCTACTCTGAGTCTTCCCTGCCTTGAATTCGGTTAT 780
Qy 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db 781 GTCTACCGTCCCTCAAGCACACCTCTGTGACCTGTGACAAAGAGAGTGTTCAGATTACAT 840
Qy 281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300

Db 841 CCCTCTCTGTCTCCAGGCCAGACACTTCTCAAGGACAAACAGACGAGGAGTCCAGTC 900
Qy 301 ArgGlyThrAlaAlaPheTyrHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
Db 901 AGAGGTACAGCAGCCTTTTACCATCATCTCCAGCTGCCAGTGGGTGCAAGCAGACTCT 960
Qy 321 ThrLysArgLysValGluGluMetGluValAspAspPheTyrAspGlyIleLysArgLeu 340
Db 961 ACTAAACGCAAGTAGAGGAATGGAAGTGGATGACTTCTATGATGGAATCAACGCTC 1020
Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
Db 1021 TATAATGAAGATAATGTCTCAGAAAATGGGGTCTGTGTGGGCTACTGATTATCAGA 1080
Qy 361 GlnGluGlyHisAlaSerProCysProProLeuGlnProValSerValMet 377
Db 1081 CAAGAGGACATGCTTCCCTTGTCCACCTTTGCAGCCTGTTTCTGTCTATG 1131

RESULT 2

US-08-969-106-5
Sequence 5, Application US/08969106
Patent No. 5986055
GENERAL INFORMATION:
APPLICANT: Yang, M.
APPLICANT: Nandabalan, K.
APPLICANT: Schulz, V.
TITLE OF INVENTION: CDK2 INTERACTIONS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/969,106
FILING DATE: 13-NOV-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mistock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7934-057
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1260 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1...1131
OTHER INFORMATION:
US-08-969-106-5

Alignment Scores:
Pred. No.: 1.83e-236 Length: 1260
Score: 1962.00 Matches: 377
Percent Similarity: 100.00% Conservativity: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-736-250-1 (1-377) x US-08-969-106-5 (1-1260)

Qy 1 MetLysPheProGlyProLeuGlnGlnArgLeuSerPheLeuLeuGluLysAlaIle 20
Db 1 ATGAAGTTTCAGGGCCCTTGGAAACACAGAGATTGCTTTCTCTGTTGGAAAGGCAATC 60

Qy 21 ThrArgGluAlaGlnMetTyrLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 61 ACTAGGGGAAGCACAGATGTGAAGATGTGAAGTGTGGGAAATGCCCTTCAATCAGAGTTT 120

Qy 41 SerProSerGlnArgAspGluValIleGlnTyrLeuAlaLysLeuLysTyrGlnPheAsn 60
Db 121 TCTCATCCAGAGAGATGAATTAATCAATGGCTGGCCAACTCAAGTACCAATTCAC 180

Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 181 CTTTACCAGAAACATTTGCTCTGGCTAGCAGTCTTTTGGATAGGTTTTAGCTACCGTA 240

Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaLys 100
Db 241 AAGGCTCATCCAAATATCTGAGTTGTATTCATCAATCAGCTGTTTTCTTAGCTGCCAAG 300

Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 301 ACTGTTGAGGAGATGAGAGATTCACAGTACTAAGGTATTGGCAGAGACAGTTTCTGT 360

Qy 121 GlyCysSerSerGluIleLeuArgMetGluArgIleLeuLeuAspLysLeuAsnTyr 140
Db 361 GGATGTTCTCATCTGAAATTTTGAGATGGAGAGAAATTTCTGGATAAGTTGAATGG 420

Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 421 GATCTTCACAGCCACACCATGAGATTTCTTCATATTTTCCATGCCATTCAGTGTCA 480

Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 481 ACTAGGCTCAGTACTTTTTCAGTTGGCCAAATGAGCCCATCTCAACATTTGGCAGTC 540

Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgLys 200
Db 541 CTTACCAAGCAACTACTTCTACGTATGCTGCAACCAACTCTCTGCAATTCAGAGGATCC 600

Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTyrLeuSer 220
Db 601 ATGCTGTCTGGCCATGTTAGTCTGGAAATGGAGAAACTCATTCCTGATTGGCTTCT 660

Qy 221 LeuThrIleGluLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
Db 661 CTTACAAATGAAGTCTTCAGAAAGCAGATGGATAGTCCAGTTGATCCATTTGTCGG 720

Qy 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
Db 721 GAGCTTGTGGCACATCACCTTTCTACTCTGCAGTCTTCCCTGCCTCTGAATTCGTTAT 780

Qy 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db 781 GTCTACCTGCCCTCAAGCACACCTCGTGTGACAAAGGAGTGTTCAGATTATCAT 840

Qy 281 ProSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
Db 841 CCTCTCTGTCCAGGCCAGACTTCTCCAGGCAACAGCAAGCCAGAGTGGCAGTC 900

Qy 301 ArgGlyThrAlaAlaPheTyrHisLeuProAlaIleSerGlyCysLysGlnThrSer 320
Db 901 AGAGGTACAGCAGCCTTTTACCATCATCTCCAGCTGCCAGTGGGTGGCAAGCAGCTCT 960

Qy 321 ThrLysArgLysValGluGluMetGluValAspPheTyrAspGlyIleLysArgLeu 340
Db 961 ACTAAACGCAAGTAGAGAGAAATGGAAGTGGATGACTTCTATGATGGAAATCAACGGCTC 1020

Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
Db 1021 TATAATGAAGATAATGTCTCAGAAATGTGGTCTCTGTGTGGCAGCTGATTTATCAAGA 1080

Qy 361 GlnGluGlyHisAlaSerProCysProLeuGlnProValSerValMet 377
Db 1081 CAAGAGGACATGCTCCCTTGTCCACCTTTGCAGCCTGTTTCTGTGATG 1131

RESULT 3

US-09-338-125-5
; Sequence 5, Application US/09338125
; Patent No. 6521412
; GENERAL INFORMATION:
; APPLICANT: Yang, M.
; APPLICANT: Mandabalan, K.
; APPLICANT: Schulz, V.
; TITLE OF INVENTION: CDK2 INTERACTIONS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/338,125
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/969,106
; FILING DATE: 13-NOV-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7934-057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1260 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...1131
; OTHER INFORMATION:
US-09-338-125-5

Alignment Scores:
Pred. No.: 1.83e-236 Length: 1260
Score: 1962.00 Matches: 377
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-736-250-1 (1-377) x US-09-338-125-5 (1-1260)

Qy 1 MetLysPheProGlyProLeuGlnGlnArgLeuSerPheLeuGluLysAlaIle 20
Db 1 ATGAAGTTTCAGGGCCCTTGGAAACACAGAGATTGCTTTCTCTGTTGGAAAGGCAATC 60

Qy 21 ThrArgGluAlaGlnMetTyrLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 61 ACTAGGGGAAGCACAGATGTGAAGTGTGGGAAATGCCCTTCAATCAGAGTTT 120

```
Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn 60
Db 121 TCTCATCCAGAGAGATGAAGTAATTCATAGCTGGCCAAACTCAAGTACCAATTCAC 180
Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 181 CTTTACCAGAAACATTTGCTCTGGTAGCAGTCTTTTGGATAGTGTTTTACGTACCGTA 240
Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaLysSerCysPhePheLeuAlaAlaLys 100
Db 241 AAGGCTCATCCAAATACTTCAGTGTATTCATTCAGCTGTCTTTCTAGCTGCCAAG 300
Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 301 ACTGTTGAGGAAGATGAGAGAATCCAGTCTAAAGGTATTGGCAAGAGACAGATTTCTGT 360
Qy 121 GlyCysSerSerSerGluIleuArgMetGluArgIleLeuAspLysLeuAsnTrp 140
Db 361 GGATGTTCTCATCTGAAATTTTGAGATGGAGAGAATTTATCTGGATAAGTTGAATTGG 420
Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 421 GATCTTCACAGCCACCAATTCAGATTTCTTCATATTTCCATGTCATTCAGTGTCA 480
Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 481 ACTAGGCTCAGTTACTTTTCAGTTTGGCCAAATGGAGCCCATCTCAACATTTGGCAGTC 540
Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
Db 541 CTTACCAAGCAACTACTTCACTGTATGGCTTGCACCAACTTCTGCAATTCAGAGGATCC 600
Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
Db 601 ATGCTTGCTCTGGCCATGTTAGTCTGGAATGGAGAACTCATCTCTGATGGCTTCT 660
Qy 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
Db 661 CTTACAAATTGAATGCTTTCAGAAAGCACAGATGATAGTCTCCAGTTCGATTCATTCG 720
Qy 241 GluLeuValAlaHisHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
Db 721 GAGCTTGTGGCACATCACTTTCTACTCTGAGTCTTCCCTGCTCTGAAATTCGTTAT 780
Qy 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db 781 GTCTACCTCTCCCTCAAGCACACCTGTGTGACCTGTGCACAAAGAGGTTCAGATTACAT 840
Qy 281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
Db 841 CCTCTCTCTGCTCCAGGCCAGACTTCTCCAAGGACACAGCAAGCCAGAAAGTGCAGTC 900
Qy 301 ArgGlyThrAlaAlaPheTyrHisHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
Db 901 AGAGGTACAGAGCCCTTTTACCATCATCTCCAGCTGCCAGTGGGTGCAGACACCTCT 960
Qy 321 ThrLysArgLysValGluGluMetGluValAspAspPheTyrAspGlyIleLysArgLeu 340
Db 961 ACTAAACCAAGTAGAGAAATGGAAGTGATGACTTCTATGATGATGATCAACAGGCTC 1020
Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
Db 1021 TATAATGAAGATAATGTCTCAGAAATGTGGTTCCTGTGTGGCACTGATTTATCAAGA 1080
Qy 361 GlnGluGlyHisAlaSerProCysProLeuGlnProValSerValMet 377
Db 1081 CAAGAGGACATGCTTCCCTTGTCCACTTTGCGACCTGTTCTGTGTCATG 1131
```

RESULT 4

US-09-023-655-899
; Sequence 899, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:

```
; APPLICANT: Cocks, Benjamin G.  
; APPLICANT: Susan G. Stuart  
; APPLICANT: Jeffrey J. Seilhamer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE  
; TITLE OF INVENTION: EXPRESSION  
; NUMBER OF SEQUENCES: 1508  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/023,655  
; FILING DATE: HEREWITH  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Zeller, Karen J.  
; REGISTRATION NUMBER: 37,071  
; REFERENCE/DOCKET NUMBER: PA-0001 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 855-0555  
; TELEFAX: (650) 845-4166  
; INFORMATION FOR SEQ ID NO: 899:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1260 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: GENEBANK  
; CLONE: g1183161  
; US-09-023-655-899
```

Alignment Scores:
Pred. No.: 1,83e-236 Length: 1260
Score: 1962.00 Matches: 377
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-736-250-1 (1-377) x US-09-023-655-899 (1-1260)

```
Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLysAlaIle 20
Db 1 ATGAAGTTTCAGGGCTTTTGGAAACACAGAGATTGCTTCTCTGTTGGAAAGCAATC 60
Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 61 ACTAGGGAACACAGAGATGGAAGTGAATGCGGAAATGCTTCCGAAATCAGATGTT 120
Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn 60
Db 121 TCTCCATCCCAGAGAGATGAAGTAATTCATAGCTGGCCAACTCAAGTACCAATTCAC 180
Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 181 CTTTACCAGAAACATTTGCTCTGGCTAGCAGTCTTTTGGATAGTGTTTTACGTACCGTA 240
Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaLysSerCysPhePheLeuAlaAlaLys 100
Db 241 AAGGCTCATCCAAATACTTCAGTGTATTCATTCAGCTGTCTTTCTAGCTGCCAAG 300
```

Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 301 ACTGTTGAGGAGATGAGAGATTCCAGTACTAAAGGTATTGGCAAGACAGATTCTGT 360
Qy 121 GlyCysSerSerGluLeuLeuArgMetGluArgIleLeuLeuAspLysLeuAsnTrp 140
Db 361 GGATGTTCTCATCTGAATTTGAGAAATGAGAGAAATATTCTGGATTAAGTTGAATGG 420
Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 421 GATCTTCACAGACACACACATTGGATTTCTCATATTTTCCATGTCATTCGACAGTGTCA 480
Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 481 ACTAGGCTCAGTTACTTTTTCAGTTTGGCCAAATGAGCCCATCTCAACATTTTGGCAGTC 540
Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
Db 541 CTTACCAAGCACTACTTCTGATGCTGATGCTGCAACCACTTCTGCAATTCAGAGGATCC 600
Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
Db 601 ATGCTTGCTCTGGCCATGTTAGTCTGGAATGAGAACTCATCTCGATTGCTTCT 660
Qy 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
Db 661 CTTACAAATTGAATGCTTTCAGAAAGCAGATGATGATGATGATGATGATGATGATGAT 720
Qy 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
Db 721 GAGCTTGGGCACATCACTTTCTACTCTGAGTCTTCCCTGCTCTGAAATTCGGTTAT 780
Qy 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db 781 GTCTACCGTCCCTCAAGCACACCTGCTGACCTGTGCAAGAGAGTTCAGATTACAT 840
Qy 281 ProSerValProGlyProAspPheSerLysAspSerLysProGluValProVal 300
Db 841 CCTCTCTGTCGCCAGGCCAGACTTCTCCAAAGACCAACAGCAAGTCCAGTC 900
Qy 301 ArgGlyThrAlaAlaPheTyrHisLeuProAlaLeuProAlaSerGlyCysLysGlnThrSer 320
Db 901 AGAGGTACAGAGAGCTTTTACCATCATCTCCAGCTGCGAGTGGTCAAGACACTCT 960
Qy 321 ThrLysArgLysValGluGluMetGluValAspPheTyrAspGlyIleLysArgLeu 340
Db 961 ACTAACGCAAGTAGAGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGA 1020
Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
Db 1021 TATAATGAAGATAATGTCACAGAAATGTTGGTCTGTGTGGCACTGATTATCAAGA 1080
Qy 361 GlnGluGlyHisAlaSerProCysProLeuGlnProValSerValMet 377
Db 1081 CAAGAGGACATGCTTCCCTTGTCCACCTTTGCAGCCTGTTCTGTGATG 1131

RESULT 5

US-09-513-999C-1907
; Sequence 1907, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59. US2.REG
; CURRENT APPLICATION NUMBER: US/09/513.999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681

; SOFTWARE: Patent.pm

; SEQ ID NO 1907
; LENGTH: 444
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 52..444
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 10
; OTHER INFORMATION: k=g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 11
; OTHER INFORMATION: n=a, g, c or t
US-09-513-999C-1907

Alignment Scores:

Pred. No.: 2.18e-84 Length: 444
Score: 748.00 Matches: 147
Percent Similarity: 99.32% Conservative: 0
Best Local Similarity: 99.32% Mismatches: 1
Query Match: 38.12% Indels: 0
DB: 4 Gaps: 0

US-09-736-250-1 (1-377) x US-09-513-999C-1907 (1-444)

Qy 113 ValLeuAlaArgAspSerPheCysGlyCysSerSerGluLeuLeuArgMetGluArg 132
Db 1 GTATGGCAKAGACAGATTCTGTGGATGTTCTCATCTGAAATTTTGAGATGGAGAGA 60
Qy 133 IleIleLeuAspLysLeuAsnTrpAspLeuHisThrAlaThrProLeuAspPheLeuHis 152
Db 61 ATTATTCGTGATAGTTGAATTTGGATCTTTCACAGCCACACCATTTGGATTTCTTCAT 120
Qy 153 IlePheHisAlaIleAlaValSerThrArgProGlnLeuLeuPheSerLeuProLysLeu 172
Db 121 ATTTTCATCCCATTCAGTGTCAACTAGGCCTCAGTTACTTTTTCAGTTTGGCCAAATTTG 180
Qy 173 SerProSerGlnHisLeuAlaValLeuThrLysGlnLeuLeuHisCysMetAlaCysAsn 192
Db 181 AGCCATCTCAACATTTGGCAGTCTTACCAGCACTACTTCTGATGGCTTGCAC 240
Qy 193 GlnLeuLeuGlnPheArgGlySerMetLeuAlaLeuAlaMetValSerLeuGluMetGlu 212
Db 241 CAATCTCGCAATTCAGAGGATCCATGCTTGTCTGGCCATGGTTAGTCTGGAATGGAG 300
Qy 213 LysLeuIleProAspTrpLeuSerLeuThrIleGluLeuLeuGlnLysAlaGlnMetAsp 232
Db 301 AAATCTATCTCGATTTGGCTTTCTTTACAAATGAACTGTCTCAGAAAGCACAGATGGAT 360
Qy 233 SerSerGlnLeuIleHisCysArgGluLeuValAlaHisLeuSerThrLeuGlnSer 252
Db 361 AGTCCCATGTTGATCCATTTGCGGAGCTTGTGGACATCACCTTTCTACTCTGCAGTCT 420
Qy 253 SerLeuProLeuAsnSerValTyr 260
Db 421 TCCCTGCTCTGAATTCGGTTAT 444

RESULT 6

US-09-023-655-913
; Sequence 913, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023.655

FILING DATE: HEREWITH

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Zeller, Karen J.

REGISTRATION NUMBER: 37,071

REFERENCE/DOCKET NUMBER: PA-0001 US

TELEPHONE: (650) 855-0555

TELEFAX: (650) 845-4166

INFORMATION FOR SEQ ID NO: 913:

SEQUENCE CHARACTERISTICS:

LENGTH: 1410 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: GENBANK

CLONE: g1236234

US-09-023-655-913

Alignment Scores:

Pred. No.:	2,05e-30	Length:	1410
Score:	326.50	Matches:	86
Percent Similarity:	55.08%	Conservative:	44
Best Local Similarity:	36.44%	Mismatches:	73
Query Match:	16.64%	Indels:	33
DB:	4	Gaps:	7

US-09-736-250-1 (1-377) x US-09-023-655-913 (1-1410)

```
QY 31 ValArgLysMetProSerAsnGlnAsn---ValSerProSerGlnArgAspGluValle 49
Db 357 ATTGAGGCTACCCCGAGAGATGATAACACACTTTGTGTCCAGGATTGAGAAATGCCAAAGTT 416
QY 50 GlnTrpLeuAlaLysLeuLysTyrglnPheAsnLeuTyrglnPheAsnLeuTyrglnPheAlaLeuAla 69
Db 417 GAAGATTTAAGGAGTTTACCCAACTTTTGTGATCTTGCACCTGAACTTTTGTCTGTGCT 476
QY 70 SerSerLeuLeuAspArgPheLeuAlaThrValLysAlaHisProLysTyrglnSerCys 89
Db 477 GTCATATTATGGACAGGTTCTTGGCTCTTATGAAGGTGAAACCTTAAACATTGTCTTGC 536
QY 90 IleAlaIleSerCysPhePheLeuAlaLysThrValGluGluAspGluArgIlePro 109
Db 537 ATTGAGGCTGTCTTTTGTGCTGCTGATAGATAGTTGAAGAGAGCTGCAATATTCCA 596
QY 110 ValLeuLysValLeuAlaArgAspSerPheCysGlyCysSerSerSerGluIleLeuArg 129
Db 597 TCCACTCATGTGATCCGGATTAGTACGTTAAATGTACTGCTTCTGACATAAAACGG 656
QY 130 MetGluArgIleIleLeuAspLysLeuAsnTrpAspLeuHisThrAlaThrProLeuAsp 149
Db 657 ATGGAAAAATAATTTTCAGAAAAATTCACATGATGATGAATGGAAGCTACTACTGCTTAAAC 716
QY 150 PheLeuHisIlePheHisAlaIleAlaVal-----SerThrArgProGlnLeuLeu 166
Db 717 TTTTGGCACTTATACCACTATTATCTTTGTCTACTTTCAGAAAGAAAGAAATATCTG 776
```

```
QY 167 PheSerLeuProLysLeuSerProSerGlnHisLeuAlaValLeuThrLysGlnLeuLeu 186
Db 777 ---AGCTTCATAAAGTAGAA-----GCT 797
QY 187 HisCysMetAlaCysAsnGlnLeuLeuGlnPhe-----ArgGlySerMetLeuAla 203
Db 798 CAGCTGAAGAGCTTGCAACTGCCGACTCATCTTTTCAAAGCAAAACCATCTGTATTAGCC 857
QY 204 LeuAlaMetValSerLeuGluMetGluLysLeuLeuPheProAspTrpLeuSerLeuThrIle 223
Db 858 TTGTGCTTCTCAATTTGGAAGTGGAAACTTTG-----AAATCTGTT 899
QY 224 GluLeuLeuGln-----LysAlaGlnMetAspSerSerGlnLeu 236
Db 900 GAATTACTGGAATTCCTTGTAGTTAAACCAATTCCAAGATTATGACACTGAGTTC 959
QY 237 IleHisCysArgGluLeuValAlaHisHisLeuSerThrLeuGlnSer 252
Db 960 TTCTACTGGAGAGAGTTGGTTTCTAAATGCTAGCCGAGTATTCTTCT 1007
```

RESULT 7

US-09-949-016-1852

Sequence 1852, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: Fast-Seq for Windows Version 4.0

SEQ ID NO 1852

LENGTH: 2039

TYPE: DNA

ORGANISM: Human

US-09-949-016-1852

Alignment Scores:

Pred. No.:	3.96e-30	Length:	2039
Score:	326.50	Matches:	114
Percent Similarity:	46.25%	Conservative:	71
Best Local Similarity:	28.50%	Mismatches:	138
Query Match:	16.64%	Indels:	78
DB:	4	Gaps:	14

US-09-736-250-1 (1-377) x US-09-949-016-1852 (1-2039)

```
QY 31 ValArgLysMetProSerAsnGlnAsn---ValSerProSerGlnArgAspGluValle 49
Db 256 ATTGAGGCTACCCCGAGAGATGATAACACACTTTGTGTCCAGGATTGAGAAATGCCAAAGTT 315
QY 50 GlnTrpLeuAlaLysLeuLysTyrglnPheAsnLeuTyrglnPheAlaLeuAla 69
Db 316 GAAGATTTAAGGAGTTTACCCAACTTTTGTGATCTTGTGCACTGAACTTTTGTCTGTGCT 375
QY 70 SerSerLeuLeuAspArgPheLeuAlaThrValLysAlaHisProLysTyrglnSerCys 89
Db 376 GTCATATTATGGACAGGTTCTTGGCTCTTATGAAGGTGAAACCTTAAACATTGTCTTGC 435
QY 90 IleAlaIleSerCysPhePheLeuAlaLysThrValGluGluAspGluArgIlePro 109
Db 436 ATTGAGGCTGTCTTTTGTGCTGCTGCTAGATAGTTGAAGAGAGCTGCAATATTCCA 495
QY 110 ValLeuLysValLeuAlaArgAspSerPheCysGlyCysSerSerSerGluIleLeuArg 129
```



```
Db 496 TCCACTCATGATGATCGATCGGATAGTCTAGTAAATGATGCTCTTCGACATAAACGG 555
Qy 130 MetGluArgIleLeuAspLysLeuAsnTrpAspLeuHisThrAlaThrProLeuAsp 149
Db 556 ATGGAAAAATAATTCAGAAAAATTCACATGATGAAATTCGCTTAAAC 615
Qy 150 PheLeuHisIlePheHisAlaIleAlaVal-----SerThrArgProGlnLeuLeu 166
Db 616 TTTTGGCACTTATACCACTACTATATCTTTGTCATACCTTCAGAAAGGAAAGAAATCTG 675
Qy 167 PheSerLeuProLysLeuSerProSerGlnHisLeuAlaValLeuThrLysGlnLeuLeu 186
Db 676 ---AGCCTTGATAACTAGAA-----GCT 696
Qy 187 HisCysMetAlaCysAsnGlnLeuGlnPhe-----ArgGlySerMetLeuAla 203
Db 697 CAGCTGAAAGCTTGCAACTGCCGACTCATCTTTCAAAGCAAAACCATCTGTATTAGCC 756
Qy 204 LeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSerLeuThrIle 223
Db 757 TTGTGCTTCTCAATTTGGAAGTGAAACTTTG-----AAATCTGTT 798
Qy 224 GluLeuLeuGln-----LysAlaGlnMetAspSerSerGlnLeu 236
Db 799 GAATTAAGTAAATCTCTTCTAGTAAATAAACAATCCAGATTAATGACACATGAGTTC 858
Qy 237 IleHisCysArgGluLeuValAlaHisLeuSerThrLeuGlnSer----- 252
Db 859 TTCTACTGGAGAGAGTGTGTTCTTAATGCTAGCGAGTATCTTCTCTCCTGAATGTGC 918
Qy 253 -----SerLeuProLeuAsn 257
Db 919 AAACCATGATTTAAGAAAGTGTGTTGGATCGTTTCAAGCGCACAGCCACGACCTCCAC 978
Qy 258 SerValTyrValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPhe 277
Db 979 AACAGCTACTATAGTGTCTGAGCTGCCAACGATACCT-----GAGGGGGTGTGTTT 1032
Qy 278 ArgLeuHisProSerSerValProGlyProAspPheSer-----LysAspAsnSerLys 295
Db 1033 GATGAAAGTGAAGTGAAGGACTCTTGTGAAGATATGAGTTGTGGAGAGAGAGTCTCAGC 1092
Qy 296 ProGluValProValArgGlyThrAlaAlaPheTyrHisHisLeuProAlaAla----- 313
Db 1093 AGCTCTCTCCAGTGCATCAAGAGTGCACCTTCTTTTCAACTTCAAGTGCACAAACA 1152
Qy 314 -----SerGlyCysLysGlnThrSerThrLysArgLysValGlu 326
Db 1153 CTGTGCTTTCATCTTAGAAATCTGATGT-----TCTGCAGAAATTTATATTATAC 1203
Qy 327 GluMetGluValAspAspPhe-----TyrAspGlyIleLysArgLeuTyrAsn 342
Db 1204 AGGTTTCAAAGCAATAAATGGGAATAGGTAGTTCCTGCTGTAGTGGCCCATCTAGTCA 1263
Qy 343 GluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArgGlnGlu 362
Db 1264 GGAATTAATATACCTGGAATACCTCTTATTTGTTATTATCAGATCA-GATCTGGCCTAT 1322
Qy 363 GlyHisAlaSerProCysPro-----ProLeuGlnProValSerValMet 377
Db 1323 TTTTATATTATCTTAAGCCATCAATGGGTAGTGCCTCTTAAACCATTAACAGTACTT 1382
```

RESULT 8

```
US-09-949-016-4342
; Sequence 4342, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
```

```
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4342
; LENGTH: 1576
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-4342
```

Alignment Scores:

```
Pred. No.: 2,11e-23 Length: 1576
Score: 271.50 Matches: 75
Percent Similarity: 53.19% Conservativeness: 50
Best Local Similarity: 31.91% Mismatches: 93
Query Match: 13.84% Indels: 17
DB: 4 Gaps: 4
```

US-09-736-250-1 (1-377) x US-09-949-016-4342 (1-1576)

```
Qy 45 ArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsnLeuTyrProGlu 64
Db 341 AGGACTTTGAAGTAAAGATCTTCTAGTCTAACTCAGTCTTGGCTTTGCACACAGAG 400
Qy 65 ThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrValLysAlaHisPro 84
Db 401 ACATTTCTCTAGCTGGAATTTACTGACAGATCTCTGCTAAATGAAGGTACAGCCC 460
Qy 85 LysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaAlaLysThrValGluGlu 104
Db 461 AAGCACCCTTGGTGTGTGGACTGAGCTGCTTTATTGCTGTAAATCAATAGAGAG 520
Qy 105 AspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCysGlyCysSerSer 124
Db 521 GAAAGGAATGTCCTATGGCAACTGACTTGTATCGAATAAGTCAATATAGGTTTACGGTT 580
Qy 125 SerGluIleLeuArgMetGluArgIleIleLeuAspLysLeuAsnTrpAspLeuHisThr 144
Db 581 TCAGACTGTATGAGATGGAAGATGATATGAGAAAGGTGTGTGGAAAGTCAAGACT 640
Qy 145 AlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSerThrArgProGln 164
Db 641 ACTACTGCTTTCAATTTCTGCACTGTATATTCCTCTTCAAGAGAACTTCCACTT 700
Qy 165 LeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaValLeuThrLysGln 184
Db 701 -----GAAAGGAGAAATAGCATTAATTTTGAAGACTAGAAAGCTCAA 742
Qy 185 LeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySerMetLeuAlaLeu 204
Db 743 CTGAAGCATGTCTATTCAGAGATCATATTTCTAAAGCAAGCTCTGTGTGGCATTG 802
Qy 205 AlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSerLeuThrIleGlu 224
Db 803 TCTATCATCTGATAGAGATCCAGACAGAGTGTAGAGTTAACAGAGGATAGAA 862
Qy 225 LeuLeuGlnLys---AlaGlnMetAspSerSerGlnLeuIleHisCysArgGluLeuVal 243
Db 863 TGTCTTTCAGAAACATTCCAAGATAAATGGCAGAGATCTGACCTTCTGGCAAGAGCTGTA 922
Qy 244 AlaHisIleSerThrLeuGlnSer-----SerLeuPro----- 255
Db 923 TCCAAATGTTTAACTGAATATTCATCAATTAAGTGTTCCTCAAAACCAATGTTTCAAGAGTTG 982
Qy 256 -----LeuAsnSerValTyrValTyrArgProLeuLysHisThr 268
Db 983 AATGGATGTTTCTGGCGCTACTGACCGCAATTTGAGCATAGC 1027
```

```

Db      863  TGTCTTCAGAACATTCCAAGATAAATGGCAGAGATCTGACCTTCTGGCAAGAGCTTGTA 92
Qy      244  AlaHisHisLeuSerThrLeuGlnSer-----SerLeuPro-----255
Db      923  TCCAAATGTTTAACTGAATATTTCATCAAAATAAGTGTCCAAACCCAAATGTTCAGAAAGTTG 982
Qy      256  -----LeuAsnSerValTy rValTy rArgProLeuIysHisThr 268
Db      983  AAATGATTTGTTTCTGGCGGTACTGCACGGCAATTGAAGCATAGC 1027

RESULT 10
US-09-023-655-912
; Sequence 912, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 912:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1602 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g1236232
US-09-023-655-912

Alignment Scores:
Pred. No.: 2,17e-23 Length: 1602
Score: 271.50 Matches: 75
Percent Similarity: 53.19% Conservative: 50
Best Local Similarity: 31.91% Mismatches: 93
Query Match: 13.84% Indels: 17
DB: 4 Gaps: 4

US-09-736-250-1 (1-377) x US-09-023-655-912 (1-1602)

Qy      45  ArgAspGluValIleClnTrpIleuAlaLysTyrGlnPheAsnLeuTy rProGlu 94
Db      365  AGCGCATTTTGAAGTAAAGATCTTCTTAGTCTAACTCAGTTCTTTGGCTTTTGACACAGAG 424

```

```
Qy 65 ThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrValLysAlaHisPro 84
Db 425 ACATTTCTAGCTGTGAATTTTACTGGACAGATTCCTGTCTAAATGAAGGTACAGCC 484
Qy 85 LysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaAlaLysThrValGluGlu 104
Db 485 AAGCACCTGGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGT 544
Qy 105 AspGluArgIleProValLeuLysValLeuAlaArgAspPheCysGlyCysSerSer 124
Db 545 GAAAGGAATGTCCTATTCGCACTGACCTGTATTCGCAATGAATCAATATAGGTTACGGTT 604
Qy 125 SerGluIleLeuArgMetGluArgIleIleLeuAspLysLeuAsnTrpAspLeuHisThr 144
Db 605 TCAGACTTGTAGAGATGGAAGATGATGTATGGAGAGGTTGTGTGGAAAGTCAAGACT 664
Qy 145 AlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSerThrArgProGln 164
Db 665 ACTACTGCTTCAATTTCTGCACTGTATTTATTCACCTCTCTCAAGAGAACTTGCACCT 724
Qy 165 LeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaValLeuThrLysGln 184
Db 725 -----GAAAGGAGAAATAGCATTAATTTTGAAGACTAGAAAGTCAA 766
Qy 185 LeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySerMetLeuAlaLeu 204
Db 767 CTGAAGCATCATTCAGCATCATATTTTCTAAAGCAAAAGCCTTCTGTGTGGCATTTG 826
Qy 205 AlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSerLeuThrIleGlu 224
Db 827 TCTATCATTCATGATAGATCCAGCAGACAGAGTGTGTAGATTAACAGAGGATAGAA 886
Qy 225 LeuLeuGlnLys---AlaGlnMetAspSerSerGlnLeuIleHisCysArgGluLeuVal 243
Db 887 TGTCTTCAGAAACATTCAGATAAATGCGCAGAGATCTGACCTTCTGCGCAAGAGCTGTA 946
Qy 244 AlaHisHisLeuSerThrLeuGlnSer-----SerLeuPro----- 255
Db 947 TCCAAATGTTTAACTGAATATTCATAAATAGTGTTCCTCAACCAAAATGTTTCAGAAAGTTG 1006
Qy 256 -----LeuAsnSerValTyrValTyrArgProLeuLysHisThr 268
Db 1007 AAATGGATGTTTCTGGCGGTACTGCGCGCAATTAAGCATAGC 1051

RESULT 11
US-09-736-250-1 (1-377) x US-09-023-655-948 (1-2212)
; Sequence 948, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESS: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023.655
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; APPLICATION NUMBER: 778
```

```
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 948:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2212 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: GI431875
; US-09-023-655-948

Alignment Scores:
Pred. No.: 6.89e-23 Length: 2212
Score: 269.50 Matches: 68
Percent Similarity: 55.71% Conservative: 49
Best Local Similarity: 32.38% Mismatches: 86
Query Match: 13.74% Indels: 7
DB: 4 Gaps: 2
```

```
US-09-736-250-1 (1-377) x US-09-023-655-948 (1-2212)
Qy 45 ArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsnLeuTyrProGlu 64
Db 167 AGGACACTTGAAGTAAAGATCTTCTTAGCTAACTCAGTCTTCTGGCTTTGACACAGAG 226
Qy 65 ThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrValLysAlaHisPro 84
Db 227 ACATTTCTAGCTGTGAATTTACTGACAGATCTCTGTCTAAATGAAGGTACAGCC 286
Qy 85 LysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaAlaLysThrValGluGlu 104
Db 287 AAGCACCTGGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGT 346
Qy 105 AspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCysGlyCysSerSer 124
Db 347 GAAAGGAATGTCCTATTCGCACTGACCTGTATTCGCAATGAATCAATATATGTTACGGTT 406
Qy 125 SerGluIleLeuArgMetGluArgIleIleLeuAspLysLeuAsnTrpAspLeuHisThr 144
Db 407 TCAGACTTGTAGAGATGGAAGATGGAAGATGGAAGATGGAAGATGGAAGATGGAAGAT 466
Qy 145 AlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSerThrArgProGln 164
Db 467 ACTACTGCTTCAATTTCTGCACTGTATTTATTCACCTCTCTCAAGAGAACTTGCACCT 526
Qy 165 LeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaValLeuThrLysGln 184
Db 527 -----GAAAGGAGAAATAGCATTAATTTTGAAGACTAGAAAGTCAA 568
Qy 185 LeuLeuHisCysMetAlaCysAsnGlnLeuLeuPheArgGlySerMetLeuAlaLeu 204
Db 569 CTGAAGCATGTCTATTCGAGATCATATTTTCTAAAGCAAAAGCCTTCTGTGTGGCATTTG 628
Qy 205 AlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSerLeuThrIleGlu 224
Db 629 TCTATCATTCGATTAGAGATCCAAAGCAGAGAGTGTGTAGAGTTAAACAGAGGAATAGAA 688
Qy 225 LeuLeuGlnLys---AlaGlnMetAspSerSerGlnLeuIleHisCysArgGluLeuVal 243
Db 689 TGTCTTCAGAAACATTCAGATAAATGCGCAGAGATCTGACCTTCTGCGCAAGAGCTGTA 748
Qy 244 AlaHisHisLeuSerThrLeuGlnSerSer 253
Db 749 TCCAAATGTTTAACTGAATATTCATCAAT 778
```

```

RESULT 12
US-09-092-770-7
; Sequence 7, Application US/09092770
; Patent No. 5973119
; GENERAL INFORMATION:
; APPLICANT: Coats, Steven R.
; APPLICANT: Bass, Michael B.
; APPLICANT: Robinson, Murray O.
; TITLE OF INVENTION: No. 5973119el Cyclin E Genes and Proteins
; FILE REFERENCE: A-524
; CURRENT APPLICATION NUMBER: US/09/092,770
; CURRENT FILING DATE: 1997-06-05
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 1214
; TYPE: RNA
; ORGANISM: Human
US-09-092-770-7

Alignment Scores:
Pred. No.: 4.2e-15 Length: 1214
Score: 204.00 Matches: 85
Percent Similarity: 43.81% Conservative: 60
Best Local Similarity: 25.68% Mismatches: 111
Query Match: 10.40% Indels: 76
DB: 2 Gaps: 15

US-09-736-250-1 (1-377) x US-09-092-770-7 (1-1214)
QY 4 ProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIleThrArgGlu 23
Db 295 CCGUCCCGCGUGCCGAC-----CUGUCCGGGUGUCUCAA----- 333
QY 24 AlaGlnMetTyrLysValAsnValArgLysMetProSer----- 36
Db 334 ---GAAGUUUG---CUGAACUGCUGAAGAAAGAAUCCGUAUCCGACGACAAACAC 387
QY 37 -----AsnGlnAsnValSerPheGlnArgAspGluValIleGlnTyrLeu 52
Db 388 UUCGAAAGUUUGCAGGUUAGCUGAAGAAAGACGACGCGGUAUCCGUAUCCGUGGUG 447
QY 53 AlaLysLeuLysTyrGlnPheAsnLeuTyrProGluThrPheAlaLeuAlaSerSerLeu 72
Db 448 CUGGAAAGUUUGCAGGUUAGCUGAAGAAAGACGACGCGGUAUCCGUAUCCGUGGUG 507
QY 73 LeuAspArgPheLeuAlaThrValLys---AlaHisProLysTyrLeuSerCysIleAla 91
Db 508 UUCGACCGUUUUGCUGACCGACCGACGAGAAAGACAUCAACAAACAAACGUGCAGCUG 567
QY 92 IleSerCysPheLeuAlaAlaLysThrValGluGluAspGluArgIleProValLeu 111
Db 568 AUCACCCUCCUGUUAUCGUCUCCUCAAACUG-----GAAGAAAUUCUACGCUCCGAA 621
QY 112 LysValLeuAlaArgAspSerPheCysGlyCysSerSerGluIleLeuArgMetGlu 131
Db 622 CAGGAAUUCGCUUAGCUUAGCUGGUGCUGGUGUCCGAAAGAAAGAAUCCGUAUCCG 681
QY 132 ArgIleLeuLeuAspLysLeuAsnTyrAspLeuHisThrAlaThrProLeuAspPheLeu 151
Db 682 CUGAUAUCCUGAAGCUGAAGAAUUGGAAUUGGAAUUGGAAUUGGAAUUGGAAUUGG 741
QY 152 HistPheHisAlaIle---AlaValSerThrArgProGlnLeuLeuPheSerLeuPro 170
Db 742 AACCUUUCUGCAGGUUAGCUGAAGAAAGACGACGCGGUAUCCGUAUCCGUGGUG 795
QY 171 LysLeuSerProSerGlnHisLeuAlaValLeuThrLysGlnLeuLeuHisCysMetAla 190
Db 796 CAGUAC-----UCCAGGAAACCUUACUCCAGUCCGACGUGGUG----- 837
QY 191 CysAsnGlnLeuLeuGlnPheArgGlySerMetLeuAlaLeuAlaMetValSerLeuGlu 210
Db 191 CysAsnGlnLeuLeuGlnPheArgGlySerMetLeuAlaLeuAlaMetValSerLeuGlu 210

838 -----GACCUGUGCAUCCUGGCUAUCGACUCCUGGAA 870
QY 211 MetGluLysLeuIleProAspTyrTrpLeuSerLeu-----ThrIleGluLeuLeu 226
Db 871 UUCAGUACCGUAUCCUGGCGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGG 930
QY 227 GlnLysAlaGln---MetAspSerSerGlnLeuIleHisCysArgGluLeuValAlaHis 245
Db 931 AAAAAAGCUCCGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGG 990
QY 246 HisLeuSerThrLeuGlnSerSerLeuProLeu-----AsnSerValTyr 260
Db 991 UUCGUUAAACGUGUUAUAAUCCACUCCUCCGUGUAAACUGAAAAACUUAACAAAAUCC 1050
QY 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db 1051 AUGGA-AGACCGUCACAAUCA-----GAC 1076
QY 281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
Db 1077 CCACACCAACUACCGGC-----UAU 1097

301 ArgGlyThrAlaAlaPheTyrHisHisLeuPro 311
Db 1098 GCUGGAAGAAUUAACUACUACCAACACCUUCCG 1130

RESULT 13
US-09-222-851-7
; Sequence 7, Application US/09222851
; Patent No. 6165753
; GENERAL INFORMATION:
; APPLICANT: Coats, Steven R.
; APPLICANT: Bass, Michael B.
; APPLICANT: Robinson, Murray O.
; TITLE OF INVENTION: No. 6165753el Cyclin E Genes and Proteins
; FILE REFERENCE: A-524
; CURRENT APPLICATION NUMBER: US/09/222,851
; CURRENT FILING DATE: 1998-12-30
; EARLIER APPLICATION NUMBER: 09/092,770
; EARLIER FILING DATE: 1998-06-05
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 1214
; TYPE: RNA
; ORGANISM: Human
US-09-222-851-7

Alignment Scores:
Pred. No.: 4.2e-15 Length: 1214
Score: 204.00 Matches: 85
Percent Similarity: 43.81% Conservative: 60
Best Local Similarity: 25.68% Mismatches: 111
Query Match: 10.40% Indels: 76
DB: 3 Gaps: 15

US-09-736-250-1 (1-377) x US-09-222-851-7 (1-1214)
QY 4 ProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIleThrArgGlu 23
Db 295 CCGUCCCGCGUGCCGAC-----CUGUCCGGGUGUCUCAA----- 333
QY 24 AlaGlnMetTyrLysValAsnValArgLysMetProSer----- 36
Db 334 ---GAAGUUUG---CUGAACUGCUGAAGAAAGAAUCCGUAUCCGACGACAAACAC 387
QY 37 -----AsnGlnAsnValSerPheGlnArgAspGluValIleGlnTyrLeu 52
Db 388 UUCGAAAGUUUGCAGGUUAGCUGAAGAAAGACGACGCGGUAUCCGUAUCCGUGGUG 447
QY 53 AlaLysLeuLysTyrGlnPheAsnLeuTyrProGluThrPheAlaLeuAlaSerSerLeu 72
Db 448 CUGGAAAGUUUGCAGGUUAGCUGAAGAAAGACGACGCGGUAUCCGUAUCCGUGGUG 507
QY 73 LeuAspArgPheLeuAlaThrValLys---AlaHisProLysTyrLeuSerCysIleAla 91
Db 508 UUCGACCGUUUUGCUGACCGACCGACGAGAAAGACAUCAACAAACAAACGUGCAGCUG 567
QY 92 IleSerCysPheLeuAlaAlaLysThrValGluGluAspGluArgIleProValLeu 111
Db 568 AUCACCCUCCUGUUAUCGUCUCCUCAAACUG-----GAAGAAAUUCUACGCUCCGAA 621
QY 112 LysValLeuAlaArgAspSerPheCysGlyCysSerSerGluIleLeuArgMetGlu 131
Db 622 CAGGAAUUCGCUUAGCUUAGCUGGUGCUGGUGUCCGAAAGAAAGAAUCCGUAUCCG 681
QY 132 ArgIleLeuLeuAspLysLeuAsnTyrAspLeuHisThrAlaThrProLeuAspPheLeu 151
Db 682 CUGAUAUCCUGAAGCUGAAGAAUUGGAAUUGGAAUUGGAAUUGGAAUUGGAAUUGG 741
QY 152 HistPheHisAlaIle---AlaValSerThrArgProGlnLeuLeuPheSerLeuPro 170
Db 742 AACCUUUCUGCAGGUUAGCUGAAGAAAGACGACGCGGUAUCCGUAUCCGUGGUG 795
QY 171 LysLeuSerProSerGlnHisLeuAlaValLeuThrLysGlnLeuLeuHisCysMetAla 190
Db 796 CAGUAC-----UCCAGGAAACCUUACUCCAGUCCGACGUGGUG----- 837
QY 191 CysAsnGlnLeuLeuGlnPheArgGlySerMetLeuAlaLeuAlaMetValSerLeuGlu 210
Db 191 CysAsnGlnLeuLeuGlnPheArgGlySerMetLeuAlaLeuAlaMetValSerLeuGlu 210

```

Qy 73 LeuaspArgPheLeuAlaThrVallys---AlaHisProLysTyrLeuSerCysIleAla 91
Db 508 UUCGACCGUUAUGAUGCUGACCGAGAAAGACAUCAACAAAAACAUCAUGCUGAUCGCGU 567
Qy 92 IleSerCysPheLeuAlaAlaLysThrValGluGluAspGluArgIleProValLeu 111
Db 568 AUCACCUCCUGUUAUGCUGUCCAAACUG-----GAAGAUAUCUACGCUCCGAACUG 621
Qy 112 LysValLeuAlaArgAspSerPheCysGlyCysSerSerGluIleLeuArgMetGlu 131
Db 622 CAGGAUAUCGCUUAACGACGCGUUGCUGCGAAGAACGCAUCCUGCGUAGGAA 681
Qy 132 ArgIleIleLeuAspLysLeuAsnTrpAspLeuHisThrAlaThrProLeuAspPheLeu 151
Db 682 CUGAUAUCUCCUGAAGCUGAAUUGGAACUGGCGCGGUAUCCAUCAUCUCCUGCGU 741
Qy 152 HisIlePheHisAlaIle---AlaValSerThrArgProGlnLeuPheSerLeuPro 170
Db 742 AACCUUGUUCGAGGUGAGCUGCUGAAGAACGCGUCCGAAAGUUCUG-----CUGCCG 795
Qy 171 LysLeuSerProSerGlnHisLeuAlaValLeuThrLysGlnLeuLeuHisCysMetAla 190
Db 796 CAGUAC-----UCCACGAGAAACCUCAUCCAGAACGCGUCAGCUGCUG----- 837
Qy 191 CysAsnGlnLeuGlnPheArgGlySerMetLeuAlaLeuAlaMetValSerLeuGlu 210
Db 838 -----GACCGUGUGCAUCCUGGCUAUGCAGCUCUCCUGGAA 870
Qy 211 MetGluLysLeuIleProAspTrpLeuSerLeu-----ThrIleGluLeuLeu 226
Db 871 UUCGACGUAUUGAUGAUGCUGCUGCUGCGUCCAUCCUCCAUCCGAAAGUUGU 930
Qy 227 GlnLysAlaGln---MetAspSerSerGlnLeuLeuHisCysArgGluLeuValAlaHis 245
Db 931 AAAAAAGCUGCGUUGAUGGAGGACUCCUCCGAAUGGUGUAGCUGGAGUUGCCG 990
Qy 246 HisLeuSerThrLeuGlnSerLeuProLeu-----AsnSerValTyr 260
Db 991 UUCGUUAACGUGUUAUAAUCCACUCCCGGUAUAAACUGAAACCUCAAAAAAUCCCG 1050
Qy 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db 1051 AUGGA-AGACCGUACACAUCCA-----GAC 1076
Qy 281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
Db 1077 CCACACCAUCCUGGC-----UAU 1097
Qy 301 ArgGlyThrAlaAlaPheTyrHisLeuPro 311
Db 1098 CGUGAAGAAAGUUAACUACUACUACACACCUCCG 1130

RESULT 14

US-09-092-770-1
; Sequence 1, Application US/09092770
; Patent No. 5973119
; GENERAL INFORMATION:
; APPLICANT: Coats, Steven R.
; APPLICANT: Bass, Michael B.
; APPLICANT: Robinson, Murray O.
; TITLE OF INVENTION: No. 5973119el Cyclin E Genes and Proteins
; FILE REFERENCE: A-524
; CURRENT APPLICATION NUMBER: US/09/092,770
; CURRENT FILING DATE: 1997-06-05
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1215
; TYPE: DNA
; ORGANISM: Human

Alignment Scores:

Pred. No.: 4,21e-15 Length: 1215
Score: 204.00 Matches: 75
Percent Similarity: 47.60% Conservatives: 54
Best Local Similarity: 27.68% Mismatches: 96
Query Match: 10.40% Indels: 46
DB: 2 Gaps: 12

US-09-736-250-1 (1-377) x US-09-092-770-1 (1-1215)

Qy 4 ProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIleThrArgGlu 23
Db 295 CCTCACCTTGGCTGAT-----TTAAGCTGGGATGTTCAAAA----- 333
Qy 24 AlaGlnMetTrpLysValAsnValArgLysMetProSer----- 36
Db 334 ---GAAGCTGG---CTAAACATGTTAAAAAGAGAGACAGATATGTTTCATGACAAACAT 387
Qy 37 -----AsnGlnAsnValSerProSerGlnArgAspGluValIleGlnTrpLeu 52
Db 388 TTTGAAGTTCTGCATTCTGACTTGGAAACACAGATGAGGTCCATACATTCTAGACTGGCTT 447
Qy 53 AlaLysLeuLysTyrGlnPheAsnLeuTyrProGluThrPheAlaLeuAlaSerSerLeu 72
Db 448 TTAGAGTATGTGAGTATACACACTTCATAGGAAACATTTTATCTTGACACAGACTTT 507
Qy 73 LeuAspArgPheLeuAlaThrValLys---AlaHisProLysTyrLeuSerCysIleAla 91
Db 508 TTTGATAGTTTATGTTGACACAAAGGATATAATAAATAATATGCTTCAACTCATTTGA 567
Qy 92 IleSerCysPhePheLeuAlaAlaLysThrValGluGluAspGluArgIleProValLeu 111
Db 568 ATTACCTCATTTATTCATTGCTTCCAAACTT-----GAGGAATCTATGCTCTCTAAACTC 621
Qy 112 LysValLeuAlaArgAspSerPheCysGlyCysSerSerGluIleLeuArgMetGlu 131
Db 622 CAAGAGTTGCTTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 681
Qy 132 ArgIleIleLeuAspLysLeuAsnTrpAspLeuHisThrAlaThrProLeuAspPheLeu 151
Db 682 CTCATTATTTAAAGGCTTTAAATGGAACCTTTGCTCTGTAAACAATCATCTCTCTGCTA 741
Qy 152 HisIlePheHisAlaIle---AlaValSerThrArgProGlnLeuLeuPheSerLeuPro 170
Db 742 AATCTCTTCTCCAAAGTTGATGCTCTTAAAGATGCTCTCTAAAGTTCTT-----CTACCT 795
Qy 171 LysLeuSerProSerGlnHisLeuAlaValLeuThrLysGlnLeuLeuHisCysMetAla 190
Db 796 CAGTAT-----TCTCAGGAACATTCATTCAATAAGTCTCAGCTTTTA----- 837
Qy 191 CysAsnGlnLeuGlnPheArgGlySerMetLeuAlaLeuAlaMetValSerLeuGlu 210
Db 838 -----GATCTGTGTTATTCTAGCCATTGATTCATTAGAG 870
Qy 211 MetGluLysLeuIleProAspTrpLeuSerLeu-----ThrIleGluLeuLeu 226
Db 871 TTCCAGTACAGAAATACGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 930
Qy 227 GlnLysAlaGln---MetAspSerSerGlnLeuLeuHisCysArgGluLeuValAlaHis 245
Db 931 AAGAAGCCCTCAGGTTTGGAGTGGACAGTATTTTCAGAAATGTTGATGTTGATGTTGATGTT 990
Qy 246 HisLeuSerThrLeuGlnSerSerLeuProLeu 256
Db 991 TTTGTCAATGTAGTAAAGTACTACTAGTCCAGTG 1023

RESULT 15

US-09-222-851-1
; Sequence 1, Application US/09222851
; Patent No. 6165753
; GENERAL INFORMATION:
; APPLICANT: Coats, Steven R.
; APPLICANT: Bass, Michael B.

Search completed: February 11, 2005, 07:41:43
Job time : 309.793 secs

Alignment Scores:		
Pred. No.:	4, 218-15	1215
Score:	204.00	75
Percent Similarity:	47.60%	Matches: 54
Best Local Similarity:	27.68%	Conservative: 96
Query Match:	10.40%	Mismatches: 46
DB:	3	Indels: 12
		Gaps: 1

Qy	4	ProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIleThrArgGlu	23
Db	295	CCTTCACCTTCCCTGAT-----TTAAGCTGGGGATGTTTCAAAA	333
Qy	24	AlaGlnMetTrpLysValAsnValArgLysMetProSer	36
Db	334	-----GAAGTCTGG-----CTAAACATGTTAAAAAGAGAGCAGATATGTTCATGACAAACAT	387
Qy	37	-----AsnGlnAsnValSerProSerGlnArgAspGluValIleGlnTrpLeu	52
Db	388	TTTGAAGTTCTGCATTCTGACTTGGAAACACAGATGAGTCCATACTTCTAGACTGGCTT	447
Qy	53	AlaLysLeuLysTyrrGlnPheAsnLeuTyrrProGlnThrPheAlaLeuAlaSerLeu	72
Db	448	TTAGAGTATGTGAAGTATPACACACTCATAGGGAACATTTTATCTGTGCACAGACTTT	507
Qy	73	LeuAspArgPheLeuAlaThrValLys---AlaHisProLysTyrrLeuSerCysIleAla	91
Db	508	TTTGATAGATTTATGTTGACACAAAGGATATAATAAATAATGCTTCAACTCATTTGGA	567
Qy	92	IleSerCysPhePheLeuAlaLysThrValGluGluAspGluArgIleProValLeu	111
Db	568	ATTACCTCATTTATCATGCTTCCAAACTT-----GAGGAATPCTATGCTCTCTAAACTC	621
Qy	112	LysValLeuAlaArgAspSerPheCysGlyCysSerSerSerGlnIleLeuArgMetGlu	131
Db	622	CAAGAGTTTGCTTTACGTCACTGATGGTGCTTGCAGTGAAGAGGATATCTTAAGGATGGAA	681
Qy	132	ArgIleIleLeuAspLysLeuAsnTrpAspLeuHisThrAlaThrProLeuAspPheLeu	151
Db	682	CTCATATATATAAGGCTTTAAATGGGAACCTTTGTCTGTAAACAATCATCTCTCGCTA	741
Qy	152	HisIlePheHisAlaIle---AlaValSerThrArgProGlnLeuLeuPheSerLeuPro	170
Db	742	AATCTCTTTCTCCAAGTTGATGCTCTTAAAGATGCTCTTAAAGTCTT-----CTACCT	795
Qy	171	LysLeuSerProSerGlnHisLeuAlaValLeuThrLysGlnLeuLeuHisCysMetAla	190
Db	796	CAGTAT-----TCTCAGGAACAATTCATTCAATATAGCTCAGCTTTTA-----	837
Qy	191	CysAsnGlnLeuLeuGlnPheArgGlySerMetLeuAlaLeuAlaMetValSerLeuGlu	210
Db	838	-----CATCTGTGTATTCTAGCCATTGATTCATTAGAG	870
Qy	211	MetGluLysLeuIleProAspTrpLeuSerLeu-----ThrIleGluLeuLeu	226
Db	871	TTCCAGTACAGAACTACTGACTCTGCTGCTTGTGCCATTTTACTCCATTGAAGTGGTT	930

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model
Run on: February 11, 2005, 05:55:30 ; Search time 1613.1 Seconds
(without alignments)
1379.008 Million cell updates/sec
Title: US-09-736-250-1
Perfect score: 1962
Sequence: 1 MKRFGPLENORLSFLEKAI.....LSRQGHASCPPLQPVSM 377

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0
Searched: 5378673 seqs, 2950229984 residues
Total number of hits satisfying chosen parameters: 10757346
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO.spool/US09736250/runat_07022005_154926_20490/app.query.fasta_1.718
-DB=Published Applications NA -QFMT=fastap -SUFFIX=rnnpb -MINMATCH=0.1
-LOOPEL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HRAPSIZ=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09736250 @CGN 1 1 582 @runat_07022005_154926_20490
-NCPU=6 -ICPU=3 -NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
19: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1962	100.0	1134	12	US-09-736-250-2
2	1962	100.0	1260	17	US-10-172-118-1396
3	1962	100.0	1260	17	US-10-342-887-1396
4	1962	100.0	1260	17	US-10-641-643-893
5	1962	100.0	1889	9	US-09-867-701-10907
6	1841	93.8	2755	10	US-09-814-353-21586
7	811	41.3	490	17	US-10-242-535A-30212
8	811	41.3	490	17	US-10-085-783A-30212
9	770.5	39.3	2146	10	US-09-814-353-21594
10	731	37.3	444	17	US-10-242-535A-16032
11	731	37.3	444	17	US-10-085-783A-16032
12	638	32.5	389	17	US-10-242-535A-6834
13	638	32.5	389	17	US-10-085-783A-6834
14	625	31.9	369	17	US-10-242-535A-33391
15	625	31.9	369	17	US-10-085-783A-33391
16	621	31.7	516	10	US-09-814-353-18045
17	486	24.8	348	9	US-09-728-445-666
18	414	21.1	350	17	US-10-242-535A-20816
19	414	21.1	350	17	US-10-085-783A-20816
20	408	20.8	486	10	US-09-814-353-17297
21	377.5	19.2	426	10	US-09-814-353-4614
22	377.5	19.2	426	10	US-09-814-353-10913
23	367	18.7	387	9	US-09-796-692-3935
24	367	18.7	387	14	US-10-040-862-3935
25	367	18.7	387	17	US-10-057-475B-3935
26	367	18.7	387	17	US-10-154-884B-3935
27	367	18.7	387	18	US-10-764-324-3935
28	346	17.6	447	9	US-09-777-564-1252
29	346	17.6	447	14	US-10-015-219-1252
30	331	16.9	666	17	US-10-240-425-64
31	326.5	16.6	1410	17	US-10-641-643-913
32	326.5	16.6	2044	10	US-09-873-367C-246
33	326.5	16.6	2044	15	US-10-171-581-243
34	326.5	16.6	2044	17	US-10-170-385-322
35	326.5	16.6	2044	17	US-10-172-118-1035
36	326.5	16.6	2044	17	US-10-240-425-1439
37	326.5	16.6	2044	17	US-10-342-887-1025
38	326.5	16.6	2692	13	US-10-002-600-15
39	326.5	16.6	5811	13	US-10-002-600-15
40	321	16.4	420	9	US-09-960-352-9810
41	315.5	16.1	889	9	US-09-867-701-10906
42	284	14.5	288	17	US-10-242-535A-57578
43	284	14.5	288	17	US-10-085-783A-57578
44	281.5	14.3	477	10	US-09-814-353-5374
45	281.5	14.3	477	10	US-09-814-353-11661

ALIGNMENTS

RESULT 1
US-09-736-250-2
; Sequence 2, Application US/09736250
; Publication No. US20050014139A1
; GENERAL INFORMATION:
; APPLICANT: SUMITOMO ELECTRIC INDUSTRIES, LTD.
; APPLICANT: NAKAMURA, Takeshi
; TITLE OF INVENTION: HUMAN CYCLIN I AND GENES ENCODING THE SAME
; FILE REFERENCE: 050212-0278
; CURRENT APPLICATION NUMBER: US/09/736,250
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 09/054,492
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: PCT/JP96/02905
; PRIOR FILING DATE: 1996-10-07
; PRIOR APPLICATION NUMBER: 284663/1995
; PRIOR FILING DATE: 1995-10-05
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2

```
; LENGTH: 1134
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-736-250-2

Alignment Scores:
Pred. No.: 9,44e-231 Length: 1134
Score: 1962.00 Matches: 377
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-09-736-250-1 (1-377) x US-09-736-250-2 (1-1134)

Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle 20
Db 1 ATGAAGTTTCCAGGGCCCTTTGGAACACAGAGATTGCTTTCCCTGTTGGAAAGGCAATC 60

Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 61 ACTAGGGAAGCACAGATGTGAAAGTGAATGTGGGAAATGCCTTCAATCAGATGTT 120

Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn 60
Db 121 TCTCCATCCAGAGATGAAGTAATTCATGTGGCTGGCCAAACTCAAGTACCAATTCAC 180

Qy 61 LeuTyrProGluThrPheAlaIleuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 181 CTTTACCAGAAACATTTGCTGTGGCTAGCAGTCTTTTGGATAGATGTTTTAGCTACCGTA 240

Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaLys 100
Db 241 AAGGCTCATCCAAATACTTGGTGTGATTCATGCATCAGCTGTTTTCCTAGCTGCCAG 300

Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 301 ACTGTGTAGGAAGATGAGAGATTCAGTACTAAAGGTATTGGCAAGAGACAGATTTCTGT 360

Qy 121 GlyCysSerSerGluLeuLeuArgMetGluArgIleLeuAspLysLeuAsnTrp 140
Db 361 GGATGTTCTCATCTGAAATTTGAGAAATGAGAGAAATTTCTGGATGAATGAAATGG 420

Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 421 GATCTTCACAGCCACACACCATGGAATTTCTTATATTTTCCATGCAATTCAGTGTCA 480

Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 481 ACTAGGCTCAGTTTACTTTTCAGTTTGGCCAAATGAGCCCATCTCAACATTTGGCAGTC 540

Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
Db 541 CTTACCAAGCAACTACTTCTACTGTATGGCTGGCAACCAACTTCTGCAATTCAGAGGATCC 600

Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
Db 601 ATGCTTGCTCTGGCCATGTTAGTCTGGAATGAGAAACTCATCTCTGATTTGCTTTCT 660

Qy 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
Db 661 CTTCAATTTGAATGCTTTTCAAGAAACACAGATGATAGTCTCCCAATTCATTCATGTCGG 720

Qy 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
Db 721 GAGCTTGTGGCAGATCACCTTTTACTCTGAGTCTTCCCTGCTGCTGAAATCCGTTTAT 780

Qy 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db 781 GTCTACCGTCCCTCAAGCACACCTGGTGTGACAAAGGAGTGTTCAGATTACAT 840

Qy 281 ProSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
Db 841 CCCTCTCTGTCCAGGCCCCAGACTTCTCCAGACCAACAGCAAGCCAGAGTCCAGTC 900

Qy 301 ArgGlyThrAlaAlaPheTyrHisHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
Db 901 AGAGGTACAGAGCCCTTTTACCATCATCTCCAGCTGCCAGTGGGTGGAAGACACCTCT 960

Qy 321 ThrLysArgLysValGluGluMetGluValAspAspPheTyrAspGlyIleLysArgLeu 340
Db 961 ACTAAACGCCAAAGTAGAGGAATGGAAGTGGATGACTTCTTATGATGAATCAACGGCTC 1020

Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
Db 1021 TATAATGAAGATAATGTCTCAGAAATGTGGTCTCTGTGTGGCACTGATTTATCAAGA 1080

Qy 361 GluGluGlyHisAlaSerProCysProLeuGlnProValSerValMet 377
Db 1081 CAAGAGGACATGCTTCCCTTGTCCACCTTTGAGCCCTTGTCTGTCTGTCATG 1131

RESULT 2
US-10-172-118-1326
; Sequence 1326, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 1326
; LENGTH: 1260
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM_006835
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-1326

Alignment Scores:
Pred. No.: 1.12e-230 Length: 1260
Score: 1962.00 Matches: 377
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-09-736-250-1 (1-377) x US-10-172-118-1326 (1-1260)

Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle 20
Db 1 ATGAAGTTTCCAGGGCCCTTTGGAACACAGAGATTGCTTTCCCTGTTGGAAAGGCAATC 60

Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 61 ACTAGGGAAGCACAGATGTGAAAGTGAATGTGGGAAATGCCTTCAATCAGATGTT 120

Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn 60
Db 121 TCTCCATCCAGAGATGAAGTAATTCATGTGGCTGGCCAAACTCAAGTACCAATTCAC 180

Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 181 CTTTACCAGAAACATTTGCTGTGGCTAGCAGTCTTTTGGATAGATGTTTTAGCTACCGTA 240
```


Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaAlaLys 100
Db 241 AAGGCTCATCAAAATACTTGAGTTGATTGCAATCAGCTGTTTTCTTCTAGCTGCCAAG 300
Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 301 ACTGTTGAGGAGATGAGAGATTCAGTACTAAGGATTTGGCAGAGACAGTTTCTGT 360
Qy 121 GlyCysSerSerGluIleLeuArgMetGluArgIleLeuLeuAspLysLeuAsnTyr 140
Db 361 GGATGTTTCTCATCTGAAATTTGAGAAATGAGAGAAATTTCTGGATAAGTTGAAATGG 420
Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 421 GATCTTCACACAGCCACACCATCTGATTTCTCATATTTTCCATGTCATTCAGTGTCA 480
Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 481 ACTAGGCTCAGTTACTTTTTCAGTTTGGCCAAATTTGAGCCATCTCAACATTTGGCAGTC 540
Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
Db 541 CTTACCAAGCAACTACTTCTGATGTCCTGCAACCACTCTGCAATTCAGAGGATCC 600
Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTyrLeuSer 220
Db 601 ATGCTTCTCTGGCCATGTTAGTCTGGAATGAGAAATCTCATTTCTGATTTGCTTTCT 660
Qy 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
Db 661 CTTACAAATTTGACCTTTTTCAGAAAGCAGATGATGATGCTCCAGTTGATCCATTTGCTGG 720
Qy 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
Db 721 GAGCTTGTGGCACATCACTTTCTACTCTGCAGTCTTCCCTGCCTCTGAAATTCGGTTAT 780
Qy 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db 781 GTCTACCGTCCCTCAAGCACACCTGTCAGCTGTGACAAAGAGGTTCAGATTACAT 840
Qy 281 ProSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
Db 841 CCTCTCTGTCCAGGCCAGACTTCTCCAGAGCAACAGCAAGCCAGAGTCCAGTC 900
Qy 301 ArgGlyThrAlaAlaPheTyrHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
Db 901 AGAGGTACAGCAGCCTTTTACCATCATCTCCAGCTGCCAGTGGTGCAAGCAGACCTCT 960
Qy 321 ThrLysArgLysValGluGluMetGluValAspAspPheTyrAspGlyIleLysArgLeu 340
Db 961 ACTAAACGCCAAGTAGAGGAATGGAATGGAGTGGATGACTTCTATGATGGAATCAACGGCTC 1020
Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
Db 1021 TATTAATGAAGATATGCTTCGAAATTTGGGTTCTGTGTGGCATGATTTATCAAGA 1080
Qy 361 GlnGluGlyHisAlaSerProCysProProLeuGlnProValSerValMet 377
Db 1081 CAAGAGGACATGCTTCCCTTGTCCACCTTTGAGCCTGTTTCTGTGTCATG 1131

RESULT 3

US-10-342-887-1326
; Sequence 1326, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernards, Rene

; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10/342,887
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 1326
; LENGTH: 1260
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-342-887-1326

Alignment Scores:

Pred. No.: 1,12e-230 Length: 1260
Score: 1962.00 Matches: 377
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-09-736-250-1 (1-377) x US-10-342-887-1326 (1-1260)

Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle 20
Db 1 ATGAAGTTTCCAGGCGCTTTGGAAACACAGAGATTGCTTCTTCTGTTGGAAAGGCAATC 60
Qy 21 ThrArgGluAlaGlnMetTyrLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 61 ACTAGGAAGACAGATGTGGAAGTGAATGTGCGAAATGCTTCAAAATCAGAAATGTT 120
Qy 41 SerProSerGlnArgAspGluValIleGlnTyrLeuAlaLysLeuLysTyrGlnPheAsn 60
Db 121 TCCTCATCCAGAGAGATGAAGTAATTCATGCTGGCCAACTCAAGTACCAATTCAC 180
Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 181 CTTTACCAGAAACATTTGCTCTGGCTAGCAGCTCTTTGGATAGTGTTCCTAGCTACCGTA 240
Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaAlaLys 100
Db 241 AAGGCTCATCAAAATACTTGAGTTGATTGATTCAGTCTGTTTCTTCTAGCTGCCAAG 300
Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 301 ACTGTTGAGGAAGATGAGAAATTCAGTACTAAAGGTATTTGGCAGAGACAGTTTCTGT 360
Qy 121 GlyCysSerSerGluIleLeuArgMetGluArgIleIleLeuAspLysLeuAsnTyr 140
Db 361 GGATGTTTCTCATCTGAAATTTTGGAGATGAGAGAAATTTCTGGATAAGTTGAAATGG 420
Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 421 GATCTTCACACAGCCACACCATCTGATTTCTCATATTTTCCATGTCATTCAGTGTCA 480
Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 481 ACTAGGCTCAGTTACTTTTTCAGTTTGGCCAAATTTGAGCCATCTCAACATTTGGCAGTC 540
Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
Db 541 CTTACCAAGCAACTACTTCTGATGTCCTGCAACCACTCTGCAATTCAGAGGATCC 600
Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTyrLeuSer 220
Db 601 ATGCTTCTCTGGCCATGTTAGTCTGGAATGAGAAATCTCATTTCTGATTTGCTTTCT 660
Qy 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240

Db 661 CTTACATTAAGTCTTTCAGAAAGCACAGATGATAGTCCAGTTGATCCATTCGCG 720
Qy
Db 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
Db 721 GAGCTTGGGCACATCCTTCTACCTGCTGAGTCTTCCCTGCTGAAATCCGTTAT 780
Qy 261 ValTyrArgProLeuHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db 781 GTCTACCGTCCCTCAAGCACACCTGGTGACCTGTGCAAAAGGAGTGTTCAGATTACAT 840
Qy 281 ProSerValProGlyProAspPheSerLysAspLysSerLysProGluValProVal 300
Db 841 CCCTCCTCTGTCAGGCGCCAGACTTCTCCAAAGACAAACAGCAAGCCAGAGTCCAGTC 900
Qy 301 ArgGlyThrAlaAlaPheTyrHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
Db 901 AGAGTACAGAGCCTTTTACCATCATCTCCAGCTGCCAGTGGGTGCAAGCACCTCT 960
Qy 321 ThrLysArgLysValGluMetGluValAspPheTyrAspGlyValLysArgLeu 340
Db 961 ACTAAACGCAAGTAGAGGAATGGAAGTGGATGATCTTATGATGGAATCAACGGCTC 1020
Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
Db 1021 TATTAATGAAGATAATGTCTCAGAAATGTGGTCTCTGTGTGGCACTGATTTATCAAGA 1080
Qy 361 GlnGluGlyHisAlaSerProCysProProLeuGlnProValSerValMet 377
Db 1081 CAAGAGGACATGTTCCCTTGTCCCTTTCAGCTTTCAGCTGTTCTGTGCAIG 1131

RESULT 4
US-10-641-643-899
; Sequence 899, Application US/10641643
; Publication No. US20040077003A1
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; Susan G. Stuart
; Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
; GENE EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESS: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 5.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/641,643
; FILING DATE: 14-Aug-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 899:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1260 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: GENBANK

CLONE: G1183161

SEQUENCE DESCRIPTION: SEQ ID NO: 899 ;
US-10-641-643-899

Alignment Scores:
Pred. No.: 1,12e-230 Length: 1260
Score: 1962.00 Matches: 377
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-09-736-250-1 (1-377) x US-10-641-643-899 (1-1260)

Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaLe 20
Db 1 ATGAAGTTTCAGGGCCTTTGGAAACCCAGAGATTGCTTCTCTGTTGGAAAGGCAATC 60
Qy 21 ThrArgGluAlaGlnMetTyrLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 61 ACTAGGGAAGACAGAGTGTGGAAGTGAATGTGCGAAATGCTTCAAAATCAGAAATGTT 120
Qy 41 SerProSerGlnArgAspGluValIleGlnTyrLeuAlaLysLeuLysTyrGlnPheAsn 60
Db 121 TCTCCATCCAGAGAGATGAATTAATTCATGCTGGCCAACTCAAGTACCAATTCAC 180
Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 181 CTTTACCAGAAACATTTGCTCTGGGTAGCAGTCTTTTGGATAGGTTTATGCTACCGTA 240
Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaLeuSerCysPhePheLeuAlaLys 100
Db 241 AAGGCTCATCCAAATACITTGAGTTGATTTGCAATCAGCTGTTTTCCTAGCTGCCAAG 300
Qy 101 ThrValGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 301 ACTGTTGAGGAAGATGAGAGAAATCCAGTACTTAAGGTATTTGCAAGAGACAGTTTCTGT 360
Qy 121 GlyCysSerSerSerGluLeuLeuArgMetGluArgIleLeuLeuAspLysLeuAsnTyr 140
Db 361 GGATGTTCTCTCATCTGAAATTTTGGAGATGAGAGAAATTAATCTGGATAAGTTGAATGG 420
Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaLeuAlaValSer 160
Db 421 GATCTTCACACAGCCACACCATTTGGATTTTCTCATATTTTCCATGCCATTCAGTGCTCA 480
Qy 161 ThrArgProGlnLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 481 ACTAGGCTCAGTTACTTTTTCAGTTTGGCCAAATTTGAGCCCACTCAACATTTGGCAGTC 540
Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuGlnPheArgGlySer 200
Db 541 CTTTACCAAGCAACTACTTCACTGATGCGCTGCAACCAACTTCTCAATTCAGAGGATCC 600
Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTyrLeuSer 220
Db 601 ATGCTTGTCTGGCCATGTTAGTCTGGAAATGAGAAACTCAATCTCTGATGGCTTCT 660
Qy 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
Db 661 CTTTACAAATTTGAATGCTTTCAGAAAGCACAGATGGATAGTCTCCAGTTGATCCATTTGCGG 720
Qy 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
Db 721 GAGCTTGTGGCACATCACCTTTCTACTGCTGCTTCCCTGCTGCTGCTGCTGCTGCTTAT 780
Qy 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db 781 GTCTACCGTCCCTCAAGCACACCTTGGTGGTGTGACCTGTGTGACAAAGAGGTTCAGATTACAT 840
Qy 281 ProSerSerValProGlyProAspPheSerLysAsnSerLysProGluValProVal 300

```
Db 841 CCCTCCTCTGTCAGGCCAGACTTCTCCAGGACACACAGCAAGCCAGAGTCCAGTC 900
Qy 301 ArgGlyThrAlaPheTyrHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
Db 901 AGAGGTACAGCAGCCTTTTACCATCACTCCAGCTGCCAGTGGGTGCAGCAGACCTCT 960
Qy 321 ThrLysArgLysValGluGluMetGluValAspPheTyrAspGlyLeuLysArgLeu 340
Db 961 ACTAAACGCAAGTAGAGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAAT 1020
Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
Db 1021 TATTAATGAAGATAATGCTCAGAAATGTTGGTCTGTGTGTGGCAGCTGATTTATCAAGA 1080
Qy 361 GlnGluGlyHisAlaSerProCysProProLeuGlnProValSerValMet 377
Db 1081 CAAGAGGACATGCTTCCCTTGTCCACCTTTGAGCCTGTTCTGTGTCATG 1131

RESULT 5
US-09-867-701-10907
; Sequence 10907, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.457
; CURRENT APPLICATION NUMBER: US/09/867,701
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10907
; LENGTH: 1889
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-867-701-10907

Alignment Scores:
Pred. No.: 2,19e-230 Length: 1889
Score: 1962.00 Matches: 377
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-736-250-1 (1-377) x US-09-867-701-10907 (1-1889)
Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle 20
Db 544 ATGAAGTTTCAGGGCCTTTGGAAACACAGAGATTGCTTTCTCTGTTGGAAAGGCAATC 603
Qy 21 ThrArgGluAlaGlnMetTyrLysValAsnValArgLysMetProSerAsnGluAsnVal 40
Db 604 ACTAGGGAAGCACAGATGTGGAATGTAATGTGGGAAATGCCTTCAATCAGATGTT 663
Qy 41 SerProSerGlnArgAspGluValIleGlnTyrLeuAlaLysLeuLysTyrGlnPheAsn 60
Db 664 TCTCATCCAGAGAGATGAAGTAATTCATGCGTGGCCAAACTCAAGTACCAATCAAC 723
Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 724 CTTTACCAGAAACATTTGCTCTGGCTAGCAGTCTTTTGGATAGTGTTCCTAGCTACCGTA 783
Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaLys 100
Db 784 AAGGCTCATCAAAATCTTGGTGTGATTCGAATCAGCTGTTTCTTCTAGCTGCCAAG 843
Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 844 ACTGTTGAGGAAGATGAGAGAAATCCAGTACTAAAGGTAATTTGGCAAGAGACAGTTTCTGT 903
```

```
Qy 121 GlyCysSerSerSerGluIleLeuArgMetGluArgIleIleLeuAspLysLeuAsnTyr 140
Db 904 GGATGTTCTCTCATCTGAAATTTTGAAGATGAGAGAAATTTCTGGATAAGTTGAAATGG 963
Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 964 GATCTTCCACAGCAGCCACCATTTGATTTCTTCATATTTTCCATGCAATTCAGTGTCA 1023
Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 1024 ACTAGGCTCAGTTACTTTTTCAGTTTGCCTTGCCTTGCCTTGCCTTGCCTTGCCT 1083
Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
Db 1084 CTTACCAAGCAACTACTTCTGATGCTGCAACCAACTTCTGCAATTCAGAGGATCC 1143
Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTyrLeuSer 220
Db 1144 ATGCTTCTCTGGCCATGGTTAGTCTGGAATGGAATGGAATGGAATGGAATGGAATGGA 1203
Qy 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
Db 1204 CTTACAAATGCACTGCTTTCAGAAAGCACAGATGATGATGATGATGATGATGATGAT 1263
Qy 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
Db 1264 GAGCTTGTGGCACATCACTTCTTACTCTGCACTTCTTCTTCTTCTTCTTCTTCTTCT 1323
Qy 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db 1324 GTCTACCGTCCCTTCAAGCACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1383
Qy 281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
Db 1384 CCTCTCTCTCTCCAGGCCAGACTTCTCCAGGACACAGCAAGCAAGCAAGCAAGCAAG 1443
Qy 301 ArgGlyThrAlaPheTyrHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
Db 1444 AGAGGTACAGCAGCCTTTTACCATCATCTCCAGCTGCCAGTGGGTGGTGGTGGTGGTGG 1503
Qy 321 ThrLysArgLysValGluGluMetGluValAspPheTyrAspGlyIleLysArgLeu 340
Db 1504 ACTAAACGCAAGTAGAGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGA 1563
Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
Db 1564 TATTAATGAAGATAATGCTCAGAAATGTTGGTCTGTGTGTGGCAGCTGATTTATCAAGA 1623
Qy 361 GlnGluGlyHisAlaSerProCysProProLeuGlnProValSerValMet 377
Db 1624 CAAGAGGACATGCTTCCCTTGTCCACCTTTGAGCCTGTTCTGTGTCATG 1674
```

RESULT 6

```
US-09-814-353-21586
; Sequence 21586, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: M01-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
```

; PRIOR APPLICATION NUMBER: US 60/216,820
 ; PRIOR FILING DATE: 2000-07-07
 ; PRIOR APPLICATION NUMBER: US 60/220,661
 ; PRIOR FILING DATE: 2000-07-25
 ; PRIOR APPLICATION NUMBER: US 60/257,672
 ; PRIOR FILING DATE: 2000-12-21
 ; NUMBER OF SEQ ID NOS: 22037
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 21586
 ; LENGTH: 2755
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-814-353-21586

Alignment Scores:

Pred. No.: 3,27e-215 Length: 2755
 Score: 1841.00 Matches: 358
 Percent Similarity: 94.96% Conservative: 0
 Best Local Similarity: 94.96% Mismatches: 1
 Query Match: 93.83% Indels: 18
 Gaps: 1
 DB: 10

US-09-736-250-1 (1-377) x US-09-814-353-21586 (1-2755)

QY 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle 20
 Db 847 ATGAAGTTTCCAGGGCCCTTGGAAACCCAGAGATTGCTTCTCTGTTGAAAAGGCAATC 906
 QY 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
 Db 907 ACTAGGGAAGCACAGATGTGAAGTGAATGTGGGAAAATGGCTTCAATTCAGAAATGTT 966
 QY 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn 60
 Db 967 TCTCCATCCAGAGAGATGAATTAATCAATGGTGGCCAACTCAAGTACCAATTCAC 1026
 QY 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
 Db 1027 CTTTACCAGAAACATTTTCTCTGGCTAGCAGTCTCTTTGGATAGGTTTTCAGCTACCGTA 1086
 QY 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaLys 100
 Db 1087 AAGGCTCATCTT----- 1098
 QY 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgSerPheCys 120
 Db 1099 -----GAGGAAGATGAGAGATTCAGTACTAAAGGTATTGGCAAGAGACAGATTCTGT 1152
 QY 121 GlyCysSerSerSerGluIleLeuArgMetGluArgIleLeuLeuAspLysLeuAsnTrp 140
 Db 1153 GGATGTTCTCATCTGAAATTTTGAAGATGGAGAGAATATTCTGGATAAGTTGAAATGG 1212
 QY 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
 Db 1213 GATCTTCACAGCCACACCAATTTGATTTCTTCAATTTTCCATGCAATTCAGTGTCA 1272
 QY 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
 Db 1273 ACTAGGCCCTCAGTTACTTTTTCAGTTTGGCCAAATGAGCCCATCTCAACATTTGGCAGTC 1332
 QY 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgLysSer 200
 Db 1333 CTTACCAGCAACACTTCTACTGTATGGCCCTGCAACCAACTTCTGCAATTCAGAGGATCC 1392
 QY 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
 Db 1393 ATGCTTGTCTGGCCATGTTAGTCTGGAATGGAGAACTCATCTCTGATGGCTTCT 1452
 QY 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
 Db 1453 CTTCAATTTGAATGCTTTCAGAAAGCACAGATGATAGTCCCACTGATCCATTTGTCGG 1512
 QY 241 GluLeuValAlaAlaHisLeuSerThrLeuGlnSerLeuProLeuAsnSerValTyr 260

Db 1513 GAGCTTGTGGCACATCACCTTTTCTACTCTGCAGTCTTCCCTGCTCTGAATTCGTTTAT 1572
 QY 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
 Db 1573 GTCTACCGTCCCTCAAGCACACCTGTCCTGTCACCAAGAGAGTGTTCAGATTACAT 1632
 QY 281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
 Db 1633 CCTTCTCTGTCCAGGCCCCAGACTTCTCCAGGACCAACAGCAAGCCAGAGTCCAGTC 1692
 QY 301 ArgGlyThrAlaAlaPheTyrHisHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
 Db 1693 AGAGGTACAGCAGCCTTTTACCATCATCTCCAGTCCAGTGGGTGGTCAAGCAGACCTCT 1752
 QY 321 ThrLysArgLysValGluGluMetGluValAspPheTyrAspGlyLysLeuArgLeu 340
 Db 1753 ACTAAACGCAAGTAGAGGAAATGGAGAGTGGAGACTTCTATGATGGAATCAACAGGCTC 1812
 QY 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
 Db 1813 TATAATGAAGATTAATGTCTCAGAAAATGTGGTCTGTGTGGCAGTGAATTTATCAAGA 1872
 QY 361 GlnGluGlyHisAlaSerProCysProLeuGlnProValSerValMet 377
 Db 1873 CAAGAGGACATGCTTCCCTTGTCTACCTTTCAGCCTGTTTCTGTGTCATG 1923

RESULT 7

US-10-242-535A-30212
 ; Sequence 30212, Application US/10242535A
 ; Publication No. US20040013663A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ChondroGene Inc.
 ; APPLICANT: Liev, C.C.
 ; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
 ; FILE REFERENCE: 4231/2005
 ; CURRENT APPLICATION NUMBER: US/10/242,535A
 ; CURRENT FILING DATE: 2002-09-12
 ; PRIOR APPLICATION NUMBER: US 10/085,783
 ; PRIOR FILING DATE: 2002-02-28
 ; PRIOR APPLICATION NUMBER: US 60/305,340
 ; PRIOR FILING DATE: 2001-07-13
 ; PRIOR APPLICATION NUMBER: US 60/275,017
 ; PRIOR FILING DATE: 2001-03-12
 ; PRIOR APPLICATION NUMBER: US 60/271,955
 ; PRIOR FILING DATE: 2001-02-28
 ; NUMBER OF SEQ ID NOS: 58994
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 30212
 ; LENGTH: 490
 ; TYPE: DNA
 ; ORGANISM: Human
 US-10-242-535A-30212

Alignment Scores:

Pred. No.: 1,39e-89 Length: 490
 Score: 811.00 Matches: 157
 Percent Similarity: 98.77% Conservative: 4
 Best Local Similarity: 96.32% Mismatches: 2
 Query Match: 41.34% Indels: 0
 DB: 17 Gaps: 0

US-09-736-250-1 (1-377) x US-10-242-535A-30212 (1-490)

QY 114 LeuAlaArgAspSerPheCysGlyCysSerSerGluIleLeuArgMetGluArgIle 133
 Db 1 ATGGCCAGAGAGAGTTTCTGTGGATGTTCTCTCACTGAAATTTGAGAAATGGAGAGATT 60
 QY 134 IleLeuAspLysLeuAsnTrpAspLeuHisThrAlaThrProLeuAspPheLeuHisIle 153
 Db 61 ATTCGTGATAGTTGAATTTGGGATCTTTACAGCCACACCATTTGGATTTTCTCATATT 120
 QY 154 PheHisAlaIleAlaValSerThrArgProGlnLeuLeuPheSerLeuProLysLeuSer 173

Db 121 TTCATGCCATTCAGTGTCACTAGGCTCAGTTACTTTTCAGTTTCCCAAAATTGAGC 180
Qy 174 ProSerGlnHisLeuAlaValLeuThrLysGlnLeuHisCysMetAlaCysAasnGln 193
Db 181 CCATCTCAACATTGGCAGTCTTACCAAGCAACTACTTCACTGTATGGCTCGCAACCA 240
Qy 194 LeuLeuGlnPheArgGlySerMetLeuAlaLeuAlaMetValSerLeuGluMetGluLys 213
Db 241 CTTCTGCAATTCAGAGGATCCATGCTTCTGCGCATGGTGTAGTCTGGAAATGGAGAA 300
Qy 214 LeuLeuProAspTrpLeuSerLeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSer 233
Db 301 CTCATTCCTGATGGCTTCTTACAAATTTGAATGCTTACAGAACACACATGATGATG 360
Qy 234 SerGlnLeuIleHisCysArgGluLeuValAlaHisLeuSerThrLeuGlnSerSer 253
Db 361 TCCAGTGTGATCCATTGTCGGAGCTTGTGGCACATCACCTTCTCTCAGTCTTCC 420
Qy 254 LeuProLeuAasnSerValTyArgProLeuLysHisThrLeuValThrCysAsp 273
Db 421 CTGCTCTGAAATTCGTTTATGTCTACCGTCCCTCAAGCACACCCCTGGTGTGAC 480
Qy 274 LysGlyVal 276
Db 481 AAAGGAGTG 489

RESULT 8

US-10-085-783A-30212
; Sequence 30212, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liaw, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 30212
; LENGTH: 490
; TYPE: DNA
; ORGANISM: Human
US-10-085-783A-30212

Alignment Scores:
Pred. No.: 1.39e-89 Length: 490
Score: 811.00 Matches: 157
Percent Similarity: 98.77% Conservative: 4
Best Local Similarity: 96.32% Mismatches: 2
Query Match: 41.34% Indels: 0
DB: 17 Gaps: 0

US-09-736-250-1 (1-377) x US-10-085-783A-30212 (1-490)

Qy 114 LeuAlaArgAspSerPheCysGlySerSerGluIleLeuArgMetGluArgIle 133
Db 1 ATTGCCACAGAGAAGTTTCTGTGGATGTTCTCATCTGAAATTTTGGAGATGAGAGATT 60
Qy 134 IleLeuAspLysLeuAasnTrpAspLeuHisThrAlaThrProLeuAspPheLeuHisIle 153
Db 61 ATTCTGGATAGGTGAATTTGGATCTTTACACAGCACACCATTTGGATTTTCTTCATATT 120
Qy 154 PheHisAlaIleAlaValSerThrArgProGlnLeuLeuPheSerLeuProLysLeuSer 173
Db 121 TTCATGCCATTCAGTGTCACTAGGCTCAGTTACTTTTCAGTTTCCCAAAATTGAGC 180

Qy 174 ProSerGlnHisLeuAlaValLeuThrLysGlnLeuHisCysMetAlaCysAasnGln 193
Db 181 CCATCTCAACATTGGCAGTCTTACCAAGCAACTACTTCACTGTATGGCTCGCAACCA 240
Qy 194 LeuLeuGlnPheArgGlySerMetLeuAlaLeuAlaMetValSerLeuGluMetGluLys 213
Db 241 CTTCTGCAATTCAGAGGATCCATGCTTCTGCGCATGGTGTAGTCTGGAAATGGAGAA 300
Qy 214 LeuLeuProAspTrpLeuSerLeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSer 233
Db 301 CTCATTCCTGATGGCTTCTTACAAATTTGAATGCTTACAGAACACACATGATGATG 360
Qy 234 SerGlnLeuIleHisCysArgGluLeuValAlaHisLeuSerThrLeuGlnSerSer 253
Db 361 TCCAGTGTGATCCATTGTCGGAGCTTGTGGCACATCACCTTCTCTCAGTCTTCC 420
Qy 254 LeuProLeuAasnSerValTyArgProLeuLysHisThrLeuValThrCysAsp 273
Db 421 CTGCTCTGAAATTCGTTTATGTCTACCGTCCCTCAAGCACACCCCTGGTGTGAC 480
Qy 274 LysGlyVal 276
Db 481 AAAGGAGTG 489

RESULT 9

US-09-814-353-21294
; Sequence 21294, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21294
; LENGTH: 2146
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-814-353-21294

Alignment Scores:
Pred. No.: 1.55e-83 Length: 2146
Score: 770.50 Matches: 154
Percent Similarity: 91.18% Conservative: 1
Best Local Similarity: 90.59% Mismatches: 12
Query Match: 39.27% Indels: 3
DB: 10 Gaps: 1

US-09-736-250-1 (1-377) x US-09-814-353-21294 (1-2146)

Qy 210 GluMetGluLysLeuIleProAspTrpLeuSerLeuThrIleGluLeuGlnLysAla 229
Db 815 GAGCAGCCTATGTATTAATTAATGATCACTGTGTGGCTTTT---TTTTTTTCTCTGCC 871

QY 230 GlnMetAspSerSerGlnLeuIleHisCysArgGluLeuValAlaHisHisLeuSerThr 249
Db 872 CAGATGGATAGTCCAGTTGATCCATGTCGGAGCTGTGGCACATCACCTTTCTACT 931
QY 250 LeuGlnSerSerLeuProLeuAsnSerValTyrValTyrArgProLeuIleHisThrLeu 269
Db 932 CTGCGAGTCTTCCCTGCTCTGAATTCGGTTATGTCATCCGTCCTCAAGCACACCCCTG 991
QY 270 ValThrCysAspLysGlyValPheArgLeuHisProSerSerValProGlyProAspPhe 289
Db 992 GTGACCTGTGACAAAGAGGTGTCAGATTACATCCCTCTCTGTCGCCAGGCCAGACTTC 1051
QY 290 SerLysAspAsnSerLysProGluValProValArgGlyThrAlaAlaPheTyrHisHis 309
Db 1052 TCCAAGGACAAACAGCAAGCCAGAGTGCAGGTACAGGAGCTTTTACCATCAT 1111
QY 310 LeuProAlaAla-SerGlyCysLysGlnThrSer-ThrLysArgLysValGlnGluMetG 329
Db 1112 CTCCAGAGCTGCCAGTGGGTGCAAGCAGCTCTTACTAAACGCAAGTAGAGGAATGG 1171
QY 329 luValAspAspPheTyrAspGlyIleLysArgLeuTyrAsnGluAspAsnValSerGluA 349
Db 1172 AAGTGGATGACTTCTATGATGAATCAACGGCTCTATAATGAAGATTAATGTCAGAAA 1231
QY 349 snValGlySerValCysGlyThrAspLeuSerArgGlnGluGlyHisAlaSerProCysP 369
Db 1232 ATGTGGGTCTGTGTGGCACTGATTTATCAAGACAAGAGGAGCATGCTTCCCTTGTG 1291
QY 369 roProLeuGlnProValSerValMet 377
Db 1292 CACCTTTCAGCCTGTTTCTGTGCATG 1317

RESULT 10

US-10-242-535A-16032
; Sequence 16032, Application US/10242535A
; Publication No. US20040013663A1

GENERAL INFORMATION:

; APPLICANT: ChondroGene Inc.
; APPLICANT: Liaw, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; PRIOR FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16032
; LENGTH: 444
; TYPE: DNA
; ORGANISM: Human
US-10-242-535A-16032

Alignment Scores:

Pred. No.: 8,43e-80 Length: 444
Score: 731.00 Matches: 145
Percent Similarity: 98.64% Conservative: 0
Best Local Similarity: 98.64% Mismatches: 2
Query Match: 37.26% Indels: 0
DB: 17 Gaps: 0

US-09-736-250-1 (1-377) x US-10-242-535A-16032 (1-444)

QY 124 SerSerGluIleLeuArgMetGluArgIleIleLeuAspLysLeuAsnTrpAspLeuHis 143
Db 3 TCATCTGAAATTTTGAGAAATGAGAGAAATTTCTGGATAAGTTGAATGGATCTTCAC 62

QY 144 ThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSerThrArgPro 163
Db 63 ACAGCCACACCATTTGGATTTTCTCATATTTCCATGCCATTGCGAGTCAACTAGGCT 122
QY 164 GlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaValLeuThrLys 183
Db 123 CAGTTACTTTTCACTTTGGCCAAATTGAGCCCATCTCAACATTTGGCAGTCTTACCAG 182
QY 184 GlnLeuLeuHisCysMetAlaCysAsnGlnLeuGlnPheArgGlySerMetLeuAla 203
Db 183 CAATCTTACTGTATGGCTGCAACAACTCTGCAATTCAGAGGATCCATCTTGCT 242
QY 204 LeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSerLeuThrIle 223
Db 243 CTGSCCATGTTAGTCTGGAAATGGAGAACTCATCTGATTTGGCTTTCTTACAAAT 302
QY 224 GluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArgGluLeuVal 243
Db 303 GAATCTGCTTCAGAAAGCACAGATGGATAGCTCCAGTTGATCCATTTGTCGGAGCTTGTG 362
QY 244 AlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyrValTyrArg 263
Db 363 GCATCATCACCTTTCTACTCTGAGTCTCCCTGCTCTGAATTCCTGTTATGCTACCCG 422
QY 264 ProLeuLysHisThrLeuVal 270
Db 423 TCCCTCAAGCACACCCCTGGTG 443

RESULT 11

US-10-085-783A-16032
; Sequence 16032, Application US/10085783A
; Publication No. US20040037841A1

GENERAL INFORMATION:

; APPLICANT: ChondroGene Inc.
; APPLICANT: Liaw, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; PRIOR FILING DATE: 2002-02-28
; CURRENT APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16032
; LENGTH: 444
; TYPE: DNA
; ORGANISM: Human
US-10-085-783A-16032

Alignment Scores:

Pred. No.: 8,43e-80 Length: 444
Score: 731.00 Matches: 145
Percent Similarity: 98.64% Conservative: 0
Best Local Similarity: 98.64% Mismatches: 2
Query Match: 37.26% Indels: 0
DB: 17 Gaps: 0

US-09-736-250-1 (1-377) x US-10-085-783A-16032 (1-444)

QY 124 SerSerGluIleLeuArgMetGluArgIleIleLeuAspLysLeuAsnTrpAspLeuHis 143
Db 3 TCATCTGAAATTTTGAGAAATGAGAGAAATTTCTGGATAAGTTGAATGGATCTTCAC 62
QY 144 ThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSerThrArgPro 163
Db 63 ACAGCCACACCATTTGGATTTTCTCATATTTCCATGCCATTGCGAGTCAACTAGGCT 122
QY 164 GlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaValLeuThrLys 183

Db 123 CAGTTACTTTTCAGTTGGCCCAATTGAGCCCATCTCAACATTTGGGAGCTCTTACCAAG 182
Qy 184 GlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySerMetLeuAla 203
Db 183 CAACTACTTCACTGTATGGCTGCAACCACTTCTGCAATTCAGAGGATCCATGCTTGT 242
Qy 204 LeuAlaMetValSerLeuLeuGluMetGluLysLeuLeuProAspTrpLeuSerLeuThrIle 223
Db 243 CTGGCCCATGGTTAGTCTGGAAATGGAGAACTCATCTGATTTGGCTTTCTTCTACAAAT 302
Qy 224 GluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuLeuHisCysArgGluLeuVal 243
Db 303 GAACCTGTTTCAAGAACACAGATGATGATCCACGTTGATCCATTTGGGAGCTTGTG 362
Qy 244 AlaHisHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyrValTyrArg 263
Db 363 GCACATCACCTTTCTACTGTGAGTCTTCCCTGCTCTGAAATCCGTTTATGTCATCCCG 422
Qy 264 ProLeuLysHisThrLeuVal 270
Db 423 TCCCTCAAGCACACCTCGGTG 443
RESULT 12
US-10-242-535A-6834
; Sequence 6834, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US 10/242,535A
; PRIOR FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6834
; LENGTH: 389
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (358)..(358)
; OTHER INFORMATION: n is a, c, g, or t
US-10-242-535A-6834
Alignment Scores:
Pred. No.: 1.93e-68 Length: 389
Score: 638.00 Matches: 128
Percent Similarity: 98.46% Conservative: 0
Best Local Similarity: 98.46% Mismatches: 1
Query Match: 32.52% Indels: 1
DB: 17 Gaps: 0
US-09-736-250-1 (1-377) x US-10-242-535A-6834 (1-389)
Qy 2 LysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIleThr 21
Db 2 AAGTTTCAGGGCCCTTGGAAACACAGATGTTCTTCTCTGTTGGAAAGCCATCACT 61
Qy 22 ArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnValSer 41
Db 62 AGGGAAGCACAGATGTGAAAGTGAATGTGGGAAATGCCTTCAATCAGATGTTTCT 121
Qy 42 ProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsnLeu 61
Db 121
Qy 62 TysProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrValLys 81
Db 182 TACCCAGAACATTTGCTCTGGCTAGCAGTCTTTTGGTAGTCTTTTACCGTAAAG 241

Db 122 CCATCCAGAGAGATGAGTAATTCAATGCTGCCCAAACTCAAGTACCATTCAACCTT 181
Qy 62 TyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrValLys 81
Db 182 TACCCAGAACATTTGCTCTGGCTAGCAGTCTTTTGGTAGTCTTTTACCGTAAAG 241
Qy 82 AlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaLysThr 101
Db 242 GCTCATCCCAAAATACCTTGTATTGCAATCAGCTGTTTTTCTTAGCTGCCAAGCT 301
Qy 102 ValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPhe-CysG1 121
Db 302 GTTGAGGAAGATGAGAGAAATCCAGTACTAAAGGTATTGGCAGAGACAGATTTCTGNGGG 361
Qy 121 YCysSerSerSerGluIleLeuArgMet 130
Db 362 ATGTTCTCTCATCTGAAATTTTGAGATG 389
RESULT 13
US-10-085-783A-6834
; Sequence 6834, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US 10/085,783A
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6834
; LENGTH: 389
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (358)..(358)
; OTHER INFORMATION: n is a, c, g, or t
US-10-085-783A-6834
Alignment Scores:
Pred. No.: 1.93e-68 Length: 389
Score: 638.00 Matches: 128
Percent Similarity: 98.46% Conservative: 0
Best Local Similarity: 98.46% Mismatches: 1
Query Match: 32.52% Indels: 1
DB: 17 Gaps: 0
US-09-736-250-1 (1-377) x US-10-085-783A-6834 (1-389)
Qy 2 LysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIleThr 21
Db 2 AAGTTTCAGGGCCCTTGGAAACACAGATGTTCTTCTCTGTTGGAAAGCCATCACT 61
Qy 22 ArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnValSer 41
Db 62 AGGGAAGCACAGATGTGAAAGTGAATGTGGGAAATGCCTTCAATCAGATGTTTCT 121
Qy 42 ProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsnLeu 61
Db 122 CCATCCAGAGAGATGAGTAATTCAATGCTGCCCAAACTCAAGTACCATTCAACCTT 181
Qy 62 TyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrValLys 81
Db 182 TACCCAGAACATTTGCTCTGGCTAGCAGTCTTTTGGTAGTCTTTTACCGTAAAG 241

Qy 82 AlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaAlaLysThr 101
Db 242 GCTCATCCAAATACTTGGTGTGATTGCAATCAGCTGTTTCTTCTAGCTGCCAAGACT 301
Qy 102 ValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPhe-CysG1 121
Db 302 GTTGAGGAGATGAGAGAAATCCAGTACTAAAGGTATTGGCAAGAGACAGTTTCTGTGGGG 361
Qy 121 yCysSerSerGluLeuLeuArgMet 130
Db 362 AGTTCTTCATCTGAATTTTGGAGATG 389

RESULT 14

US-10-242-535A-33391
; Sequence 33391, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 33391
; LENGTH: 369
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2)..(2)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (25)..(25)
; OTHER INFORMATION: n is a, c, g, or t
US-10-242-535A-33391

Alignment Scores:
Pred. No.: 7,07e-67 Length: 369
Score: 625.00 Matches: 119
Percent Similarity: 99.17% Conservative: 1
Best Local Similarity: 98.35% Mismatches: 1
Query Match: 31.86% Indels: 0
DB: 17 Gaps: 0

US-09-736-250-1 (1-377) x US-10-242-535A-33391 (1-369)

Qy 208 SerLeuGluMetGluLysLeuIleProAspTrpLeuSerLeuThrIleGluLeuGln 227
Db 4 AGTCTGGAATGGAGAACTCNTTCTGATGGCTTCTTCTTACAAATGAAGTCTTCAG 63
Qy 228 LysAlaGlnMetAspSerSerGlnLeuIleHisCysArgGluLeuValAlaHisLeu 247
Db 64 AAAGCACAGATGGATAGTCCAGTTGATCCATTGTCGGGAGCTTGTGGCACATCACCCT 123
Qy 248 SerThrLeuGlnSerSerLeuProLeuAsnSerValTyrArgProLeuLysHis 267
Db 124 TCTACTCTGAGCTTCCCTGCCCTCGAATTCGGTTTATGTCTACCGTCCCTCAAGCAC 183
Qy 268 ThrLeuValThrCysAspLysGlyValPheArgLeuHisProSerSerValProGlyPro 287
Db 184 ACCCTGGTGACCTGTGACAAAGGAGTGTTCAGATTACATCCCTCTCTGTGCCAGGCCCA 243

Qy 288 AspPheSerLysAspAsnSerLysProGluValProValArgGlyThrAlaAlaPheTyr 307
Db 244 GACTTCTCCAGGACAAACAGCAGCAAGTGCAGTCCAGGTAGCAGCCCTTTTAC 303
Qy 308 HisHisLeuProAlaAlaSerGlyCysLysGlnThrSerThrLysArgLysValGluGlu 327
Db 304 CATCATCTCCAGCTGCCAGTGGGTGCAAGCAGACCTCTACTAAACGCAAGTAGAGAA 363
Qy 328 Met 328
Db 364 ATT 366

RESULT 15

US-10-085-783A-33391
; Sequence 33391, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 33391
; LENGTH: 369
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2)..(2)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (25)..(25)
; OTHER INFORMATION: n is a, c, g, or t
US-10-085-783A-33391

Alignment Scores:
Pred. No.: 7,07e-67 Length: 369
Score: 625.00 Matches: 119
Percent Similarity: 99.17% Conservative: 1
Best Local Similarity: 98.35% Mismatches: 1
Query Match: 31.86% Indels: 0
DB: 17 Gaps: 0

US-09-736-250-1 (1-377) x US-10-085-783A-33391 (1-369)

Qy 208 SerLeuGluMetGluLysLeuIleProAspTrpLeuSerLeuThrIleGluLeuGln 227
Db 4 AGTCTGGAATGGAGAACTCNTTCTGATGGCTTCTTCTTACAAATGAAGTCTTCAG 63
Qy 228 LysAlaGlnMetAspSerSerGlnLeuIleHisCysArgGluLeuValAlaHisLeu 247
Db 64 AAAGCACAGATGGATAGTCCAGTTGATCCATTGTCGGGAGCTTGTGGCACATCACCCT 123
Qy 248 SerThrLeuGlnSerSerLeuProLeuAsnSerValTyrArgProLeuLysHis 267
Db 124 TCTACTCTGAGCTTCCCTGCCCTCGAATTCGGTTTATGTCTACCGTCCCTCAAGCAC 183
Qy 268 ThrLeuValThrCysAspLysGlyValPheArgLeuHisProSerSerValProGlyPro 287
Db 184 ACCCTGGTGACCTGTGACAAAGGAGTGTTCAGATTACATCCCTCTCTGTGCCAGGCCCA 243
Qy 288 AspPheSerLysAspAsnSerLysProGluValProValArgGlyThrAlaAlaPheTyr 307

Db	244	GACTTCTCCAAGGACACAGCAGCCAGAAAGTGCCAGTCAGAGGTACAGCAGCCTTTTAC	303
Qy	308	HisHisLeuProAlaAlaSerGlyCysLysGlnThrSerThrLysArgLysValGluGlu	327
Db	304	CATCATCTCCAGCTGCCAGTCAGTGGGTGCAAGCAGACCTCTACTAAACGCAAAAGTAGAGAA	363
Qy	328	Met	328
Db	364	ATT	366

Search completed: February 11, 2005, 10:20:36
 Job time : 1619.1 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 11, 2005, 03:23:50 ; Search time 5876.76 Seconds
(without alignments)
2441.859 Million cell updates/sec

Title: US-09-736-250-1

Perfect score: 1962

Sequence: 1 MKFPGLNQLSLLEKAI.....LSROEGHASPPLQPVSV 377

Scoring table:

	BLOSUM62	Xgapop 10.0	Xgapext 0.5
Ygapop 10.0			0.5
Ygapop 6.0			7.0
Delop 6.0			7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US09736250/runat_07022005_154924_20414/app_query.fasta_1.718
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOPCL=0 -LOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09736250 @CGN 1 1 4385 @runat_07022005_154924_20414 -NCPU=3
-NO.MMAP -LARGQUERY -NEG SCORE=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*	1: gb est1.*
2: gb est2.*	
3: gb_hcc.*	
4: gb_est3.*	
5: gb_est4.*	
6: gb_est5.*	
7: gb_est6.*	
8: gb_gsl1.*	
9: gb_gsl2.*	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1509	97.3	1134	9	AY412158 Homo sapi
2	1851	94.3	2348	3	BC029328 Mus muscu
3	1841	93.8	2045	3	AK050465 Mus muscu
4	1817	92.6	2739	3	AK079476 Mus muscu
5	1746	89.0	1110	9	AY412160 Mus muscu
6	1593	81.2	1085	7	CR754276 Mus muscu
7	1577	80.4	967	7	CR754276 CR754276
8	1535	78.2	992	7	CN647834 ILLUMIGEN
9	1456	74.2	920	5	CB646424 ILLUMIGEN
					BQ673277 AGENCOURT

RESULT 1	LOCUS	AY412158	Homo sapiens CCNI gene, genomic survey sequence.	1134 bp	DNA	linear	GSS 16-DEC-2003
DEFINITION	LOCUS	AY412158	Homo sapiens CCNI gene, genomic survey sequence.	1134 bp	DNA	linear	GSS 16-DEC-2003
ACCESSION	AY412158	GI:39768123					
VERSION	AY412158.1	GI:39768123					
KEYWORDS	GSS.						
SOURCE	Homo sapiens (human)						
REFERENCE	1 (bases 1 to 1134)						
AUTHORS	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreria, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.						
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios						
JOURNAL	Science 302 (5652), 1960-1963 (2003)						
PUBMED	14671302						
REFERENCE	2 (bases 1 to 1134)						
AUTHORS	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreria, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.						
TITLE	Direct Submision						
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA						
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.						
FEATURES	Location/Qualifiers						
	1..1134						

Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 10 Row: i Column: 3
This clone has the following problem: no 5' EST match.

FEATURES

Location/Qualifiers
1. 2348
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:3583701"
/tissue_type="Mammary tumor. Metallothionien-TGF alpha model. 10 month old virgin mouse. Taken by biopsy."
/clone_lib="NCI CGAP_Mam1"
/lab_host="DH10B"
/note="vector: pCMV-SPORT6"

ORIGIN

Alignment Scores:
Pred. No.: 1.99e-186 Length: 2348
Score: 1851.00 Matches: 355
Percent Similarity: 97.08% Conservative: 11
Best Local Similarity: 94.16% Mismatches: 11
Query Match: 94.34% Indels: 0
DB: 3 Gaps: 0

US-09-736-250-1 (1-377) x BC029328 (1-2348)

Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaile 20
Db 160 ATGAAGTTTCAGGACCTTGGAAACACAGAGATTGCTCTCTGTTGGAAAGGCAATC 219
Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 220 TCCAGGGAAGCCAGATGTGGAGGTGAATGTGCCGAAATATACCTACAAATCGAATGTT 279
Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLysLysLysLysLysLys 60
Db 280 TCTCATCCAGAGAGATGAATTAATCAATGGTTGCCAACTCAATACCATGCTTCAAC 339
Qy 61 LeuTrpProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 340 CTCTATCCAGAAACATTTGCTCTGCCAAGCAGTCTTTGGATAGTGTTCAGTACAGTA 399
Qy 81 LysAlaHisProLysTrpLeuSerCysIleAlaLysSerCysPhePheLeuAlaLys 100
Db 400 AAAGCCCATCCAAATATTTGAATTTGATTTGCAATCAGCTGTTTTTTTCTGGCTGCTAAG 459
Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 460 ACTGTTGAGGAAGATGAGAAATTTCCAGTGTCAAGGTATTGGCAAGACAGATTCTGT 519
Qy 121 GlyCysSerSerGluIleLeuArgMetGluArgIleLeuLeuAspLysLeuAsnTrp 140
Db 520 GGATGTTCTCATCTGAGATTTTCAGATTCGAGAGATTTATCTGGATAATTCGAATGG 579
Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 580 GATCTTCACCGGTACACCATTTGGATTTTCTTCACATTTTCCATGTCATTCGCGTCA 639
Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 640 ACTAGGCTCTAGTACTTTTCAGTTTGGCCAAATGAGCCCATCTCAACATTTGGCAGTC 699
Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
Db 700 CTGACCAAGCAGCTGCTTCACTGTATGGCTTGCACCACTCTTCGACATTCGAAGGCTCC 759
Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220

Db 760 ATGCTTGCTCTGCCCAGTGTAGTCTGGAATGAGAAATCATCTCTGATTGCTTCCT 819
Qy 221 LeuThrIleGluLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
Db 820 CTTACGATGAACCTGCTTCAGAAAGCACAGATGCAGAGCTCCCGATGATCCATGTCG 879
Qy 241 GluLeuValAlaHisLysLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTrp 260
Db 880 GAGCTGTGTCATATCACCTTTCTGCTGTCAGTCTGCCCTGCTCTAAATTCGTTTAT 939
Qy 261 ValTrpArgProLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db 940 GTCTACCGTCCCTCAGACACACCTGTAACCTGTGACAAAGAGCATTCATTAATCAT 999
Qy 281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
Db 1000 CCTCTCTGCTCTCAGGCCAGATTTCTCCAGGACAAACAGAGCCAGAGTCCAGTC 1059
Qy 301 ArgGlyThrAlaAlaPheTrpHisLeuProAlaLysSerGlyCysLysGlnThrSer 320
Db 1060 CGAGGTCCAGCAGCTTCCACCTGTCATCTCCCGCTGCCAGTGGGTGCAAGCAACCTCT 1119
Qy 321 ThrLysArgLysValGluGluMetGluValAspAspPheTrpAspGlyIleLysArgLeu 340
Db 1120 GCTAAACGGAAGATGGAGAGATGGAGGTGGATGACTTCTACGATGGGATCAACGGCTC 1179
Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
Db 1180 TATAATGAGGACCAATGGTCTGAGATGTGGTCTGTATGTGGCACTGATTTATCAAG 1239
Qy 361 GlnGluGlyHisAlaSerProCysProLeuGlnProValSerValMet 377
Db 1240 CAAGAGGGCCATGTTCCCTCTGTCACCTTTCAGCTTTCCTGTCATG 1290
RESULT 3
AK050465 2045 bp mRNA linear HTC 03-APR-2004
LOCUS Mus musculus adult pancreas islet cells cDNA, RIKEN full-length
DEFINITION enriched library, clone:C820001G04 product:cyclin I, full insert
sequence.
AK050465
AK050465.1 GI:26341217
VERSION HTC; CAP trapper.
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE
2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20493374
PUBMED 11042159
REFERENCE
3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kiteunai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Izawa, M., Ohara, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE PUBMED REFERENCE AUTHORS	20530913 11076861 4 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium. Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001) 5 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002) 6 (bases 1 to 2045) Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T., Hori, F., Imocani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akashira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toyata, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission	Alignment Scores: Pred. No.: 1.88e-185 Score: 1841.00 Percent Similarity: 96.55% Best Local Similarity: 93.63% Query Match: 93.83% DB: 3 Gaps: 0 US-09-736-250-1 (1-377) x AK050465 (1-2045)	2045 353 11 13 0 0
TITLE JOURNAL REFERENCE AUTHORS	1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuGluLysAlaIle 20 628 ATGAAGTTTCACGACCTTTGGAAACACACAGATTGCTCTCTGTTGGAAAGGCAATC 687 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40 688 TCCAGGGAAGCCAGATGTGGAAGGTGAATGTGCCGAAAATACCTCAAAATCAGAATGTT 747 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn 60 748 TCTCCATCCACGAGAGATGAGTAATTCATGTGTGCCAACTCAATACCACTTCAAC 807 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80 808 CTCTATCCAGAAACATTTGCTCTGCGCAAGCAGTCTTTTGGTAGGTTTTAGCTACAGTA 867 81 LysAlaHisProLysTyrLeuSerCysIleAlaLysSerCysPheLeuAlaLys 100 868 AAGCCCATCCAAAATATTGTAATTTATGCAATCAGCTGTTTTTTCTGGCTGCTAAG 927 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120 928 ACTGTTGGAAGATGAGAAATTCAGTGTCTAAAGTATTGCGACAGACAGCAGTTCTGT 987 121 GlyCysSerSerGluLeuLeuArgMetGluArgIleLeuLeuAspLysLeuAsnTrp 140 988 GGATGTTCTCTCATCTCAGATTTTGAGATGGAGAGAATTTATCTGATAAATGAATTGG 1047 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160 1048 GATCTTCACAGCGCTACACATTTGGAATTTCTTCAATTTCCATGCCATTCGGGTGCA 1107 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180 1108 GCTAGGCTTCAGTTACTTTTCAGTTTGCCCAATTTGAGCCCATCTCAACATTTGGCAGTC 1167 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200 1168 CTGACCAAGCAGCTGCTTCACTGTATGGCTGCAACCAACTTCTGCAGTTCAAGGGTCC 1227 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220 1228 ATGCTTGCTCTGGCCATGTTAGTCTGGAATGGAGAACTCATTCTCATTTGGCTTCCT 1287 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240 1288 CTTTACGATTGAACCTGCTTCAGAAAGCACAGATGGACAGCTCCAGTTGATCCACTGCG 1347 241 GluLeuValAlaHisHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260 1348 GAGCTGGTGGCATATCACCTTTCTGCTCTGCAGTCTGCCCTGCTGCTAAATTCGTTAT 1407 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280 1408 GTCTACCGTCCCTCAAGCACACCTCTGGTAACCTGTGACAAAGGACATTCATTTACAT 1467 281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300 1468 CCTCTCTGCTCTCAGGCCAGATTCTTCCAAGGACCAACAGCAAGCAGAGTGCAGTC 1527 301 ArgGlyThrAlaAlaPheTyrHisHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320		
COMMENT	Submitted (16-JUL-2001) Yoshihide Hayaishizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Cells were provided by Hiroo Iwata (Department of Reproductive Materials Field of Tissue Engineering Institute for Frontier Medical Sciences, Sakyoku-ku, Kyoto, 606-8507, Japan) whose assistance we gratefully acknowledge. Please visit our web site for further details. URL: http://genome.gsc.riken.jp/ URL: http://fantom.gsc.riken.jp/ Location/Qualifiers		
FEATURES SOURCE	1..2045 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J" /db_xref="FANTOM_DB:C820001G04" /db_xref="taxon:10090" /clone="C820001G04" /cell_type="islet cells" /tissue_type="pancreas" /clone_lib="RIKEN full-length enriched mouse cDNA library" /dev_stage="adult" 628..1761 /note="unnamed protein product; cyclin I (MGI:1341077, GB NM_017367, evidence: BLASTN, 98%, match=1534) putative" /codon_start=1 /protein_id="BAC34271.1" /db_xref="GI:26341218" /translation="MKPPGLEHRLSSLLERAIISREAWKYNVPKIPNQNVSQ RDEVQWLAKLYQFNLYPETFLASLLRFLATVKHAKYLNCAISCFPLAAKTV EEDKIPVLKVLARDSFCGSSSEILMERIILDKLNDWIDLTATPDLFLHFAIAVS ARPLLPSLQPSQSLAVLTQQLHCWACNQLQFPGSMALAVSLEMEKLIPTW LPTLIELQAKMDSSQLIHRELVAYHLALQSLPLNSVYVYRPLKHLVLCIDGA FKLHPSSVSGPDSKNSKEPVRGPAFHLPLPAASGCKQTSAKRKRVEEMVEDDFF DGIKRLYNEDNGPENVSGVGTDLRSRGEHASFCCPPIQPVSM"		
CDS			
ORIGIN			

Db 1528 CGAGGTCAGCAGCTTCCACCTGCATCTCCCGCTGCCAGTGGTGCAGCAACCACTCT 1587

Qy 321 ThrIysArgLysValGluGluMetGluValAspPheTyrAspGlyIleIysArgLeu 340

Db 1588 GCTAAACGGAAGTCGAGGAGATGAGGTGATGACCTTCTACGATGGGATCAAGCGGCTC 1647

Qy 341 TyrHsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360

Db 1648 TATTAATGAGGACAATGGTCCTGAGAATGTGGTCTCTGTATGTGCACCTGATTTATCAAG 1707

Qy 361 GlnGluGlyHisAlaSerProCysProProLeuGlnProValSerValMet 377

Db 1708 CAAGAGGCCATGCTTCCCTGTCCACCTTGACCTGTGTCTGTGTCATG 1758

RESULT 4

AK079476

LOCUS

DEFINITION Mus musculus 16 days neonate thymus cDNA, RIKEN full-length enriched library, clone: A130017J05 product: cyclin I, full insert sequence.

ACCESSION AK079476

VERSION AK079476.1 GI:26098528

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE

AUTHORS Carninci, P. and Hayashizaki, Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Mech. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

REFERENCE

AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20499374

PUBMED 11042159

REFERENCE

AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagasaka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yanamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913

PUBMED 11076861

REFERENCE

AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409, 685-690 (2001)

REFERENCE

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

REFERENCE

AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Oheato, N.,

Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

Direct Submission

Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL: http://genome.gsc.riken.jp/

URL: http://fantom.gsc.riken.jp/.

FEATURES

source

1..2739

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6J"

/db_xref="FANTOM DB:A130017J05"

/db_xref="taxon:10090"

/clone="A130017J05"

/tissue_type="thymus"

/clone_lib="RIKEN full-length enriched mouse cDNA library"

/dev_stage="16 days neonate"

567..1701

/notes="cyclin I (MGD|MG1:1341077, GB|NM_017367, evidence: BLASTN, 98%, match=1534)

putative"

2723..2728

/notes="putative"

2739

/notes="putative"

ORIGIN

Alignment Scores:

Pred. No.: 1..182 Length: 2739

Score: 1817.00 Matches: 351

Percent Similarity: 95.77% Conservative: 11

Best Local Similarity: 92.86% Mismatches: 15

Query Match: 92.61% Indels: 1

DB: 3 Gaps: 0

US-09-736-250-1 (1-377) x AK079476 (1-2739)

Qy 1 MetLysPheProGly-ProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaI 20

Db 567 ATGACGTTTCAGACCCCTTGGAACCAACAGAGATTGCTCTCTGTGGAAAGGCAAT 626

Qy 20 eThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVa 40

Db 627 CTCACGGGAAGCCACAGATGTGAAGGTGAATGTGCCGAACATACCTACCAATCATGT 686

Qy 40 lSerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAs 60

Db 687 TTCTCCATCCAGAGAGATGAAGTAATTAATGTTATGCAATCAGCTGTTTTTCTGGCTGCTAA 746

Qy 60 nLeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVa 80

Db 747 CCTCTATCCAGAACATTTGCTCTGCAAGCAGTCTTTTGATAGGTTTTTAGCTACAGT 806

Qy 80 lLysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaLaLy 100

Db 807 AAAAGCCCATCCAAAATATTGAATGTTATGCAATCAGCTGTTTTTCTGGCTGCTAA 866

Qy 100 sThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCy 120

```
Db 867 GACTGTTGAGGAAGATGAGAAATTCAGTCTCTAAAGGTATTGGCAAGACAGACTTCTGT 926
Qy 120 sGlyCysSerSerGluLeuAArgMetGluArgIleLeuAAspLysLeuAAsnTr 140
Db 927 TGGATGTTCTTCATCTGAGATTTTGGAGATGGAGAGATTAATCTCGGATAAATGGAATG 986
Qy 140 pAspLeuHisThrAlaThrProLeuAAspPheLeuHisIlePheHisAlaIleAlaValSe 160
Db 987 GGATCTTCACACGCTACACCATTTGATTTCTTTCACATTTTCCATGCCATTGGCGTGC 1046
Qy 160 rThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVa 180
Db 1047 AGCTAGGCTCAGTTACTTTTCAGTTTGGCCAAATTCAGCCCATCTCAACATTTGGCAGT 1106
Qy 180 lLeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuPheArgGlySe 200
Db 1107 CCTGACCAAGCAGTCTTCTACTGTATGGCTGCAACCACTTCTGCAGTTCAAGGGTC 1166
Qy 200 rMetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSe 220
Db 1167 CATGCTTGCTCTGGCCATGTTAGTCTGGAATGGAGAACTCATTTCTGATTGGCTTCC 1226
Qy 220 rLeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysAr 240
Db 1227 TCTTACGATTTGAATCTGTCAGAAAGCACAGATGGACAGCTCCCGAGTTGATCCACTGTGC 1286
Qy 240 gGluLeuValAlaHisIleLeuSerThrLeuGlnSerSerLeuProLeuLeuSerValTy 260
Db 1287 GGAGCTGGTGCATATACCTTTCTGCTCTGCATGTGCTGCTCTTAATTCCTGTTA 1346
Qy 260 rValTyArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHi 280
Db 1347 TGTCTACGTCCTCCCTCAAGCACACCTGGTAACCTGTGACAAAGAGCAATTCAAATTACA 1406
Qy 280 sProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVa 300
Db 1407 TCCCTCTCTCTCTCAGGCCAGATTTCTCAAGCAACACAGCAAGCAGAGTGCAGT 1466
Qy 300 lArgGlyThrAlaAlaPheTyHisIleLeuProAlaAlaSerGlyCysLysGlnThrSe 320
Db 1467 CCGAGTCCAGCAGCTTCCAGCTGCATCTCCCGCTGCCAGTGGTGCAAGCAAACTC 1526
Qy 320 rThrLysArgLysValGluGluMetGluValAspAspPheTyArgGlyIleLysArgLe 340
Db 1527 TGTAAACGGAAAGTGGAGAGATGGAGTGGATGACTTCTACGATGGATCAAGCGCT 1586
Qy 340 uTyAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerAr 360
Db 1587 CTATAATGAGACAATGCTCTCGAATGTGGGTCTGTATGTGGCACTGATTTATCAAG 1646
Qy 360 gGlnGluGlyHisAlaSerProCysProProLeuGlnProValSerValMet 377
Db 1647 GCAAGAGGGCCATGCTCCCTCTCCACCTTTCAGCCCTGTTCTGTGATG 1698

RESULT 5
LOCUS AY412160
DEFINITION Mus musculus CCNI gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION AY412160
VERSION AY412160.1 GI:39768125
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1110)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
Location/Qualifiers
1..1110
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
<1..>1110
/genes="CCNI"
/locus_tag="HCM4464"
ORIGIN
Alignment Scores:
Pred. No.: 1,07e-175 Length: 1110
Score: 1746.00 Matches: 345
Percent Similarity: 94.43% Conservative: 11
Best Local Similarity: 91.51% Mismatches: 14
Query Match: 88.99% Indels: 9
DB: Gaps: 1
US-09-736-250-1 (1-377) x AY412160 (1-1110)
Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle 20
Db 1 ATCAAGTTCCTCAGACCTTTGGAAACACAGAGATTGTTCTCTGTTGGAAGGGCAATC 60
Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 61 TCCGAGGAGGCCAGATGTGGAAGTGAATGTCCGAAATACCTACAAATCAGATGTT 120
Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLysLysTrpGlnPheAsn 60
Db 121 TCTCCATCCAGAGATGAAGTAATTCATATGTTGGCCAACTCAAAATACCAATTCAC 180
Qy 61 LeuTyProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 181 CTATATCCAGAAACATTTGCTCTGGCAAGCAGTCTTTTGGATAGGTTTTTGTCTACAGTA 240
Qy 81 LysAlaHisProLysTyLeuSerCysIleAlaIleSerCysPhePheLeuAlaAlaLys 100
Db 241 AAAGCCCATCAAAATATTGTAATTTGATTTGCAATCAGCTGTTTTTTCTGGCTGCTAAG 300
Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 301 ACTGTTGAGGAAGATGAGAAATTCAGTCTTAAAGGTATTGGCAAGACAGCTTCTGT 360
Qy 121 GlyCysSerSerGluIleLeuAArgMetGluArgIleIleLeuAspLysLeuAsnTrp 140
Db 361 GGATGTTCTCATCTGAGATTTTGGAGATGGAGAGATTAATTTCTGGATAAATGGAATGG 420
Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 421 GATCTTCACACGGCTACACCATTTGGATTTTCTTTCACA--TTCCATGCCATTGGCGTCA 478
Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 479 GCTAGGCTCAGTTACTTTTCAGTTTGGCCAAATTCAGCCCATCTCAACATTTGGCAGTC 538
Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
Db 539 CTGACCAAGCAGTGTCTTCACTGTATGGCTGCAACCACTTCTGCAGTTTCAAGGGTCC 598
```

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous

Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuLeuLeuProAspTyrLeuSer 220
 Db 599 ATGTTGCTGCTGGCCATGTTAGTCTGGAAATGAGAAACTCATCTCGATGGCTTCCT 658
 Qy 221 LeuThrileGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuLeuHisCysArg 240
 Db 659 CTTAGATTGACCTGCTTCAGAAAGCAGAC-----TGTCGG 696
 Qy 241 GluLeuValAlaHisHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
 Db 697 GAGCTGGTGGCATATACCTTCTGCTCTGCAGTCTGCCCTCAAAATTCGGTTAT 756
 Qy 261 ValTyrArgProLeuLysHisHisLeuValThrCysAspLysGlyValPheArgLeuHis 280
 Db 757 GTCTACCGTCCCTCAAGCACACCTGTGTAACTGTGACAAAGGAGCATTCAAATATCAT 816
 Qy 281 ProSerSerValProGlyProAspPheSerLysAspSerLysProGluValProVal 300
 Db 817 CCTCTCTGCTCAGGCCAGATTTCTCCAGGACACACAGCCAGAGTCCAGTC 876
 Qy 301 ArgGlyThrAlaAlaPheTyrHisHisLeuProAlaLeuSerGlyCysLysGlnThrSer 320
 Db 877 CGAGTCCAGCAGCGCTTCCACTGTCATCTCCCGCTGCCAGTGGGTGCAAGCAAACTCT 936
 Qy 321 ThrLysArgLysValGluGluMetGluValAspPheTyrAspGlyLysArgLeu 340
 Db 937 GCTAAACGGAAGTGGAGGAGATGGAGTGGATGACTTCTACGATGGGATCAAGCGGCTC 996
 Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
 Db 997 TATATGAGGACATGGTCTGAGATGTGGTCTGTATGTGGCAGCTGATTTATCAAGG 1056
 Qy 361 GlnGluGlyHisAlaSerProCysProProLeuGlnProValSerValMet 377
 Db 1057 CAAGAGGCGCCATGCTTCCCTCCCTGTCACCTTTGCGAGCTGTTCTGTGTCATG 1107

RESULT 6
 LOCUS CR754276 1085 bp mRNA linear EST 02-SEP-2004
 DEFINITION CR754276 Rattus norvegicus muscle Sprague-Dawley Rattus norvegicus
 cDNA clone GP0AAA12ZH09, mRNA sequence.

ACCESSION CR754276 GI:51866233
 VERSION EST.
 KEYWORDS Rattus norvegicus (Norway rat)
 SOURCE Rattus norvegicus
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.

REFERENCE 1 (Bases 1 to 1085)
 AUTHORS Cros, N., Tkatchenko, A. V., Pisani, D. F., Leclerc, L., Leger, J. J.,
 Marini, J. F. and Decheane, C. A.
 TITLE Analysis of altered gene expression in rat soleus muscle atrophied
 by disuse

J. Cell. Biochem. 83 (3), 508-519 (2001)
 JOURNAL 21479502
 MEDLINE 11596118
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequençage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
 Genoscope sequence ID: GP0AAA12ZH09CP1.
 Location/Qualifiers

FEATURES
 source
 1. 1085
 /organism="Rattus norvegicus"
 /mol_type="mRNA"
 /strain="Sprague-Dawley"
 /db_xref="taxon:10116"
 /clone="GP0AAA12ZH09"
 /sex="Female"
 /tissue_type="muscle"
 /clone_lib="Rattus norvegicus muscle Sprague-Dawley"
 /note="Vector: pCKII-TOPO; Pietu G., Cros N., Leger J. J.,

Decheane C.A. Subtracted library from atrophied and control soleus muscles subtraction was performed according to Diatchenko et al. (Diatchenko L, Lau YF, Campbell AP, Chenchik A, Moqadam F, Huang B, Lukyanov S, Lukyanov K, Gurekaya N, Sverdlov ED, Siebert PD. Suppression subtractive hybridization: a method for generating differentially regulated or tissue-specific cDNA probes and libraries. Proc Natl Acad Sci U S A. 1996; 93 :6025-30) Rats were female Sprague Dawley between 200 and 220g. Soleus muscle atrophy was performed by 14 days of hindlimb suspension."

ORIGIN

Alignment Scores: 2.45e-159 Length: 1085
 Pred. No.: 1593.00 Matches: 318
 Score: 94.54% Conservative: 11
 Percent Similarity: 91.38% Mismatches: 18
 Best Local Similarity: 81.19% Indels: 3
 Query Match: 7 Gaps: 0
 DB:

US-09-736-250-1 (1-377) x CR754276 (1-1085)

Qy 31 ValArgLysMetProSerAsnGlnAsnValSerProSerGlnArgAspGluValileGln 50
 Db 1 GTACCAAAATACCTCAAAACCAGATGTTTCTCCATCCAGAGAGAGCAATA-ATTGAG 59
 Qy 51 TrpLeuAlaLysLeuLysTyrGlnPheAsnLeuTyrProGluThrPheAlaLeuAlaSer 70
 Db 60 TGGTTGGCCAAACTCAATACCAGTTCAACTTATCCAGAAACATTTGCTCTGCGAAGC 119
 Qy 71 SerLeuLeuAspArgPheLeuAlaThrValLysAlaHisProLysTyrLeuSerCysIle 90
 Db 120 AGTCTTTGGATAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 179
 Qy 91 AlaIleSerCysPhePheLeuAlaLysThrValGluGluAspGluArgIleProVal 110
 Db 180 GCATCAGCTGTTTTTTTCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 239
 Qy 111 LeuLysValLeuAlaArgAspSerPheCysGlyCysSerSerSerGluIleLeuArgMet 130
 Db 240 CTAAGGATTTGGCAAGACAGAGTCTTCTGTTGAGTGTCTCTCATCTGAGATTTTCCAGATG 299
 Qy 131 GluArgIleLeuLeuAspLysLeuAsnTrpAspLeuHisThrAlaThrProLeuAspPhe 150
 Db 300 GAGAGAAATTTCTGGATAAATTGAATTTGGATCTTCCACAGCCACACCATTTGGATTTT 359
 Qy 151 LeuHisIlePheHisAlaIleAlaValSerThrArgProGlnLeuLeuPheSerLeuPro 170
 Db 360 CTTTCCATTTTCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 419
 Qy 171 LysLeuSerProSerGlnHisLeuAlaValLeuThrLysGlnLeuLeuHisCysMetAla 190
 Db 420 AGATTGAGCCCGTCTCAACTTGGCAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 479
 Qy 191 CysAsnGlnLeuLeuGlnPheArgGlySerMetLeuAlaLeuAlaMetValSerLeuGlu 210
 Db 480 TGCAACCAACTTCTGCGAGTTCAAGAGTCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 539
 Qy 211 MetGluLysLeuLeuProAspTrpLeuSerLeuThrIleGluLeuLeuGlnLysAlaGln 230
 Db 540 ATGAGAAACTCATTTCCCGATTTGCTTCTTCAATTTGAATTTGCTTCAAGAGCAGCAG 599
 Qy 231 MetAspSerSerGlnLeuLeuHisCysArgGluLeuValAlaHisHisLeuSerThrLeu 250
 Db 600 ATGGACAGCTCCCGATTTGATCCACTGTGCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 659
 Qy 251 GlnSerSerLeuProLeuAsnSerValTyrValTyrArgProLeuLysHisThrLeuVal 270
 Db 660 CAGTCTTCCCTGCTCTAAATTTCCGTTTATGCTTACCGTCCCTTCAAGAGCAGCAGCCTGCTG 719
 Qy 271 ThrCysAspLysGlyValPheArgLeuHisProSerSerValProGlyProAspPheSer 290

Db 720 ACCTGTGCAAGAGCGGTTCAANTATACATCCCTCTCTATCTCAGGCCAGATTCTCC 779

Qy 291 LysAspAsnSerLysProGluValProValArgGlyThrAlaAlaPheTyrHisHisLeu 310

Db 780 AAGGACACAGACAGCCAGAGTGCAGTCCAGAGTCCAGAGCTTCCACCTCCATCTC 839

Qy 311 ProAlaAlaSerGlyCysGlyGlnThrSerThrLysArgLysValGluGluMetGluVal 330

Db 840 CCTGCTGTGAGTGGTGCAGCATACCTCTGTCTAAACGGAAGTGGAGAGATGAGGTG 899

Qy 331 AspAspPhe-TyrAspGlyLysArgLysLeuTyrHisGlnAspAsnValSerGluAsnVa 350

Db 900 GACGACTTGTATATGACGGGATCAACGGCTCTTATAACGA-GACAGTTGTTCCGAGAATGT 958

Qy 350 LcylSerValCysGlyThrAspLeuSerArgGlnGluGlyHisAlaSerProCysProPr 370

Db 959 GGGCTCTGTGTTTGCATGATTTATCCAGACAGAGGGCCATGCCCTTCCCTGTCCACC 1018

Qy 370 LcylGlnProValSerValMet 377

Db 1019 TTTGCGAGCTGTATCTGTAATG 1040

RESULT 7

LOCUS CN647834

DEFINITION ILLUMIGEN MCQ 29127 Katze MMPL2 Macaca mulatta cDNA clone

CCNI (Hs.369110), mRNA sequence.

ACCESSION CN647834

VERSION CN647834.1 GI:47161277

KEYWORDS EST.

SOURCE Macaca mulatta (rhesus monkey)

ORGANISM Macaca mulatta

REFERENCE 1 (bases 1 to 967)

AUTHORS Katze,M.G., Thomas,M., Korth,M., Iadonato,S.P. and Magnus,C.L.

TITLE Large-scale Rhesus Macaque cDNA Sequencing

JOURNAL Unpublished (2003)

COMMENT Contact: C. Magnus

ILLUMIGEN Biosciences Inc.

2203 Airport Way S, Suite 450, Seattle, WA 98134, USA

Tel: 2063780400

Fax: 2063780408

Email: cmagness@illumigen.com

Sequenced on 2004.03.25. 786 Q20 bases.

PCR Primers

FORWARD: CCCTCACTAAAGGGAACAAA

BACKWARD: CACTATAGGCGGAATTGGGTA

Insert Length: 967 Std Error: 0.00

Plate: CL000123 row: A column: 11

Seq primer: CCCTCACTAAAGGGAACAAA

POLYA=No.

FEATURES

source

1..967

/organism="Macaca mulatta"

/mol_type="mRNA"

/strain="Indian"

/db_xref="taxon:9544"

/clone="IBIUM:7202"

/sex="male"

/dev_stage="newborn infant"

/lab_host="E. coli SOLR"

/clone_lib="Katze MMPL2"

/note="Organ: placenta; Vector: Uni-ZAP XR; Site 1: EcoR I; Site 2: Xho I; Created from Stratagene ZAP-CDNA Synthesis kit (catalog #200400) and ZAP-CDNA Gigapack III Gold Cloning Kit (Catalog #200450)"

ORIGIN

Alignment Scores: 1.06e-157 Length: 967

Pred. No.:

Score: 1577.00 Matches: 302

Percent Similarity: 99.67% Conservative: 1

Best Local Similarity: 99.34% Mismatches: 1

Query Match: 80.38% Indels: 0

DB: 7 Gaps: 0

US-09-736-250-1 (1-377) x CN647834 (1-967)

Qy 74 AspArgPheLeuAlaThrValLysAlaHisProLysTyrLeuSerCysIleAlaIleSer 93

Db 1 GACAGGTTTTTAGTACTCCGTAAGGCTCATCCAAAATACTTTGAGTTGTATTGCAATCAGC 60

Qy 94 CysPhePheLeuAlaAlaLysThrValGluGluAspGluArgIleProValLeuLysVal 113

Db 61 TGTITTTTCTAGCTGCCAGACTGTTGAGGAAGATGAGAGAAATTCAGTACTATAAGGTA 120

Qy 114 LeuAlaArgAspSerPheCysGlyCysSerSerGluIleLeuArgMetGluArgIle 133

Db 121 TTGGCAAGAGACAGATTTCTGTGGATGTTCTCATCTCGAAATTTTGAGAATGGAGAAAT 180

Qy 134 IleLeuAspLysLeuAsnTyrAspLeuHisThrAlaThrProLeuAspPheLeuHisIle 153

Db 181 ATTCTGGATAAGTTGAATTTGGGATCTTCACACAGCCACACCATTTGGATTTTCTTCATATT 240

Qy 154 PheHisAlaIleAlaValSerThrArgProGlnLeuLeuPheSerLeuProLysLeuSer 173

Db 241 TTCCATGCTATTGGGTATCACTAGGCCTCAGTTACTTTTTCAGTTTGCCCAATTTGAGC 300

Qy 174 ProSerGlnHisLeuAlaValLeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGln 193

Db 301 CCATCTCAACATTTGGCAGTCTTACCAGCAACTACTTCACTGTATGGCTGCAACCAA 360

Qy 194 LeuLeuGlnPheArgGlySerMetLeuAlaLeuAlaMetValSerLeuGluMetGluLys 213

Db 361 CTCTGCAATTCAGAGATCCATGCTTCTGCGCATGTTAGTTGGAAATGGAGAAA 420

Qy 214 LeuIleProAspTrpLeuSerLeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSer 233

Db 421 CTTATTCTTAATTTGGCTTTCTCTTACAAATTGAATGCTTTCAGAAAGCACAGATGGATAGC 480

Qy 234 SerGlnLeuIleHisCysArgGlyLeuValAlaHisHisLeuSerThrLeuGlnSerSer 253

Db 481 TCCAGTGTGATCCACTGTGCGGAGCTTGTGGCATCATCCCTTTCTACTCTGCAGTCTTCC 540

Qy 254 LeuProLeuAsnSerValTyrValTyrArgProLeuLysHisThrLeuValThrCysAsp 273

Db 541 CTGCCTCTAAATTTCCGTTTATGTTCTACCGTCCCTCAGACACACCTTGTGACTGTGAC 600

Qy 274 LysGlyValPheArgLeuHisProSerSerValProGlyProAspPheSerLysAspAsn 293

Db 601 AAAGGAGTGTTCAGATTACATCCCTCTCTGTCCAGGCCAGACTTCTCCAAGGCAAC 660

Qy 294 SerLysProGluValProValArgGlyThrAlaAlaPheTyrHisHisLeuProAlaAla 313

Db 661 AGCAAGCCAGAGTGCAGTGCAGAGTACAGACGCTTTTACCATCATCTCTCCAGTGTCC 720

Qy 314 SerGlyCysLysGlnThrSerThrLysArgLysValGluGluMetGluValAspAspPhe 333

Db 721 AGTGGGTGCAGAGCAGACCTCTGCTAAACGCAAGTAGAGAGATGGAGTGCATCTTC 780

Qy 334 TyrAspGlyLysLysArgLeuTyrAsnGluAspAsnValSerGluAsnValGlySerVal 353

Db 781 TATGATGAATCAAAAGGGCTCTATAATGAAGATAATGTCTCAGAAATATGTGGTCTGTG 840

Qy 354 CysGlyThrAspLeuSerArgGlnGluGlyHisAlaSerProCysProLeuGlnPro 373

Db 841 TGTGGCACTGATTTATCAAGCAAGAGGGACATGCTTCCCTTGTCCACCTTTTGACGCT 900

Qy 374 ValSerValMet 377

Db 901 GTTCTGTCTCATG 912

RESULT 8

C0646424 992 bp mRNA linear EST 23-JUL-2004
 LOCUS ILLUMIGEN MCQ 39156 Katze MPPB2 Macaca mulatta cDNA clone
 DEFINITION IBTUM:23419 5' similar to Bases 612 to 991 highly similar to human
 Unigene Ha.518825, mRNA sequence.
 C0646424
 C0646424.1 GI:50567918
 EST.
 KEYWORDS
 SOURCE
 ORGANISM Macaca mulatta (rhesus monkey)
 Macaca mulatta
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 Cercopithecinae; Macaca.
 REFERENCE
 1 (bases 1 to 992)
 Katze M.G., Thomas M., Korth M., Iadonato S.P. and Magness C.L.
 Large-scale Rhesus Macaque cDNA Sequencing
 Unpublished (2003)
 CONTACT: C. Magness
 Illumigen Biosciences Inc.
 2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
 Tel: 2063780400
 Fax: 2063780408
 Email: cmagness@illumigen.com
 Sequenced on 2004.05.25 741 Q20 bases. Library Preparation: Prof.
 Michael Katze Lab at University of Washington DNA Sequencing:
 Illumigen Biosciences Inc. For further information, see
 http://www.macaque.org
 PCR PRIMERS
 FORWARD: CCCTCACTAAAGGGAACAAA
 BACKWARD: CACTATAGGCGCAATGGGTA
 Insert Length: 992 Std Error: 0.00
 Plate: C000214 row: F column: 05
 Seq primer: CCCTCACTAAAGGGAACAAA
 POLYA-Yes.
 FEATURES
 source
 Location/Qualifiers
 1..992
 /organism="Macaca mulatta"
 /mol_type="mRNA"
 /strain="Indian"
 /db_xref="taxon:9544"
 /clone="IBTUM:23419"
 /sex="male"
 /tissue_type="blood"
 /cell_type="PBMC"
 /dev_stage="adult"
 /lab_host="Electromax DH10B"
 /clone_lib="Katze MPPB2"
 /note="Vector: pDONR 222; Site_1: BsrG I; Site_2: BsrG I;
 Created from CloneMiner cDNA Library Construction kit
 (catalog #18249-029)"
 ORIGIN
 Alignment Scores:
 Pred. No.: 3.44e-153 Length: 992
 Score: 1535.00 Matches: 308
 Percent Similarity: 96.06% Conservative: 9
 Best Local Similarity: 93.33% Mismatches: 8
 Query Match: 78.24% Indels: 5
 DB: 7 Gaps: 0
 US-09-736-250-1 (1-377) x C0646424 (1-992)
 QY 13 SerPheLeuLeuGluLysAlaIleThrArgGluAlaGlnMetTrpLysValAsnValArg 32
 DB 6 TCTTCTCTGTTGGAAAGGCAATCACTAGGAGGCGCAGATGTGAAAGTGAATGGCG 65
 QY 33 LysMetProSerAsnGlnAsnValSerProSerGlnArgAspGluValIleGlnTrpLeu 52
 DB 66 AAAATGCTTCAATCAGAAATGTTCTCCATCCAGAGATGAAGTAATCAATGGCTG 125
 QY 53 AlaLysLeuLysTyGlnPheAsnLeuTyProGluThrPheAlaLeuAlaSerSerLeu 72
 DB 126 GCCAAACTCAAGTACCAATTCACCTTTACCCAGAAACATTTGCTCTGGCTAGCAGTCTT 185

QY 73 LeuAspArgPheLeuAlaThrValLysAlaHisProLysTyTrpLeuSerCysIleAlaIle 92
 DB 186 TTGGACAGAGGTTTTAGTACCGTAAAGGCTCATCCAAAATACTTGTAGTTGCAATC 245
 QY 93 SerCysPhePheLeuAlaAlaLysThrValGluGluAspGluArgIleProValLeuLys 112
 DB 246 AGCTGTTTTTCTTAGCTGCCAAGACTGTTGAGAGAGTGAAGAAATCCAGTACTAAAG 305
 QY 113 ValLeuAlaArgAspSerPheCysGlyCysSerSerGluLeuLeuArgMetGluArg 132
 DB 306 GTATTGGCAAGACAGACTTTCTGTGGATGTTCTCATCTGAAATTTTGAGAAATGGAGAGA 365
 QY 133 IleIleLeuAspLysLeuAsnTrpAspLeuHisThrAlaThrProLeuAspPheLeuHis 152
 DB 366 ATTATTCTGATAAGTTGAATTTGGATCTTTCACACAGCCACACCATTTGGATTTTCTTCAT 425
 QY 153 IlePheHisAlaIleAlaValSerThrArgProGlnLeuLeuPheSerLeuProLysLeu 172
 DB 426 ATTTTCCATGCTATTTGGGTATCAACTAGGCGCTCAGTTACTTTTCAGTTTGCCCAAAATG 485
 QY 173 SerProSerGlnHisLeuAlaValLeuThrLysGlnLeuLeuHisCysMetAlaCysAsn 192
 DB 486 AGCCCATCTCAACTTTGGCAGTCTTACCAGCAACTACTTCACTGTATGGCTGCAAC 545
 QY 193 GlnLeuLeuGlnPheArgGlySerMetLeuAlaLeuAlaMetValSerLeuGluMetGlu 212
 DB 546 CAACTTCTGCAATTCAGAGATCCATGCTTGTCTGCGCATGGTGTAGTCTGGAAATGGAG 605
 QY 213 LysLeuIleProAspTrpLeuSerLeuThrIleGluLeuLeuGlnLysAlaGlnMetAsp 232
 DB 606 AAACCTTAATCTTAATTTGGCTTTCTTTACAAATTTGACTGCTTACAGAAAGCACATGGAT 665
 QY 233 SerSerGlnLeuIleHisCysArgGluLeuValAlaHisHisLeuSerThrLeuGlnSer 252
 DB 666 AGCTCCCAAGTTGATCCACTGTGGGAGCTTTGTGCACATCACCTTTTCTACTCTCAGTCT 725
 QY 253 SerLeuProLeuAsnSerValTyArgProLeuLysHisThrLeuValThrCys 272
 DB 726 TCCCTGCTCTAAATTCGGTTTATGCTACCGTCCCTCAATCACACGCTGTGACCTGT 785
 QY 273 AspLysGlyValPheArgLeuHisProSerSerValProGlyProAspPheSerLysAsp 292
 DB 786 GACAAAGAGTGTTCAGATTACATCCCTCTCTGTCCAGGCCAGACTTTTCTCCAGAC 845
 QY 293 AsnSerLysProGluValProValArgGly-ThrAlaAla-PheTyHisHisLeuProA 312
 DB 846 AACAGCAGCCAAAGAGTCCAGTCAAAGGTTACAGCAGCCTTTTACCATCTTCTCCCA 905
 QY 312 laAla-SerGlyCysLysGln-ThrSerThrLysArgLysValGluMetGluValAs 331
 DB 906 CTGCCAGGGGGTGCAAGCAAAACCTCTGCCAAACGCAAAAAAAGAGAAATGGA 965
 QY 331 p-AspPheTyArgGlyIle 337
 DB 966 AAGAAATTCATGAAGGAATC 985
 RESULT 9
 LOCUS B0673277
 DEFINITION AGENCOURT_8354951 NIH_MGC_102 Homo sapiens cDNA clone IMAGE:6275333
 5', mRNA sequence.
 ACCESSION B0673277
 VERSION B0673277.1 GI:21784111
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 1 (bases 1 to 920)
 NIH-MGC http://mgs.nci.nih.gov/
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Rubin Laboratory
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: L1CM2458 row: f column: 06
 High quality sequence stop: 691.
 Location/Qualifiers
 1. 920
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6275333"
 /tissue type="epidermoid carcinoma, cell line"
 /lab host="DH10B (phage-resistant)"
 /clone lib="NIH MGC 102"
 /note="Organ: salivary gland; Vector: pOTB7; Site_1: XhoI;
 Site_2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCACGAG(G). Library constructed
 by Ling Hong in the laboratory of Gerald M. Rubin
 (University of California, Berkeley) using ZAP-cDNA
 synthesis kit (Stratagene) and Superscript II RT (Life
 Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.: 8.74e-145 Length: 920
 Score: 1456.00 Matches: 294
 Percent Similarity: 96.75% Conservative: 4
 Best Local Similarity: 95.45% Mismatches: 7
 Query Match: 74.21% Indels: 4
 DB: 5 Gaps: 0

US-09-736-250-1 (1-377) x BQ673277 (1-920)

QY 9 AenGlnArgLeuSerPheLeuGluGluLysAlaIleThr-ArgGluAlaGlnMetTrpLy 28
 Db 2 AACCAGAGATTGTTCTTCTGTTGAAAGCAATCACTAAGGGAAGCACAGATGTGGAA 61
 QY 28 sValAsnValArgLysMetProSerAsnGlnAsnValSerProSerGlnArgAspGluVa 48
 Db 62 AGTGAATGTCGGAAATGCCTTCAATCAGAAITTTCTCATCCAGAGATGAAGT 121
 QY 48 lileGlnTrpLeuAlaLysLeuLysTyrGlnPheAsnLeuTyrProGluThrPheAlaLe 68
 Db 122 AATTCAATGGTGGCCAACTCAAGTACCAATTCACCTTTACCAGAAACATTTGCTCT 181
 QY 68 uAlaSerSerLeuLeuAspArgPheLeuAlaThrValLysAlaHisProLysTyrLeuSe 88
 Db 182 GGCTAGCAGCTCTTTGGATAGCTTTTGTAGTACCCTAAGAGCTCATCAAAATCTTGAG 241
 QY 88 rCysIleAlaIleSerCysPhePheLeuAlaAlaLysThrValGluGluAspGluArgIl 108
 Db 242 TTGTATTGCATCAGCTGTTTTTTCCTAGCTGCCAGACTGTTGAGAGATGAGAGAT 301
 QY 108 eProValLeuLysValLeuAlaArgAspSerPheCysGlyCysSerSerGluIleLe 128
 Db 302 TCCAGTACTAAAGGTATTGGCAAGACAGATTTCTGTGGATGTTCTCATCTGAATTTT 361
 QY 128 uArgMetGluArgIleLeuLeuAspLysLeuAsnTrpAspLeuHisThrAlaThrProLe 148
 Db 362 GAGATGGAGAGAATATTCTGGATAAGTGAATGGATCTTCACAGCCACCATTT 421
 QY 148 uAspPheLeuHisIlePheHisAlaIleAlaValSerThrArgProGlnLeuLeuPheSe 168
 Db 422 GGATTTCTTCATATTTCCATGCATGCAATGTCAGTGTCACTAGGCTCAGTACTTTTCAG 481
 QY 168 rLeuProLysLeuSerProSerGlnHisLeuAlaValLeuThrLysGlnLeuLeuHisCy 188

Db 482 TTTGCCCAATTTGAGCCATCTCAACATTTGGAGTCTTACCAGCAACTACTTCACTG 541
 QY 188 sMetAlaCysAsnGlnLeuLeuGlnPheArgGlySerMetLeuAlaLeuAlaMetValSe 208
 Db 542 TATGGCCTGCAACCAACTTCTGCAATTCAGAGGATCCATGCTTGTCTGGCCATGGTTAG 601
 QY 208 rLeuGluMetGluLysLeuIleProAspTrpLeuSerLeuThrIleGluLeuGlnLy 228
 Db 602 TCTGGAATGGAGAACTCATTTCTGATGGCTTCTTTTACAAATGAACGTCTTCAGAA 661
 QY 228 sAlaGlnMetAspSerSerGlnLeuIleHisCysArgGluLeuValAlaHisLeuSe 248
 Db 662 AGCACAGATGGATAGTCTCCAGTTGATCCATTTGCGGAGCTTGTGGCACATCACCTTTC 721
 QY 248 rThrLeuGlnSerSerLeuProLeuAsnSerValTyrValTyrArgProLeuLysHisTh 268
 Db 722 TACTCTGAGTCTTCCCTGCTCTGAATTCGGTTATGTCTAGCGTCCCTCAG-CACAC 780
 QY 268 rLeuValThrCysAspLysGlyValPheArgLeuHis-ProSerSerValProGlyProA 288
 Db 781 CCTGTGACCTGTGACCAAGAGGTGTTTCAGATTACATCCCTCTCTGTCCCGGCCAG 840
 QY 288 spPheSerLysAspAsnSerLysProGluVal-ProValArgGlyThrAlaAlaPheTyr 307
 Db 841 ACTTCTCCAGGNACAAAGCAGCCAGAGTGGCCAGTCAGAGTACAGAGTACACAGCCTTTT 900
 QY 308 HisHisLeuProAlaAla 313
 Db 901 CATCATCTCCCACTGCC 918

RESULT 10

CN646807

LOCUS

DEFINITION

ILLUMIGEN MCQ 27149 Katze MMR Macaca mulatta cDNA clone IBIUW:8232

5' similar to Bases 1 to 982 highly similar to human CCNI

(Hs.369110), mRNA sequence.

CN646807

CN646807.1

GI:47160250

EST.

Macaca mulatta (rhesus monkey)

Macaca mulatta

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;

Cercopithecinae; Macaca.

1 (bases 1 to 982)

Katze, M.G., Thomas, M., Korth, M., Iadonato, S.P. and Magness, C.L.

Large-scale Rhesus Macaque cDNA Sequencing

Unpublished (2003)

Contact: C. Magness

Illumigen Biosciences Inc.

2203 Airport Way S, Suite 450, Seattle, WA 98134, USA

Tel: 2063780400

Fax: 2063780408

Email: cmagness@illumigen.com

Sequenced on 2004.03.11. 833 Q20 bases.

PCR Primers

FORWARD: CCCTCACTAAAGGGAACAAA

BACKWARD: CACTATAGGCGGAATGGGTA

Insert length: 983 Std Error: 0.00

Plate: CL000143 row: G column: 10

Seq primer: CCCTCACTAAAGGGAACAAA

POLYA=No.

Location/Qualifiers

1..983

/organism="Macaca mulatta"

/mol_type="mRNA"

/strain="Indian"

/db_xref="taxon:9544"

/clone="IBIUV:8232"

/sex="female"

/dev_stage="adult"

/lab_host="E. coli SOLR"

FEATURES

source

```
/clone_lib="Katze MBR"
/notes="Organ: brain; Vector: Uni-ZAP XR; Site 1: EcoR I;
Site 2: Xho I; Created from Stratagene ZAP-cDNA Synthesis
kit (catalog #200400) and ZAP-cDNA Gigapack III Gold
Cloning kit (Catalog #200450)"

ORIGIN
Alignment Scores:
Pred. No.: 3.06e-143 Length: 983
Score: 1442.00 Matches: 281
Percent Similarity: 98.95% Conservatives: 3
Best Local Similarity: 97.91% Mismatches: 0
Query Match: 73.50% Indels: 0
DB: 7 Gaps: 0

US-09-736-250-1 (1-377) x CN646807 (1-983)
Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle 20
Db |||||
22 ATGAAGTTTCCAGGCTTTGGAAACCCAGAGATTGCTTTCCTGTGGAAAGGCATC 181
Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db |||||
182 ACTAGGAGCGCAGATGTGGAAATGATGTGGAAATGCTTCAATCAGATGTT 241
Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn 60
Db |||||
242 TCTCCATCCAGAGATGAAGTAATTAATTCAGTGGCCCAACTCAAGTACCAATTCAAC 301
Qy 61 LeuTyrProGlnThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db |||||
302 CTTTACCACCAAAACATTTGCTGGCTAGCAGTCTTTTGACAGGTTTTAGCTACCGTA 361
Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaAlaLys 100
Db |||||
362 AAGCTCATCCAAATCTTGAGTTGTTATGCAATCAGCTGTTTTCCTAGCTGCCAAG 421
Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db |||||
422 ACTGTTGAGGAAGATGAGAAATTCAGTACTAAAGGTATTTGGCAAGACAGTTCCTGT 481
Qy 121 GlyCysSerSerGluIleLeuArgMetGluArgIleIleLeuAspLysLeuAsnTrp 140
Db |||||
482 GGATGTTCCATCTGAAATTTTGAGAAATGAGAGAAATTTCTGGATAAGTTGAAATGG 541
Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db |||||
542 GATCTTCACACAGCCACCATTTGGATTTCTTCATATTTCCATGCTATTCGGTATCA 601
Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db |||||
602 ACTAGGCTCAGTTACTTTTCAGTTTCCCAAAATGAGCCCATCTCAACATTTGGCAGTC 661
Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
Db |||||
662 CTTACCAAGCAACTACTTCTACTGTATGCTGCAACCAACTCTGCAATTCAGAGGATCC 721
Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
Db |||||
722 ATGCTTGCTCTGGCCATGTTAGTCTGGAAATGAGAAACTTATTCCTAATTTGGCTTCT 781
Qy 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
Db |||||
782 CTTACAATTGAATGCTTCAGAAAGCACAGATGATAGTCCCAAGTTGATCCACTGTCGG 841
Qy 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
Db |||||
842 GAGCTTGTCGACATCATCTTCTACTCTGAGTCTTCCCTGCTCTTAAATTCGGTTAT 901
Qy 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db |||||
902 GTCTACCGTCCCTCAAGCACACCCCTGGTACCTGTGACAAAGGAATGTTCAAAATTACTT 961
```

```
281 ProSerSerValProGlyPro 287
|||
962 CCTCTCTGTGGTCCACGCCCA 982

RESULT 11
LOCUS BUS28295 920 bp mRNA linear EST 13-SEP-2002
DEFINITION AGENCOURT_10180275 NIH_MGC_101 Homo sapiens cDNA clone
IMAGE:6538220 5', mRNA sequence.
ACCESSION BUS28295
VERSION BUS28295.1 GI:22838736
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 920)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLC2702 row: g column: 20
High quality sequence stop: 651.
FEATURES
source
1..920
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6538220"
/tissue_type="epidermoid carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 101"
/notes="Organ: lung; Vector: pOTB7; Site 1: EcoRI; Site 2:
XhoI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
Laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

ORIGIN
Alignment Scores:
Pred. No.: 4.51e-143 Length: 920
Score: 1440.00 Matches: 291
Percent Similarity: 95.77% Conservatives: 3
Best Local Similarity: 94.79% Mismatches: 11
Query Match: 73.39% Indels: 3
DB: 5 Gaps: 0

US-09-736-250-1 (1-377) x BUS28295 (1-920)
Qy 11 ArgLeuSerPheLeuLeuGluLysAlaIleThrArgGluAlaGlnMetTrpLysValAsn 30
Db |||||
2 AGATTTGCTTTCTGTGGAAAGGA-ATCCTAGGGAAGCAGACAGATGTGGAAAGTGAAT 60
Qy 31 ValArgLysMetProSerAsnGlnAsnValSerProSerGlnArgAspGluValIleGln 50
Db |||||
61 GTGCGGAAATGCTTCAATCAGATGTTTCTTCATCCAGAGAGATGAGTAAATTCAA 120
Qy 51 TrpLeuAlaLysLeuLysTyrGlnPheAsnLeuTyrProGlnThrPheAlaLeuAlaSer 70
Db |||||
121 TGGCTGGCCAACTCAAGTACCAATTCACCTTTACCCAGAAACATTTGCTCTGGCTAGC 180
Qy 71 SerLeuLeuAspArgPheLeuAlaThrValLysAlaHisProLysTyrLeuSerCysIle 90
```

181 AGTCTTTGGATAGTGTCTTTAGTACCTACCGTAAAGGCTCATCCAAATACTTGAGTTGATT 240
 QY
 91 AlalileSerCysPhePheLeuAlaAlaLysThrValGluGluAspGluArgIleProVal 110
 Db
 241 GCAATCAGCTGTTTTCTTCTAGCTGCCAAGACTGTTGAGGAAGATGAGAGAATTCAGTA 300
 QY
 111 LeuLysValLeuAlaArgAspSerPheCysGlyCysSerSerSerSerGluLeuLeuArgMet 130
 Db
 301 CTAAGGTATTTGGCAGAGACAGTTCTGTGGATGTTCTCATCTGAAATTTTGAAGATG 360
 QY
 131 GluArgIleLeuLeuAspLysLeuAsnTrpAspLeuHisThrAlaThrProLeuAspPhe 150
 Db
 361 GAGAGAATTTCTCGATAGTGAAGTCTGTGGATGTTCTCATCTGAAATTTTGAAGATG 420
 QY
 151 LeuHisIlePheHisAlaIleAlaValSerThrArgProGlnLeuLeuPheSerLeuPro 170
 Db
 421 CTTATATTTTCCATGCAATGCGATGTCAGTGTCACTAGGCTCAGTTTACTTTTTCGCC 480
 QY
 171 LysLeuSerProSerGlnHisLeuAlaValLeuThrLysGlnLeuLeuHisCysMetAla 190
 Db
 481 AAATTTAGCCCATCTCAACATTTGGCAGTCTTACCAAGCACTTACTTCTGATGGCC 540
 QY
 191 CysAsnGlnLeuLeuGlnPheArgGlySerMetLeuAlaLeuAlaMetValSerLeuGlu 210
 Db
 541 TGCAACCAACTTCTGCAATTCAGAGATCCATGCTGCTGGCCATGGTTAGTCTGAA 600
 QY
 211 MetGluLysLeuLeuProAspTrpLeuSerLeuThrIleGluLeuLeuGlnLysAlaGln 230
 Db
 601 ATGAGAAACTCATCTCTGATGCTGCTTCTTCAACATTTGAACCTGCTTCAAGAACACAG 660
 QY
 231 MetAspSerSerGlnLeuLeuHisCysArgGluLeuValAlaHisLeuSerThrLeu 250
 Db
 661 ATGATAGTCTCCAGTTGATCCATTTGTCGGAGCTTGTGGCACTCACTTTTACTCTG 720
 QY
 251 GlnSerSerLeuProLeuAsnSerValTrpValTrpArgProLeuLysHisThrLeuVal 270
 Db
 721 CAGCTTTCCCTGCTCTGAAATTCGGTTATGCTTACCTCCCTTCAAGCACACCTCGTG 780
 QY
 271 ThrCysAspLysGlyValPheArgLeuHisProSerSerValProGlyProAspPheSer 290
 Db
 781 ACCCTGTGACAGGAGTGTTCAGATTACATCCCTCTCTGTCACCAAGCCCAACTTCTCC 840
 QY
 291 LysAspAsnSerLys-ProGluValProValArgGlyThrAlaAla-PheTyrHisHisL 310
 Db
 841 AAGGACAACAGCAAGCCAGATGCCAGTCCGAGCAGACAGCAGCCCTTTTACCATCATC 900
 QY
 310 euProAlaAlaSerGly 315
 Db
 901 TTCCAGTTGCCAATGGG 917

RESULT 12
 BU538306
 LOCUS
 DEFINITION AGENCOURT_10181155 NIH_MGC_107 Homo sapiens cDNA clone
 IMAGE:6568838 5', mRNA sequence.
 BU538306
 VERSION BU538306.1 GI:22848747
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 963)
 NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-x@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: LICM2755 row: c column: 14
 High quality sequence stop: 646.
 Location/Qualifiers
 1. 963
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6568838"
 /tissue_type="adenocarcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_107"
 /notes="Organ: breast; Vector: pOTB7; Site_1: EcoRI; Site_2: XhoI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

FEATURES

source

ORIGIN

Alignment Scores:
 Pred. No.: 3 94e-142 Length: 963
 Score: 1431.50 Matches: 291
 Percent Similarity: 94.21% Conservative: 2
 Best Local Similarity: 93.57% Mismatches: 11
 Query Match: 72.96% Indels: 7
 DB: 5 Gaps: 1

US-09-736-250-1 (1-377) x BU538306 (1-963)

QY 2 LysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIleThr 21
 Db 3 AAGTTTCCAGGGCTTTGGAAAACCCAGAGATTGCTTCTGTTGTTGAAAAGGCAATCACT 62
 QY 22 ArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnValSer 41
 Db 63 AGGGAAGCACAGATGTGGAAAGTGAATGCGGAAATGCTTCAATCAGAAATGTTCT 122
 QY 42 ProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsnLeu 61
 Db 123 CCATCCAGAGAGATCAAGTAAATTCATGCTGGCCAAACTCAAGTACCAATTCACACT 182
 QY 62 TyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrValLys 81
 Db 183 TACCCAGAAACATTTGCTGCTAGCAGTCTTTTGGATAGGTTTTTAGCTACCGTAAAG 242
 QY 82 AlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaLysThr 101
 Db 243 GCTCATCCAAATVACTTGATGTGATTCATCAGCTGTTTTTCTAGCTGCAAGACT 302
 QY 102 ValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCysGly 121
 Db 303 GTTGAGGAAGATCAGAGAATTCAGTACTAAAGGTATTGGCAAGACACAGTTTCTGTGGA 362
 QY 122 CysSerSerSerGluLeuLeuArgMetGluArgIleLeuAspLysLeuAsnTrpAsp 141
 Db 363 TGTCTCTCATCTCTGAAATTTTGAATGGAGAGAAATTAATTCGGATAGTGAATTCGGAT 422
 QY 142 LeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSerThr 161
 Db 423 CTTACACAGCCACACCATTTGATTTCTCATATTTTCCATGCTGCAATTCGAGTCACT 482
 QY 162 ArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaValLeu 181
 Db 483 AGGCTCTAGTTACTTTTCAAGTTTGGCCAAATTCAGCCCATCTCAACATTTGGCAGTCT 542
 QY 182 ThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuPheArgGlySerMet 201
 Db 543 ACCAAGCACTACTTCTCAGTGTATGGCTGCAACCAACTTCTGCAATTCAGAGATCCATG 602

Qy 202 LeuAlaLeuAlaMetValSerLeuGluMetGluLeuLeuLeuProAspTrpLeuSerLeu 221
 Db 603 CTTCCTCTGGCCATGGTGTAGTCTGGAATGAGAACTCATTCCTGATGGCTTCTCTT 662
 Qy 222 ThrileGluLeuLeuGlnLysAlaGlnMetAspSerGlnLeuLeuLeuHisCysArgGlu 241
 Db 663 ACAATTGACCTGCTTCAGAAAGCAGATGATAGTCCCGAGTTGATCCATTCGCGGAG 722
 Qy 242 LeuValAlaHisHisLeu-SerThrLeuGlnSerSerLeuProLeuAsnSerValTyrVa 261
 Db 723 CTTCGTCGACATCACTTTCTACTCTGCACTCTTCCTGCTCTGAAATTCGGTATGT 782
 Qy 261 lTyrArgProLeuLysHisThrLeuValThrCysAspLysGly-ValPheArgLeuHisP 281
 Db 783 CTACCGTCCCTCAGCACACCTGCTGGTGTGACCTGTGACAAAGGAAGTGGTCAGATTACATC 842
 Qy 281 roSerSerValPro-GlyProAspPheSerLysAsp-AsnSerLysProGluValProVa 300
 Db 843 CCTCTCTGTCAGGGCCCACTTCTCCAGGACAAACAGCAAGCCACAGA----- 894
 Qy 300 lArgGlyThrAlaAlaPheTyrHis 308
 Db 895 -AGTGGCCAGTCCAGAGGGTACCAC 918

RESULT 13

CF552849 841 bp mRNA linear EST 22-SEP-2003
 LOCUS AGNCOURT 15595023 NIH_MGC_183 Homo sapiens cDNA clone
 DEFINITION IMAGE:30529710 5', mRNA sequence.

ACCSSION CF552849

VERSION EST.

KEYWORDS GI:34899683

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 841)

NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Michael Brownstein

cDNA Library Preparation: Invitrogen Corp

DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: NDA617 row: 1 column: 07

High quality sequence stop: 738.

Location/Qualifiers

1. .841

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clones="IMAGE:30529710"

/lab_host="DH10B-Tona (T1 and T5 phage resistant)"

/clone_lib="NIH_MGC_183"

/note="Organ: Pooled muscle (cardiac and skeletal);

Vector: pCMV-SPORT6.1; Site 1: EcoRV (destroyed); Site 2:

NotI; Library is oligo-dT primed and directionally cloned

(EcoRV site is destroyed upon cloning). Average insert

size 1.7. Library was constructed by Invitrogen."

ORIGIN

Alignment Scores:

Pred. No.: 2,02e-141 Length: 841

Score: 1424.00 Matches: 279

Percent Similarity: 99.64% Conservative: 0
 Best Local Similarity: 99.64% Mismatches: 1
 Query Match: 72.58% Indels: 1
 DB: 7 Gaps: 0

US-09-736-250-1 (1-377) x CF552849 (1-841)

Qy 71 SerLeuLeuAspArgPheLeuAlaThrValLysAlaHisProLysTyrLeuSerCysIle 90
 Db 3 AGTCTTTTGGATAGTTTTTTAGCTACCGTAAGGCTCATCCAAATACTTTGAGTTGATT 62
 Qy 91 AlaIleSerCysPhePheLeuAlaAlaLysThrValGluGluAspGluArgIleProVal 110
 Db 63 GCAATCAGCTGTTTTTTCCTAGCTGCCAAGACTGTTGAGGAAGATGAGAAATTCAGTA 122
 Qy 111 LeuLysValLeuAlaArgAspSerPheCysGlyCysSerSerSerGluIleLeuArgMet 130
 Db 123 CTAAAGGTATTGGCAAGAGACAGTTTCTGTGGATGTTCTCTCATCTGAAATTTTTCAGAA 182
 Qy 131 GluArgIleIleLeuAspLysLeuAsnTrpAspLeuHisThrAlaThrProLeuAspPhe 150
 Db 183 GAGAGAATTATTCTGGATAAGTTGAATTGGGATCTTCACACAGCCACACCATTTGGATTTT 242
 Qy 151 LeuHisIlePheHisAlaIleAlaValSerThrArgProGlnLeuLeuPheSerLeuPro 170
 Db 243 CTTCAATATTTTCCATGCCATTGCACTGCACTAGGCTCAGTTTACCTTTTTCAGTTTGGCC 302
 Qy 171 LysLeuSerProSerGlnHisLeuAlaValLeuThrLysGlnLeuLeuHisCysMetAla 190
 Db 303 AATTGAGCCCATCTCAACATTTGGCAGTCTTACCAAGCAACTTACTTCACTGATGGCC 362
 Qy 191 CysAsnGlnLeuLeuGlnPheArgGlySerMetLeuAlaLeuAlaMetValSerLeuGlu 210
 Db 363 TGCAACCAACTTCTGCAATTCAGAGGATCCATGCTTCTCTGGCATGGTTAGTCTGGAA 422
 Qy 211 MetGluLysLeuIleProAspTrpLeuSerLeuThrIleGluLeuLeuGlnLysAlaGln 230
 Db 423 ATGAGAAACTCACTTCTGATTGGCTTCTTACAAATTGAACCTGCTTCAAGAAAGCACAG 482
 Qy 231 MetAspSerSerGlnLeuIleHisCysArgGluLeuValAlaHisHisLeuSerThrLeu 250
 Db 483 ATGGATAGTCTCCCATGTTGATCCATTGTCGGAGGCTTGTGGCAGATCACTTTCTACTCTG 542
 Qy 251 GlnSerSerLeuProLeuAsnSerValTyrValTyrArgProLeuLysHisThrLeuVal 270
 Db 543 CAGTCTTCCCTGCTCTGAAATTCGGTTTATGCTTACCGTCCCTCTCAAGCACACCTTGGTG 602
 Qy 271 ThrCysAspLysGlyValPheArgLeuHisProSerSerValProGlyProAspPheSer 290
 Db 603 ACCTGTGACAAAGAGGT-TTCAGATTACATCCCTCTCTGTCCAGGCCAGACTTCTCC 661
 Qy 291 LysAspAsnSerLysProGluValProValArgGlyThrAlaAlaPheTyrHisLeu 310
 Db 662 AAGGACAAACAGCAAGCCAGAGTGCCAGTCAGAGGTACAGAGCCTTTTACCATCATCTC 721
 Qy 311 ProAlaAlaSerGlyCysLysGlnThrSerThrLysArgLysValGluGluMetGluVal 330
 Db 722 CCAGCTGCCAGTGGTGCAGAGCAGACCTCTACTAAACGCAAGTAGAGAAATTCGAAAGTG 781
 Qy 331 AspAspPheTyrAspGlyIleLysArgLeuTyrAsnGluAspAsnValSerGluAsnVal 350
 Db 782 GATGACTTCTATGATGGAATCAAAACGGCTCTATAATGAAGATAATGTCTCAGAAAAATGTG 841

RESULT 14

CD107527

LOCUS

DEFINITION

AGNCOURT 14020471 NIH_MGC_179 Homo sapiens cDNA clone

IMAGE:30364743 5', mRNA sequence.

CD107527

ACCSSION

VERSION

KEYWORDS

SOURCE

ORGANISM

CD107527 906 bp mRNA linear EST 15-MAY-2003

AGNCOURT 14020471 NIH_MGC_179 Homo sapiens cDNA clone

IMAGE:30364743 5', mRNA sequence.

CD107527

ACCSSION

VERSION

KEYWORDS

SOURCE

ORGANISM

CD107527 906 bp mRNA linear EST 15-MAY-2003

AGNCOURT 14020471 NIH_MGC_179 Homo sapiens cDNA clone

IMAGE:30364743 5', mRNA sequence.

CD107527

ACCSSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 906)
NIH-MGC <http://mgc.nci.nih.gov/>
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Tissue Procurement: Dr. Michael Brownstein
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

Plate: NDA421 row: j column: 16
High quality sequence start: 38
High quality sequence stop: 716.
Location/Qualifiers

FEATURES
source

1. 906
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30364743"
/tissue_type="Pituitary"
/lab_host="DH10B-Ton A (T1 and T5 phage resistances)"
/clone_lib="NIH_MGC_179"
/notes="Organ: brain; Vector: pCMV-SPORT6.1; Site 1: EcoRV
(destroyed); Site 2: NotI; Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.1 kb. Library was
constructed by (Invitrogen). Note: this is a NIH_MGC
Library."

ORIGIN

Alignment Scores:
Pred. No.: 1.63e-140 Length: 906
Score: 1416.00 Matches: 284
Percent Similarity: 96.96% Conservative: 3
Best Local Similarity: 95.95% Mismatches: 5
Query Match: 72.17% Indels: 4
DB: 6 Gaps: 0

US-09-736-250-1 (1-377) x CD107527 (1-906)

Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuGluLysAlaVal 20
Db :::
26 TTGAAGTTCCAGGCTTTGGACACACAGAGATTGCTTCCTGTTGGAAAGGCATC 85
Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db :::
86 ACTAGGAAGCACAGATGTGGAAGTGAATGTGCGGAAATGCCCTTCAATCAGATGTT 145
Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTrpGlnPheAsn 60
Db :::
146 TCTCCATCCAGAGAGATGAAGTAATTCATATGGCTGGCCAAACTCAAGTACCAATTCAC 205
Qy 61 LeuTrpProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db :::
206 CTTTACCAGAAACATTTGCTGGCTAGCAGCTTTTGGATGGTTTGTAGTACCGTA 265
Qy 81 LysAlaHisProLysTrpLeuSerCysIleAlaIleSerCysPhePheLeuAlaLys 100
Db :::
266 AAGGCTCATCAAAATCTTGAGTTGATTCATCAATCAGCTGTTTTTCTAGTGGCCAAAG 325
Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspPheCys 120
Db :::
326 ACTGTTGAGGAAGATGAGAAATTCAGTACTAAGGTATGGCAAGACAGAGATTTCTGT 385
Qy 121 GlyCysSerSerGluIleLeuArgMetGluArgIleIleLeuAspLysLeuAsnTrp 140
Db :::
386 GGATGTTCTCACTCAATTTTGAAGATGGAGAGATTATTCGGTAAGTGAATGG 445

Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db :::
446 GAATCTTACACAGCCACACCAATTTGGATTTCTTCATATTTTCCATGCAATGCAAGTGA 505
Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db :::
506 ACTAGGCTCAGTTACTTTTTCAGTTGGCCAAATTTAGCCCACTCTCAACATTTGGCAGTC 565
Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
Db :::
566 CTTACCAAGCACTACTTCTATGGCTTGAACCAACTTCTGCAATTCAGAGGATCC 625
Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
Db :::
626 ATGCTTGCTCTGGCCATGGTTAGTCTGGAATGGAGAACTCATCTCTGATTTGGCTTCT 685
Qy 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
Db :::
686 CTTTACAAATTCAGCTTTCAGAAAGCACAGATGATAGTCCCGAGTTGATCCATTCGCG 745
Qy 241 GluLeuValAlaHisIleLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTrp 260
Db :::
746 GAGCTTGTGGCACAATCACCTTTCTACTCTGAGTCTTCCCTGCTCTGAATTCGGTTAT 805
Qy 261 ValTrpArgProLeuLysHisThrLeuValThr--CysAspLysGlyValPheArgLeuH 280
Db :::
806 GTCTACCGTCCCTCAAGCACACACCTGGTGAACCTGTGACAAAGAGTGTTCAGATTAC 865
Qy 280 is-ProSerSerValPro-GlyProAspPheSerLysAsp 292
Db :::
866 ATNCCCTCTCTGCTCCCAAGCCCGACAGATTTTCTCCAGGAC 905

RESULT 15

BU501311 LOCUS 936 bp mRNA linear EST 12-SEP-2002
DEFINITION AGENCOURT_8877734 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:6338015
5', mRNA sequence.
BU501311
VERSION BU501311.1 GI:22803673
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 936)
NIH-MGC <http://mgc.nci.nih.gov/>
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov

AUTHORS

TITLE

JOURNAL

COMMENT

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLCM2530 row: i column: 24

High quality sequence stop: 600.

FEATURES

source

1. 936
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6338015"
/tissue_type="normal pigmented retinal epithelium"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_43"

/notes="Organ: eye; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library. |"

ORIGIN

Alignment Scores:
Pred. No.: 1.94e-140 Length: 936
Score: 1415.50 Matches: 289
Percent Similarity: 96.66% Conservative: 0
Best Local Similarity: 96.66% Mismatches: 6
Query Match: 72.15% Indels: 6
DB: 5 Gaps: 0

US-09-736-250-1 (1-377) x BU501311 (1-936)

```
Qy 79 ThrVallyAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAla 98
Db 1 ACCGTAAAGGCTCATCCAAATACCTTGAGTTGTATGCAATCAGCTGTTTTTCTAGCT 60
Qy 99 AlaLysThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSer 118
Db 61 GCCAAGACTGTTGAGGAAGATGAGAGAATCCAGTACTAAAGGTATTGGCAAGACAGT 120
Qy 119 PheCysGlyCysSerSerGluIleLeuArgMetGluArgIleIleLeuAspLysLeu 138
Db 121 TTCTGTGATGTTCTCTCATCTGAAATTTGAGAATGGAGAGAATATTCTGGTAAGTTG 180
Qy 139 AsnTrpAspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAla 158
Db 181 AATTGGGATCTTCACAGCCACACCATTTGATTTCTTCATATTTCCATGCCATTGCA 240
Qy 159 ValSerThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeu 178
Db 241 GTGTCAACTAGGCTCAGTTACTTTTCAAGTTTGCCAAATTTAGCCCATCTCAACATTG 300
Qy 179 AlaValLeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArg 198
Db 301 GCAGTCCCTTACCAAGCAACTACTTCACTGTATGGCTGCAACCACTTCTGCAATTCAGA 360
Qy 199 GlySerMetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrp 218
Db 361 GGATCCATGCTTGCTTGCCCATGGTTAGTCTGGAAATGGAGAACTCATTTCTGATTGG 420
Qy 219 LeuSerLeuThrIleGluLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHis 238
Db 421 CTTTCTCTTACAATTGAATGCTTCAGAAAGCACAGATGGATAGTCCAGTGTATCCAT 480
Qy 239 CysArgGluLeuValAlaHisIleLeuSerThrLeuGlnSerSerLeuProLeuAsnSer 258
Db 481 TGTCGGGAGCTTGTCGACATCACCTTTCTACTCTGCAGTCTTCCCTGCCTCTGAATTC 540
Qy 259 ValTyrValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArg 278
Db 541 GTTATGTCTACCGTCCCTCAGACACACCTGTGTGACCTGTGACAAAGGAGTGTTCAGA 600
Qy 279 LeuHisProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluVal 298
Db 601 TTACATCCCTCTCTGTCCAGGCCAGACTTCTCCAAGGACAAACAGCAAGCCAGAGAGTG 660
Qy 299 ProValArgGlyThrAlaAlaPheTyrHisIleLeuProAlaAlaSerGlyCysLysGln 318
Db 661 CCAGTCAGAGGTACAGCAGCCTTTTACCATCATCTCCAGCTGCCAGTGGGTGCAAGCAG 720
Qy 319 ThrSerThrLysArgLysValGluGluMetGluValAspAspPheTyrAspGlyIleLys 338
Db 721 ACCTTACTTAACGCACTA-GAGGAATGGGAGGG-GATGACTTCTATGATGGGATCAAA 778
Qy 339 ArgLeuTyrAsnGluAspAsnValSerGluAsnValGlySer-ValCysGlyThrAspLe 358
Db 779 CGGCTCTATATGAAGATAATGCTCCGAAATGTGGGGTCTGTGTGTGGCCCTGATT 838
Qy 358 uSerArg-GlnGluGlyHisAlaSerProCys-ProPro-LeuGlnPro 373
||||| ||||||| ||| ||||| |||||||
```

Db 839 ATCCAGACCAGGAGGACATGCCCTTCCCTTTGGCCACCTTTTGCAGCCT 887

Search completed: February 11, 2005, 07:36:28
Job time : 5890.76 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 11, 2005, 03:05:54 ; Search time 106.061 Seconds
(without alignments)
1374.757 Million cell updates/sec

Title: US-09-736-250-1

Perfect score: 377

Sequence: 1 MKFPGLNQLRSLFLEKAI.....LSRQGHASCPPLQPVSVW 377

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2105692 seqs, 386760381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	377	100.0	377	2	Aaw21965 Human cyc
2	377	100.0	377	3	Aay52185 Human cyc
3	377	100.0	377	6	Abr39934 Human pro
4	377	100.0	377	8	Adp12615 Protein e
5	296	78.5	334	7	Aae37938 Human CGD
6	276	73.2	377	8	Aam80569 Tumour-as
7	153	40.6	300	8	Adn01131 Human cel
8	131	34.7	131	3	Asg01903 Human sec
9	34	9.0	41	4	Asa011635 Human pol
10	14	3.7	14	2	Aaw21966 Human cyc
11	10	2.7	10	6	Asj20156 MHC bindi
12	9	2.4	9	5	Adg32308 HLA-A2 as
13	9	2.4	9	6	Adj19986 MHC bindi
14	9	2.4	462	5	Aaw85684 NBP46 roo
15	9	2.4	462	5	Aau78818 Dolichos
16	8	2.1	269	7	Adh44940 Human TCH
17	8	2.1	391	5	Aau81226 Human lun
18	8	2.1	391	8	Adl06559 Human tum
19	8	2.1	416	6	Abc01333 Human pro
20	8	2.1	416	7	Adh44925 Human TCH
21	8	2.1	416	8	Adn96038 Human NOV
22	8	2.1	545	4	Aab65649 Novel pro
23	8	2.1	545	8	Adi29256 Human MAR
24	8	2.1	667	2	Aaw94919 Rat phero
25	7	1.9	12	3	Aay91912 Peptide 2

26	7	1.9	12	8	ADO04715	Human int
27	7	1.9	21	2	AAW93064	Human Tan
28	7	1.9	39	8	ADO24383	Human PRO
29	7	1.9	52	2	AAW93061	Human Tan
30	7	1.9	58	3	AAW93058	Human Tan
31	7	1.9	63	2	AAW93058	Human Tan
32	7	1.9	68	4	AAW96280	Human rep
33	7	1.9	68	4	ABB10911	Human ova
34	7	1.9	73	4	AAW82834	Human imm
35	7	1.9	74	4	AAU43120	Propionib
36	7	1.9	74	6	ABM39639	Propionib
37	7	1.9	85	7	ADP07949	Bacterial
38	7	1.9	88	4	ABG04101	Novel hum
39	7	1.9	88	5	ABP03890	Human ORF
40	7	1.9	95	2	AAW37852	Chlamydia
41	7	1.9	96	5	ABB80038	Human C2H
42	7	1.9	97	4	AAO01328	Human pol
43	7	1.9	98	4	AAU22330	Human car
44	7	1.9	98	7	ADE46298	Human car
45	7	1.9	98	8	ADJ07716	Human car
46	7	1.9	104	4	ABB68248	Drosophil
47	7	1.9	108	4	AAU66549	Propionib
48	7	1.9	108	6	ABM63068	Propionib
49	7	1.9	110	4	ABB42544	Peptide #
50	7	1.9	110	4	AAW36358	Peptide #
51	7	1.9	110	4	AAW76247	Human bon
52	7	1.9	110	4	AAW63432	Human bra
53	7	1.9	115	2	AAW04930	Interfero
54	7	1.9	122	8	ADQ65672	Novel hum
55	7	1.9	123	4	AAO04444	Human pol
56	7	1.9	125	4	AAU60950	Propionib
57	7	1.9	125	6	ABM57469	Propionib
58	7	1.9	136	2	AAW93063	Human Tan
59	7	1.9	139	4	ABG08538	Novel hum
60	7	1.9	146	2	AAW00014	Chimeric
61	7	1.9	146	2	AAW99491	Chimeric
62	7	1.9	146	2	AAW99495	Chimeric
63	7	1.9	146	2	AAW30899	Synthetic
64	7	1.9	146	2	AAW30895	Synthetic
65	7	1.9	146	2	AAW30900	Synthetic
66	7	1.9	146	2	AAW22902	Biologica
67	7	1.9	146	2	AAW10152	Properly
68	7	1.9	146	2	AAW26198	Obesity p
69	7	1.9	146	2	AAW26199	Obesity p
70	7	1.9	146	2	AAW26190	Obesity p
71	7	1.9	146	2	AAW18628	Obesity p
72	7	1.9	146	2	AAW18622	Obesity p
73	7	1.9	146	2	AAW18627	Obesity p
74	7	1.9	146	2	AAW32579	Anti obes
75	7	1.9	146	2	AAW32580	Anti obes
76	7	1.9	146	2	AAW34485	Obesity p
77	7	1.9	146	2	AAW34494	Obesity p
78	7	1.9	146	2	AAW34493	Obesity p
79	7	1.9	146	2	AAW62605	Preferred
80	7	1.9	146	2	AAW69688	Obesity p
81	7	1.9	146	2	AAW69692	Obesity p
82	7	1.9	146	2	AAW69693	Obesity p
83	7	1.9	146	2	AAW51002	Anti-obes
84	7	1.9	146	2	AAW51003	Anti-obes
85	7	1.9	146	2	AAW50998	Anti-obes
86	7	1.9	146	2	AAW71301	Obesity p
87	7	1.9	146	2	AAW71310	Obesity p
88	7	1.9	146	2	AAW71835	Obesity p
89	7	1.9	146	2	AAW71844	Obesity p
90	7	1.9	146	2	AAW53336	Obesity p
91	7	1.9	146	2	AAW53335	Obesity p
92	7	1.9	146	2	AAW53331	Obesity p
93	7	1.9	148	2	AAW71848	Obesity p
94	7	1.9	150	4	ABB17457	Human ner
95	7	1.9	157	3	AAW70930	Human zil
96	7	1.9	157	3	AAW70934	Human zil
97	7	1.9	157	3	AAW70932	Human zil
98	7	1.9	157	3	AAW70929	Human zil

99	7	1.9	157	3	AA95301	Human int	172	7	1.9	193	7	ADH52125	Novel hum
100	7	1.9	157	7	ADH89073	Human zil	173	7	1.9	193	7	ADH49980	Novel hum
101	7	1.9	157	7	ADH89076	Human zil	174	7	1.9	193	7	Adi25490	Novel hum
102	7	1.9	157	7	ADH89071	Human zil	175	7	1.9	193	7	Adh90283	Novel hum
103	7	1.9	157	7	ADH89070	Human zil	176	7	1.9	193	7	Adi25660	Novel hum
104	7	1.9	163	3	AA97069	Human IL-	177	7	1.9	193	7	Adh97834	Novel hum
105	7	1.9	167	2	AAW93060	Human Tan	178	7	1.9	193	7	Adi103682	Novel hum
106	7	1.9	167	3	AA96932	Human IL-	179	7	1.9	193	7	Adi12039	Human PRO
107	7	1.9	167	3	AA96939	Human IL-	180	7	1.9	193	7	Adh90113	Novel hum
108	7	1.9	176	4	AA848081	Human ext	181	7	1.9	193	7	Adh98514	Novel hum
109	7	1.9	176	8	ADL68905	Human ext	182	7	1.9	193	7	Adi11189	Human PRO
110	7	1.9	178	2	AAW93057	Human Tan	183	7	1.9	193	7	Adi11699	Human PRO
111	7	1.9	182	4	AAU31746	Novel hum	184	7	1.9	193	7	Adh98344	Novel hum
112	7	1.9	188	4	ABB66418	Drosophil	185	7	1.9	193	7	Adh98684	Novel hum
113	7	1.9	192	3	AA95297	Human int	186	7	1.9	193	7	Adh98174	Novel hum
114	7	1.9	192	8	ADN05880	Antipori	187	7	1.9	193	7	Adi05162	Novel hum
115	7	1.9	193	3	AA96934	Processed	188	7	1.9	193	7	Adi03512	Novel hum
116	7	1.9	193	4	AA887596	Human PRO	189	7	1.9	193	7	Adi04907	Novel hum
117	7	1.9	193	5	ABG95921	Human sec	190	7	1.9	193	7	Adh78361	Human PRO
118	7	1.9	193	6	ABU90946	Novel hum	191	7	1.9	193	7	Adi119705	Novel hum
119	7	1.9	193	6	ABO34005	Human sec	192	7	1.9	193	7	Adh90453	Novel hum
120	7	1.9	193	6	ABU72022	Novel hum	193	7	1.9	193	7	Adi03172	Novel hum
121	7	1.9	193	6	ABU71576	Human sec	194	7	1.9	193	7	Adh78021	Human PRO
122	7	1.9	193	6	ABU72357	Human PRO	195	7	1.9	193	7	Adh98004	Novel hum
123	7	1.9	193	6	ABU91030	Human PRO	196	7	1.9	193	7	Adi01389	Novel hum
124	7	1.9	193	6	ABO27351	Human sec	197	7	1.9	193	7	Adi02084	Novel hum
125	7	1.9	193	6	ABU92546	Human sec	198	7	1.9	193	7	Adi03342	Novel hum
126	7	1.9	193	6	ABU81216	Human sec	199	7	1.9	193	7	Adi11529	Human PRO
127	7	1.9	193	6	ABO53330	Novel hum	200	7	1.9	193	7	Adi02431	Novel hum
128	7	1.9	193	6	ABU98333	Novel hum	201	7	1.9	193	7	Adi11869	Human PRO
129	7	1.9	193	6	ABU89338	Novel hum	202	7	1.9	193	7	Adi05506	Novel hum
130	7	1.9	193	6	ABU82545	Novel hum	203	7	1.9	193	7	Adh79578	Novel hum
131	7	1.9	193	6	ABU96509	Human PRO	204	7	1.9	193	7	Adi119535	Novel hum
132	7	1.9	193	6	ABU72179	Human PRO	205	7	1.9	193	7	Adi05336	Novel hum
133	7	1.9	193	6	ABU17199	Human tra	206	7	1.9	193	7	Adh79748	Novel hum
134	7	1.9	193	6	ABO44309	Human sec	207	7	1.9	193	7	Adi01574	Novel hum
135	7	1.9	193	6	ADA20004	Novel hum	208	7	1.9	193	7	Adi01744	Novel hum
136	7	1.9	193	6	ADB17387	Human tra	209	7	1.9	193	7	Adi01914	Novel hum
137	7	1.9	193	6	ADA20176	Novel hum	210	7	1.9	193	7	Adh79918	Novel hum
138	7	1.9	193	6	ABO34237	Human sec	211	7	1.9	193	7	Adi04736	Novel hum
139	7	1.9	193	6	ADA00473	Human sec	212	7	1.9	193	7	Adi02872	Novel hum
140	7	1.9	193	7	ADB85715	Novel hum	213	7	1.9	193	7	Adh78191	Human PRO
141	7	1.9	193	7	ADB68394	Human PRO	214	7	1.9	193	7	Adi25830	Novel hum
142	7	1.9	193	7	ADB68201	Human PRO	215	7	1.9	193	7	Adi26000	Novel hum
143	7	1.9	193	7	ADB91018	Novel hum	216	7	1.9	193	7	Adh65512	Novel hum
144	7	1.9	193	7	ADC07098	Human PRO	217	7	1.9	193	7	Adh98854	Novel hum
145	7	1.9	193	7	ADC17277	Mammalian	218	7	1.9	193	7	Adh80095	Novel hum
146	7	1.9	193	7	ADC14975	Novel hum	219	7	1.9	193	7	Adi33825	Novel hum
147	7	1.9	193	7	ADC52470	Novel hum	220	7	1.9	193	8	Adc52280	Novel hum
148	7	1.9	193	7	ADD36146	Novel hum	221	7	1.9	193	8	Adh06712	Novel hum
149	7	1.9	193	7	ADG01147	Novel hum	222	7	1.9	193	8	Adh06542	Novel hum
150	7	1.9	193	7	ADG08700	Novel hum	223	7	1.9	193	8	Adg68963	Novel hum
151	7	1.9	193	7	ADP95321	Novel hum	224	7	1.9	193	8	Adh27853	Novel hum
152	7	1.9	193	7	ADH24174	Novel hum	225	7	1.9	193	8	Adh25194	Novel hum
153	7	1.9	193	7	ADH34200	Novel hum	226	7	1.9	193	8	Adh33826	Human PRO
154	7	1.9	193	7	ADH30033	Novel hum	227	7	1.9	193	8	Adh02469	Human PRO
155	7	1.9	193	7	ADH24004	Novel hum	228	7	1.9	193	8	Adh08076	Novel hum
156	7	1.9	193	7	ADG85408	Novel hum	229	7	1.9	193	8	Adg69473	Novel hum
157	7	1.9	193	7	ADH24684	Novel hum	230	7	1.9	193	8	Adh39293	Novel hum
158	7	1.9	193	7	ADH37540	Human sec	231	7	1.9	193	8	Adg84034	Human PRO
159	7	1.9	193	7	ADH02129	Human PRO	232	7	1.9	193	8	Adg85578	Novel hum
160	7	1.9	193	7	ADH37710	Human sec	233	7	1.9	193	8	Adh06372	Novel hum
161	7	1.9	193	7	ADG85748	Novel hum	234	7	1.9	193	8	Adh30202	Novel hum
162	7	1.9	193	7	ADH24344	Novel hum	235	7	1.9	193	8	Adh24514	Novel hum
163	7	1.9	193	7	ADH38638	Novel hum	236	7	1.9	193	8	Adg69643	Novel hum
164	7	1.9	193	7	ADG83759	Human PRO	237	7	1.9	193	8	Adh07906	Novel hum
165	7	1.9	193	7	ADH29567	Novel hum	238	7	1.9	193	8	Adg85918	Novel hum
166	7	1.9	193	7	ADH27683	Novel hum	239	7	1.9	193	8	Adh39464	Novel hum
167	7	1.9	193	7	ADH37880	Human sec	240	7	1.9	193	8	Adh33656	Human PRO
168	7	1.9	193	7	ADH38057	Human sec	241	7	1.9	193	8	Adh33996	Human PRO
169	7	1.9	193	7	ADH57477	Novel hum	242	7	1.9	193	8	Adh01206	Human PRO
170	7	1.9	193	7	ADH53619	Novel hum	243	7	1.9	193	8	Adg69813	Novel hum
171	7	1.9	193	7	ADH53789	Novel hum	244	7	1.9	193	8	Adh02299	Human PRO

391	7	1.9	424	8	ADM48000	Adm48000 Polypepti	464	7	1.9	895	5	AAU86165	Aau86165 Mouse alp
392	7	1.9	428	4	AA879936	Ab879936 Coryneb	465	7	1.9	951	8	ADQ37103	Adq37103 Cell prol
393	7	1.9	428	4	ABG08766	Abg08766 Novel hum	466	7	1.9	952	7	ADC00492	Adc00492 Enterohae
394	7	1.9	428	5	AAE14780	Aae14780 Coryneb	467	7	1.9	966	6	ABM70145	Abm70145 Phototab
395	7	1.9	428	5	AB898395	Ab898395 Coryneb	468	7	1.9	973	4	AB586699	Ab586699 Drosophil
396	7	1.9	436	4	AAE59872	Ab59872 Coryneb	469	7	1.9	982	4	ABQ36919	Abq36919 Cell prol
397	7	1.9	437	2	AA880071	Adm80071 Rat sonic	470	7	1.9	996	5	ABB91788	Abb91788 Herbicida
398	7	1.9	437	2	AA880071	Adm80071 Rat sonic	471	7	1.9	1026	5	ADC00868	Adc00868 Enterohae
399	7	1.9	437	8	ADO50491	Ado50491 Rat sonic	472	7	1.9	1026	7	ADC00339	Adc00339 Enterohae
400	7	1.9	439	4	AAE00240	Aae00240 Taxus cus	473	7	1.9	1045	2	AAR66221	Aar66221 Sucrose-p
401	7	1.9	439	5	AB879398	Ab879398 Taxane sy	474	7	1.9	1045	7	ADE93716	Ade93716 Beet sucr
402	7	1.9	439	6	AB882996	Ab882996 T. cuspid	475	7	1.9	1057	4	ABG09834	Abg09834 Novel hum
403	7	1.9	439	6	AB882996	Ab882996 T. cuspid	476	7	1.9	1068	6	ABP78187	Abp78187 N. gonorr
404	7	1.9	446	5	ABP35708	Abp35708 Fungal ZB	477	7	1.9	1080	4	ABG14396	Abg14396 Novel hum
405	7	1.9	446	8	ADJ93495	Adj93495 RDS2. 5/2	478	7	1.9	1080	7	ADC00043	Adc00043 Enterohae
406	7	1.9	448	4	AAE00254	Aae00254 Taxus cus	479	7	1.9	1115	4	ABB71925	Abb71925 Drosophil
407	7	1.9	448	7	AB891967	Ab891967 Acyltrans	480	7	1.9	1190	8	ADS29513	Ads29513 Bacterial
408	7	1.9	449	5	ABP69364	Abp69364 Human pol	481	7	1.9	1228	6	ABU03505	Abu03505 Actinogene
409	7	1.9	496	2	AAW35703	Aaw35703 Carnation	482	7	1.9	1228	8	ADQ39914	Adq39914 Human myo
410	7	1.9	508	2	AAW35711	Aaw35711 Chrysanth	483	7	1.9	1236	7	ADK40931	Adk40931 Novel hum
411	7	1.9	510	8	ADN21340	Adn21340 Bacterial	484	7	1.9	1236	8	ADR15652	Adr15652 Kinase 49
412	7	1.9	513	5	AB883701	Ab883701 Human HTA	485	7	1.9	1245	4	ABG21517	Abg21517 Novel hum
413	7	1.9	513	8	ADH23368	Adh23368 Human Tip	486	7	1.9	1245	4	ABG25816	Abg25816 Novel hum
414	7	1.9	513	8	ADJ78504	Adj78504 TlP60 pro	487	7	1.9	1274	5	ABB79601	Abb79601 Human nuc
415	7	1.9	517	5	AB897525	Ab897525 Novel hum	488	7	1.9	1405	4	ABG07888	Abg07888 Novel hum
416	7	1.9	528	2	AA896267	Aar96267 Mutant Th	489	7	1.9	1554	4	ADQ93658	Adq93658 Streptoco
417	7	1.9	528	6	ADB16231	Adb16231 T. aquati	490	7	1.9	1669	4	ABG13314	Abg13314 Novel hum
418	7	1.9	540	4	ABG05292	Abg05292 Novel hum	491	7	1.9	2458	2	AAR07640	Aar07640 Deduced p
419	7	1.9	544	4	AB861602	Ab861602 Drosophil	492	7	1.9	2458	2	AAR04031	Aar04031 Full leng
420	7	1.9	550	2	AAW94922	Aaw94922 Rat phero	493	7	1.9	3700	7	ADI23890	Adi23890 Streptomy
421	7	1.9	556	4	AB869870	Ab869870 Drosophil	494	7	1.9	6291	7	ADI23927	Adi23927 Streptomy
422	7	1.9	560	3	AA842484	Aab42484 Human ORF	495	6	1.6	9	7	ADC99890	Adc99890 Murine IL
423	7	1.9	560	5	AAO17144	Aao17144 Human blo	496	6	1.6	10	4	AAG96875	Aag96875 Human com
424	7	1.9	560	5	AAO17145	Aao17145 Human blo	497	6	1.6	10	4	AAG96601	Aag96601 Human com
425	7	1.9	572	4	ABG03563	Abg03563 Novel hum	498	6	1.6	10	8	ADG98114	Adg98114 Apoptosis
426	7	1.9	573	8	ADS44435	Ads44435 Bacterial	499	6	1.6	12	3	AAB12275	Aab12275 Mutated N
427	7	1.9	574	4	AB862467	Ab862467 Drosophil	500	6	1.6	12	6	ABR59086	AbR59086 Alzheimer
428	7	1.9	578	8	ADS21175	Ads21175 Bacterial	501	6	1.6	12	8	ADN31709	Adn31709 Human Alz
429	7	1.9	622	5	ABP74053	Abp74053 Candida a	502	6	1.6	13	2	AA74214	Aar74214 Internal
430	7	1.9	639	7	ADD27949	Add27949 Arabidops	503	6	1.6	13	5	AAE24108	Aae24108 Rice CO39
431	7	1.9	639	8	ADN73509	Adn73509 Thale cre	504	6	1.6	13	7	ADM75198	Adm75198 Potential
432	7	1.9	652	4	AAU38102	Aau38102 Streptoco	505	6	1.6	13	7	ADM75463	Adm75463 Potential
433	7	1.9	663	4	AA893313	Aab93313 Human pro	506	6	1.6	13	7	ADM74934	Adm74934 Potential
434	7	1.9	663	8	ADR14479	Adr14479 Human NF-	507	6	1.6	13	7	ADM75728	Adm75728 Potential
435	7	1.9	666	8	ADS09737	Ads09737 Chinese h	508	6	1.6	14	8	ADG98131	Adg98131 Apoptosis
436	7	1.9	684	6	ABJ37930	Abj37930 NOXV prot	509	6	1.6	15	4	AAB97259	Aab97259 Human spl
437	7	1.9	685	8	ADS09695	Ads09695 House mou	510	6	1.6	16	6	ABP82862	Abp82862 G protein
438	7	1.9	685	8	ADS09693	Ads09693 House mou	511	6	1.6	16	2	AAW07268	Aaw07268 Amphiphil
439	7	1.9	685	8	ADS09731	Ads09731 Mammalian	512	6	1.6	18	8	ADG98128	Adg98128 Apoptosis
440	7	1.9	685	8	ADS09697	Ads09697 House mou	513	6	1.6	23	8	ADG98130	Adg98130 Apoptosis
441	7	1.9	685	8	ADS09726	Ads09726 House mou	514	6	1.6	22	8	AAW75019	Aaw75019 Human sec
442	7	1.9	685	8	ADS09651	Ads09651 House mou	515	6	1.6	23	5	ABG95481	Abg95481 Human nov
443	7	1.9	695	2	AAW94925	Aaw94925 Rat phero	516	6	1.6	23	6	ABO34675	AbO34675 Region of
444	7	1.9	704	6	ABJ37934	Abj37934 NOXV prot	517	6	1.6	23	7	ADI23336	Adi23336 Novel hum
445	7	1.9	709	5	AA891737	Abg91737 Purine/py	518	6	1.6	23	8	ADG98148	Adg98148 Apoptosis
446	7	1.9	723	2	AAW94905	Aaw94905 Mouse phe	519	6	1.6	23	8	ADH74338	Adh74338 Human sec
447	7	1.9	730	5	ABG91661	Abg91661 Purine/py	520	6	1.6	23	8	ADR44125	Adr44125 Human OC-
448	7	1.9	739	7	ABO65357	AbO65357 Klebsiell	521	6	1.6	24	8	ADG98126	Adg98126 Apoptosis
449	7	1.9	743	6	ABJ37932	Abj37932 NOXV prot	522	6	1.6	29	2	AAR60931	Aar60931 Hs229-Vas
450	7	1.9	752	7	ABO81381	AbO81381 Pseudomon	523	6	1.6	30	2	AAW11546	Aaw11546 Human 5'
451	7	1.9	772	8	ADS26981	Ads26981 Bacterial	524	6	1.6	30	2	AAW95024	Aaw95024 Sorbitol
452	7	1.9	789	2	AAW14055	Aaw14055 Pumpkin e	525	6	1.6	30	3	AAG55291	Aag55291 Arabidops
453	7	1.9	789	8	ADM98975	Adm98975 Diterpene	526	6	1.6	31	2	AAW13992	Aaw13992 Single ch
454	7	1.9	793	2	AAW94923	Aaw94923 Rat phero	527	6	1.6	31	7	ABM74179	Abm74179 DNA clone
455	7	1.9	798	2	AAW94924	Aaw94924 Rat phero	528	6	1.6	32	2	AAW13993	Aaw13993 Single ch
456	7	1.9	798	7	ADD48569	Add48569 Rat Prote	529	6	1.6	32	2	AAW13991	Aaw13991 Single ch
457	7	1.9	804	2	AAW94914	Aaw94914 Mouse phe	530	6	1.6	32	2	AAW13990	Aaw13990 Single ch
458	7	1.9	816	8	ADS95106	Ads95106 Human the	531	6	1.6	32	2	AAW20205	Aaw20205 H. pylori
459	7	1.9	833	2	ADI92686	Adi92686 Mutant Th	532	6	1.6	32	5	AAE16407	Aae16407 pPTG26 ca
460	7	1.9	833	5	ADI92686	Adi92686 T. aquati	533	6	1.6	32	5	AAO19536	Aao19536 Substance
461	7	1.9	833	6	ADB16226	Adb16226 T. aquati	534	6	1.6	32	6	ABJ18544	Abj18544 Gangliosi
462	7	1.9	852	2	AAW94904	Aaw94904 Mouse phe	535	6	1.6	32	7	ABO33895	AbO33895 Anti-GPI-
463	7	1.9	889	4	ABG23879	Abg23879 Novel hum	536	6	1.6	32	7	ABO33897	AbO33897 Anti-GPI-

537 6 1.6 34 4 AAm18787 Peptide #
538 6 1.6 34 4 AAm37888 Peptide #
539 6 1.6 34 4 AAm31295 Peptide #
540 6 1.6 34 4 AAm23146 Protein #
541 6 1.6 34 4 AAm71018 Human bon
542 6 1.6 34 4 AAm58520 Human bra
543 6 1.6 34 4 AAm52733 Human liv
544 6 1.6 34 5 AAg40809 Human pep
545 6 1.6 34 6 AAd95130 Protein d
546 6 1.6 34 6 AAg36681 Chicken s
547 6 1.6 34 7 AAm01737 Chicken s
548 6 1.6 34 8 AAm97052 Botulinum
549 6 1.6 35 3 AAm56225 Human sec
550 6 1.6 35 4 AAm13693 Peptide #
551 6 1.6 35 4 AAm32624 Peptide #
552 6 1.6 35 4 AAm26093 Peptide #
553 6 1.6 35 4 AAm27473 Human pep
554 6 1.6 35 4 AAm18122 Protein #
555 6 1.6 35 4 AAm65831 Human bon
556 6 1.6 35 4 AAm53454 Human bra
557 6 1.6 35 4 AAg47477 Human liv
558 6 1.6 35 4 AAm01443 Peptide #
559 6 1.6 35 5 AAg35465 Human pep
560 6 1.6 35 5 AAg35465 Human pep
561 6 1.6 37 3 AAg65541 Arabidops
562 6 1.6 37 4 AAm76961 Human bon
563 6 1.6 38 2 AAm88826 Polypepti
564 6 1.6 38 3 AAm34255 Human sec
565 6 1.6 38 3 AAg11009 Arabidops
566 6 1.6 38 3 AAg55177 Arabidops
567 6 1.6 38 4 AAm50768 Human sec
568 6 1.6 38 6 ABo45025 Novel hum
569 6 1.6 38 7 ABo26505 Protein a
570 6 1.6 38 8 ABo54386 Human gen
571 6 1.6 39 3 AAg15094 Arabidops
572 6 1.6 39 4 AAm31153 Peptide #
573 6 1.6 39 4 AAm25509 Human pro
574 6 1.6 40 4 AAm15982 Peptide #
575 6 1.6 40 4 AAm34977 Peptide #
576 6 1.6 40 4 AAm28482 Peptide #
577 6 1.6 40 4 AAm29799 Peptide #
578 6 1.6 40 4 AAm20385 Protein #
579 6 1.6 40 4 AAm68159 Human bon
580 6 1.6 40 4 AAm55784 Human bra
581 6 1.6 40 4 AAg49811 Human liv
582 6 1.6 40 4 AAm03717 Peptide #
583 6 1.6 40 5 AAg37689 Human pep
584 6 1.6 42 4 AAm18300 Peptide #
585 6 1.6 42 4 AAm13867 Peptide #
586 6 1.6 42 4 AAm32812 Peptide #
587 6 1.6 42 4 AAm37335 Peptide #
588 6 1.6 42 4 AAm26274 Peptide #
589 6 1.6 42 4 AAm30785 Peptide #
590 6 1.6 42 4 AAm32081 Peptide #
591 6 1.6 42 4 AAm17642 Human pep
592 6 1.6 42 4 AAm18294 Protein #
593 6 1.6 42 4 AAm22622 Protein #
594 6 1.6 42 4 AAm65998 Human bon
595 6 1.6 42 4 AAm70463 Human bra
596 6 1.6 42 4 AAm53619 Human liv
597 6 1.6 42 4 AAg47664 Human liv
598 6 1.6 42 4 AAg52150 Human liv
599 6 1.6 42 4 AAm01610 Peptide #
600 6 1.6 42 5 AAg35646 Human pep
601 6 1.6 42 5 AAg40101 Human pep
602 6 1.6 42 6 AAm26678 Seed deve
603 6 1.6 43 2 AAm33554 Sequence
604 6 1.6 43 2 AAm49199 Human cal
605 6 1.6 43 2 AAm63146 Sequence
606 6 1.6 43 2 AAm80716 S. pneumo
607 6 1.6 43 3 AAm10577 Human cal
608 6 1.6 43 4 AAm69635 Targeting
609 6 1.6 43 5 AAm24790 Human cal

610 43 8 ADJ38329 Human cal
611 43 8 ADM57746 Human cal
612 44 8 ADS05593 Staphyloc
613 45 4 AAg12463 Novel hum
614 45 6 ABo14059 Novel hum
615 46 8 AAm60756 Human sec
616 46 8 ADM05385 Antipsori
617 47 2 AAY27654 Human sec
618 47 8 AAg78465 Human sec
619 48 1 AAm82386 Human spl
620 48 2 AAm15041 Human thy
621 48 3 AAm98484 Thymopoie
622 48 3 AAY59029 Peptide 1
623 48 3 AAY59028 Peptide 1
624 48 4 AAm45837 Nucleic a
625 48 4 AAm04274 Nucleic 1
626 49 3 AAY98483 Thymopoie
627 49 4 AAm45836 Nucleic a
628 49 4 AAm04273 Nucleic 1
629 49 8 AAg98121 Apoptosis
630 49 8 ABo58069 Human gen
631 50 2 AAm15042 Rat thymo
632 50 4 AAm58238 Propionib
633 50 6 AAm54757 Propionib
634 51 7 AAm49311 WW domain
635 52 5 AAm01606 Human ORF
636 53 4 AAm56530 Propionib
637 53 4 AAm53101 Propionib
638 53 4 AAg19128 Novel hum
639 53 6 AAm49620 Propionib
640 53 6 AAm53049 Propionib
641 54 3 AAg57041 Arabidops
642 54 5 AAm00824 Human ORF
643 55 5 AAm00846 Human ORF
644 56 4 AAm17368 Human ner
645 57 3 AAm87302 Human sig
646 57 5 AAg77449 Selected
647 57 5 AAm11351 Yeast sel
648 57 7 AAm11835 Human sec
649 58 3 AAm76213 Human sec
650 58 3 AAg57040 Arabidops
651 58 4 AAm90572 Human imm
652 59 4 AAm19354 Peptide #
653 59 4 AAm38712 Peptide #
654 59 4 AAm32178 Peptide #
655 59 4 AAm23776 Protein #
656 59 4 AAm71898 Human bon
657 59 4 AAm62221 Propionib
658 59 4 AAm59345 Human bra
659 59 4 AAg53580 Human liv
660 59 5 AAm06509 Human ORF
661 59 5 AAg41711 Human pep
662 59 6 AAm58740 Propionib
663 59 7 AAm78992 KLK2-EXTb
664 60 2 AAY36383 Fragment
665 60 4 AAm43876 Propionib
666 60 6 AAm40395 Propionib
667 60 6 AAd11842 Human nov
668 61 4 AAm48735 Propionib
669 61 5 AAm02276 Human ORF
670 61 5 AAm05669 Human ORF
671 61 6 AAm45254 Propionib
672 61 8 AAm48215 Streptoco
673 62 5 AAm03086 Human ORF
674 62 5 AAm07062 Human ORF
675 62 5 AAm32215 Human ORF
676 63 4 AAm11880 Human pol
677 63 4 AAg23791 Novel hum
678 63 4 AAm29530 Human cr2
679 63 6 AAd49714 Death dom
680 63 7 AAm05235 Bacterial
681 64 3 AAg36768 Arabidops
682 64 3 AAg12929 Arabidops

683	6	1.6	64	4	AAW15161	Aam15161 Peptide #	756	6	1.6	71	4	AAW77286	Aam77286 Human bon
684	6	1.6	64	4	AAW20020	Aam20020 Peptide #	757	6	1.6	71	4	AAU55114	AAU55114 Propionib
685	6	1.6	64	4	ABB40124	Abb40124 Peptide #	758	6	1.6	71	4	ABG24180	Novel hum
686	6	1.6	64	4	ABB34154	Abb34154 Peptide #	759	6	1.6	71	5	ABG46301	Novel pep
687	6	1.6	64	4	ABB33763	Abb33763 Peptide #	760	6	1.6	71	5	ADH32281	Novel yea
688	6	1.6	64	4	AAW37618	Aam37618 Peptide #	761	6	1.6	71	6	ABM51633	Propionib
689	6	1.6	64	4	ABB28986	Abb28986 Peptide #	762	6	1.6	72	4	AAW75744	Human col
690	6	1.6	64	4	ABB24591	Abb24591 Protein #	763	6	1.6	72	4	AAW83615	Human imm
691	6	1.6	64	4	ABB19598	Abb19598 Protein #	764	6	1.6	72	4	AAO05618	Human pol
692	6	1.6	64	4	AAW73568	Aam73568 Human bon	765	6	1.6	72	4	AAU40872	Propionib
693	6	1.6	64	4	AAW67326	Aam67326 Human bon	766	6	1.6	72	6	ABM37391	Propionib
694	6	1.6	64	4	AAW60885	Aam60885 Human bra	767	6	1.6	72	8	ABO53816	Human gen
695	6	1.6	64	4	AAW54946	Aam54946 Human bra	768	6	1.6	73	4	ABB03783	Human mus
696	6	1.6	64	4	ABG55297	Abg55297 Human liv	769	6	1.6	73	4	AAO00950	Human pol
697	6	1.6	64	4	ABG48988	Abg48988 Human liv	770	6	1.6	73	4	AAU59828	Propionib
698	6	1.6	64	4	AAW02899	Aam02899 Peptide #	771	6	1.6	73	4	AAU45926	Propionib
699	6	1.6	64	5	ABG43434	Abg43434 Human pep	772	6	1.6	73	5	ABP05551	Human ORF
700	6	1.6	64	5	ABG36969	Abg36969 Human pep	773	6	1.6	73	6	ABM42445	Propionib
701	6	1.6	64	5	AAE15374	Aae15374 Aspergill	774	6	1.6	73	6	ABM56347	Propionib
702	6	1.6	65	2	AAE55789	Aae55789 Cell deat	775	6	1.6	73	6	ABU13077	Novel hum
703	6	1.6	65	4	AAW18374	Aam18374 Peptide #	776	6	1.6	73	8	ADJ29103	Human mus
704	6	1.6	65	4	AAW65246	Aag65246 D melanog	777	6	1.6	74	4	ABG29302	Novel hum
705	6	1.6	65	4	ABW60552	Abw60552 Drosophil	778	6	1.6	74	5	AAU76252	A. thalia
706	6	1.6	65	4	AAW86392	Aam86392 Human imm	779	6	1.6	75	1	AAW82326	Protein M
707	6	1.6	65	4	AAW70535	Aam70535 Human bon	780	6	1.6	75	4	AAU63518	Propionib
708	6	1.6	65	4	AAW05971	Aam05971 Peptide #	781	6	1.6	75	6	AAU660037	Propionib
709	6	1.6	65	5	AAE19839	Aae19839 Drosophil	782	6	1.6	76	4	AAU66632	Propionib
710	6	1.6	66	3	AAW02508	Aag02508 Human sec	783	6	1.6	76	4	AAU59146	Propionib
711	6	1.6	66	4	ABG19494	Abg19494 Novel hum	784	6	1.6	76	5	ABP39442	Staphyloc
712	6	1.6	66	4	AAU21051	Aau21051 Human nov	785	6	1.6	76	6	ABM55665	Propionib
713	6	1.6	67	4	AAW62161	Aag62161 Human gen	786	6	1.6	76	6	ABM63151	Propionib
714	6	1.6	67	4	AAW62190	Aag62190 Human gen	787	6	1.6	76	8	ADS05270	Staphyloc
715	6	1.6	67	4	ABG00022	Abg00022 Novel hum	788	6	1.6	77	2	AAW44726	Amino aci
716	6	1.6	67	4	ABG02469	Abg02469 Novel hum	789	6	1.6	77	3	AAW44019	Human can
717	6	1.6	67	5	ABG63507	Abg63507 Human alb	790	6	1.6	77	4	AAW90947	Human imm
718	6	1.6	67	5	ABG63508	Abg63508 Human alb	791	6	1.6	78	3	AAW62279	Arabidops
719	6	1.6	67	8	ADL76773	Adl76773 Albumin f	792	6	1.6	78	4	AAU60256	Propionib
720	6	1.6	67	8	ADL76772	Adl76772 Albumin f	793	6	1.6	78	5	ABP10742	Human ORF
721	6	1.6	68	3	AAW00812	Aag00812 Human sec	794	6	1.6	78	5	ABG69653	Human sec
722	6	1.6	68	4	AAU44892	Aau44892 Propionib	795	6	1.6	78	6	ABM56775	Propionib
723	6	1.6	68	6	ABW41411	Bmw41411 Propionib	796	6	1.6	80	4	AAU59725	Propionib
724	6	1.6	68	6	ABU00285	Abu00285 Human nov	797	6	1.6	80	5	ABP00826	Human ORF
725	6	1.6	69	2	AAW88724	Aaw88724 Secreted	798	6	1.6	80	6	ABM56244	Propionib
726	6	1.6	69	3	AAW58275	Aag58275 Arabidops	799	6	1.6	80	7	ADC38698	Human sec
727	6	1.6	69	3	AAW51554	Aag51554 Arabidops	800	6	1.6	80	8	ADP24388	PRO poly
728	6	1.6	69	3	AAW09754	Aag09754 Arabidops	801	6	1.6	81	3	AAW57063	Human pro
729	6	1.6	69	3	AAW36534	Aag36534 Arabidops	802	6	1.6	81	4	AAW84895	Human imm
730	6	1.6	69	3	AAW51525	Aag51525 Arabidops	803	6	1.6	81	5	AAU80868	Human CAR
731	6	1.6	69	4	ABW76560	Abw76560 Human col	804	6	1.6	81	5	ABP42754	Human ova
732	6	1.6	69	4	ABB50491	Abb50491 Human sec	805	6	1.6	81	5	ABU81727	Human cas
733	6	1.6	69	4	ABB12233	Abb12233 Human GPC	806	6	1.6	81	6	ADA56818	Human sec
734	6	1.6	69	4	AAU52092	Aau52092 Propionib	807	6	1.6	81	6	ADA40667	Human sec
735	6	1.6	69	5	ABP07927	Abp07927 Human ORF	808	6	1.6	81	6	ABR47685	Human sec
736	6	1.6	69	6	ABW48611	Bmw48611 Propionib	809	6	1.6	81	7	ADE11762	Human sec
737	6	1.6	69	6	ABO44748	Abu44748 Novel hum	810	6	1.6	81	8	ADP30166	Human sec
738	6	1.6	69	7	ABO26228	Abu26228 Human pro	811	6	1.6	82	3	AAW76139	Human sec
739	6	1.6	70	2	AAW85910	Aay85910 S. pneumo	812	6	1.6	82	4	AAO08254	Human pol
740	6	1.6	70	2	AAW35938	Aay35938 Extended	813	6	1.6	82	8	ADS07055	Staphyloc
741	6	1.6	70	2	AAW28573	Aay28573 Secreted	814	6	1.6	83	3	AAW36533	Arabidops
742	6	1.6	70	4	AAU39046	Aau39046 Human sec	815	6	1.6	83	7	ADP05432	Bacterial
743	6	1.6	70	4	AAU53345	Aau53345 Propionib	816	6	1.6	85	3	AAW03573	Human sec
744	6	1.6	70	4	AAW56487	Aau56487 Propionib	817	6	1.6	85	5	ABP31152	Human ORF
745	6	1.6	70	5	ABP41876	Abp41876 Human ova	818	6	1.6	85	8	ADG22709	Cyanophag
746	6	1.6	70	5	ABW55755	Abw55755 Human pol	819	6	1.6	86	4	AAW99872	Human exc
747	6	1.6	70	6	ABU00959	Abu00959 S. pneumo	820	6	1.6	86	4	AAW86227	Human imm
748	6	1.6	70	6	ABW49864	Abw49864 Propionib	821	6	1.6	86	4	AAW43671	Human bla
749	6	1.6	70	6	ABW53006	Abw53006 Propionib	822	6	1.6	86	5	ABW79369	Human ova
750	6	1.6	70	7	AAO27232	Aao27232 Protein s	823	6	1.6	86	8	ADF71630	Human bla
751	6	1.6	70	7	ADP79004	Adp79004 K1K2-EHTJ	824	6	1.6	87	3	AAW34201	Gene 37 h
752	6	1.6	70	8	ADP19246	Adp19246 Human sec	825	6	1.6	87	3	AAW34202	Human sec
753	6	1.6	71	4	AAW92805	Aam92805 Human dig	826	6	1.6	87	4	AAU55966	Propionib
754	6	1.6	71	4	AAW37438	Aam37438 Peptide #	827	6	1.6	87	5	ABP64128	Human ORF
755	6	1.6	71	4	AAW86403	Aam86403 Human imm	828	6	1.6	87	6	ABM52485	Propionib

829	6	1.6	87	8	ADK51430	Adk51430 Murine an	902	6	1.6	104	4	AAU33672	Aau33672 Pseudomon
830	6	1.6	87	8	ADK51392	Adk51392 Murine an	903	6	1.6	104	5	AAM53044	Aam53044 Human zin
831	6	1.6	87	8	ABM82237	Abm82237 Tumour-as	904	6	1.6	104	6	ABU41310	Abu41310 Protein e
832	6	1.6	87	8	ADR40102	Adr40102 Human PKH	905	6	1.6	104	6	ABU39900	Abu39900 Protein e
833	6	1.6	87	8	ADR73444	Adr73444 Human bla	906	6	1.6	104	6	ABU15559	Abu15559 Protein e
834	6	1.6	88	4	AAU29334	Aau29334 Human dig	907	6	1.6	104	6	ABM71048	Abm71048 Staphyloc
835	6	1.6	88	4	AAU20030	Aau20030 Human liv	908	6	1.6	104	7	ADP78991	Adp78991 KIX2-EHTb
836	6	1.6	88	5	ABP23239	Abp23239 Streptococ	909	6	1.6	104	7	ADM05243	Adm05243 Human pro
837	6	1.6	88	5	ABP40891	Abp40891 Human liv	910	6	1.6	104	8	ADG78417	Adg78417 Human sec
838	6	1.6	88	7	ADJ15009	Adj15009 Human liv	911	6	1.6	105	4	AAM15243	Aam15243 Peptide #
839	6	1.6	88	8	ADK46404	Adk46404 Streptococ	912	6	1.6	105	4	ABB34233	Abb34233 Peptide #
840	6	1.6	88	8	ADR95467	Adr95467 Novel S.	913	6	1.6	105	4	AAM32704	Aam32704 Peptide #
841	6	1.6	89	4	ABM62542	Abm62542 B. melite	914	6	1.6	105	4	ABB29071	Abb29071 Peptide #
842	6	1.6	89	7	ADC96552	Adc96552 E. faeciu	915	6	1.6	105	4	AAM67412	Aam67412 Human bon
843	6	1.6	90	2	AAU37903	Aau37903 Amino aci	916	6	1.6	105	4	AAM55027	Aam55027 Human bra
844	6	1.6	90	5	ABU10594	Abu10594 cDNA enco	917	6	1.6	105	4	ABG49071	Abg49071 Human liv
845	6	1.6	90	5	ADH32283	Adh32283 Novel yea	918	6	1.6	105	4	AAM02986	Aam02986 Peptide #
846	6	1.6	91	5	ABP10026	Abp10026 Human ORF	919	6	1.6	105	7	ADH86628	Adh86628 Enterococ
847	6	1.6	91	5	ABP31979	Abp31979 Human ATP	920	6	1.6	105	7	ADK48360	Adk48360 Streptococ
848	6	1.6	91	6	ABU18519	Abu18519 Protein e	921	6	1.6	105	8	AAK28434	Aak28434 Sequence
849	6	1.6	91	8	ABO60466	AbO60466 Human gen	922	6	1.6	107	2	AAK28434	Aak28434 Heavy cha
850	6	1.6	92	4	ABE17549	AbE17549 Human ner	923	6	1.6	108	5	ABR89130	AbR89130 Human pol
851	6	1.6	92	5	ABE97780	AbE97780 Human sec	924	6	1.6	108	6	ABR41195	AbR41195 Human DIT
852	6	1.6	93	3	ABM51662	Abm51662 Human sec	925	6	1.6	108	7	ABO72605	AbO72605 Pseudomon
853	6	1.6	93	4	ABE69620	AbE69620 Drosophil	926	6	1.6	108	7	ABG19307	AbG19307 Novel hum
854	6	1.6	94	5	AAE25420	Aae25420 Human nod	927	6	1.6	110	4	AAM18435	Aam18435 Peptide #
855	6	1.6	94	5	ABP60145	AbP60145 Human tri	928	6	1.6	110	4	ABB37475	Abb37475 Peptide #
856	6	1.6	94	5	ABG69875	AbG69875 Human sec	929	6	1.6	110	4	AAM30909	Aam30909 Peptide #
857	6	1.6	94	5	ABJ04739	AbJ04739 Nod2 casp	930	6	1.6	110	4	ABB32224	Abb32224 Peptide #
858	6	1.6	94	6	ABP75798	AbP75798 Human sec	931	6	1.6	110	4	AAM70596	Aam70596 Human bon
859	6	1.6	95	2	AAW88599	Aaw88599 Secreted	932	6	1.6	110	4	AAO08741	Aao08741 Human pol
860	6	1.6	95	3	AAU65258	Aau65258 Human 5'	933	6	1.6	110	4	AAU55178	Aau55178 Propionib
861	6	1.6	95	4	ABM50366	Abm50366 Human sec	934	6	1.6	110	4	AAU51131	Aau51131 Propionib
862	6	1.6	95	4	AAU56542	Aau56542 Propionib	935	6	1.6	110	4	ABG52276	AbG52276 Human liv
863	6	1.6	95	5	ABP62916	AbP62916 Human pol	936	6	1.6	110	4	AAO60603	Aao60603 Peptide #
864	6	1.6	95	6	ABM53061	Abm53061 Propionib	937	6	1.6	110	5	ABP02171	Abp02171 Human ORF
865	6	1.6	95	6	ABO44623	AbO44623 Novel hum	938	6	1.6	110	5	ABG40267	AbG40267 Human pep
866	6	1.6	95	7	ABO26103	AbO26103 Human pro	939	6	1.6	110	6	ABM47650	Abm47650 Propionib
867	6	1.6	96	4	AAU27452	Aau27452 Novel bon	940	6	1.6	110	6	ABM51697	Abm51697 Propionib
868	6	1.6	96	4	AAO01860	Aao01860 Human pol	941	6	1.6	110	6	ABR58493	AbR58493 Human sec
869	6	1.6	96	4	ADB11174	AdB11174 Alloiococ	942	6	1.6	110	8	ADS23652	AdS23652 Bacterial
870	6	1.6	96	7	ADD36274	AdD36274 D. melanog	943	6	1.6	111	2	AAK98496	Aak98496 MAB 2E3 h
871	6	1.6	96	8	ADQ08897	AdQ08897 Drosophil	944	6	1.6	111	2	AAK98494	Aak98494 MAB 2F2 h
872	6	1.6	97	4	AAU22281	Aau22281 Human car	945	6	1.6	111	2	AAW42453	Aaw42453 Mouse ant
873	6	1.6	97	6	ABU01567	AbU01567 S. pneumo	946	6	1.6	111	2	AAW42455	Aaw42455 Mouse ant
874	6	1.6	97	7	ADE46249	AdE46249 Human car	947	6	1.6	111	3	AAK33847	Aak33847 Arabidops
875	6	1.6	97	8	ADJ07667	Adj07667 Human car	948	6	1.6	111	7	ADC08105	AdC08105 Rice prot
876	6	1.6	98	2	AAU49211	Aau49211 MAB 1A7 l	949	6	1.6	112	7	ADP26003	AdP26003 H-chain v
877	6	1.6	98	4	ABG26593	AbG26593 Novel hum	950	6	1.6	112	2	AAK35943	Aak35943 Extended
878	6	1.6	98	5	AAU11263	Aau11263 Partial h	951	6	1.6	112	5	ABP09703	AbP09703 Human ORF
879	6	1.6	98	6	ADA14771	AdA14771 Mouse art	952	6	1.6	112	5	ABU51491	AbU51491 Helicobac
880	6	1.6	98	7	ADC35313	AdC35313 Prior art	953	6	1.6	112	7	ABO33836	AbO33836 Human ant
881	6	1.6	98	7	ADF05177	AdF05177 Bacterial	954	6	1.6	112	7	ABO33834	AbO33834 Human ant
882	6	1.6	99	7	ADC88727	AdC88727 Ribosomal	955	6	1.6	112	7	ADC33367	AdC33367 Human nov
883	6	1.6	99	7	ADD36236	AdD36236 Frog orth	956	6	1.6	112	8	ADP19251	AdP19251 Human sec
884	6	1.6	99	8	ADQ08859	AdQ08859 Xenopus l	957	6	1.6	113	2	AAK21268	Aak21268 Murine VH
885	6	1.6	100	4	ABU53241	AbU53241 Human tes	958	6	1.6	113	3	AAK16745	Aak16745 Neisseria
886	6	1.6	100	5	ABP35338	AbP35338 Human ORF	959	6	1.6	113	3	AAU74309	Aau74309 Bacteriop
887	6	1.6	100	6	ADA35444	AdA35444 Acinetoba	960	6	1.6	113	3	AAU70080	Aau70080 Mouse aor
888	6	1.6	101	4	AAU93191	Aau93191 Human pol	961	6	1.6	113	3	AAK16278	Aak16278 Arabidops
889	6	1.6	101	4	AAU66900	Aau66900 Propionib	962	6	1.6	113	6	ABR58492	AbR58492 Human sec
890	6	1.6	101	4	ABG29446	AbG29446 Novel hum	963	6	1.6	113	6	ABU00147	AbU00147 Human nov
891	6	1.6	101	6	ABM63419	AbM63419 Propionib	964	6	1.6	114	3	AAK52552	Aak52552 Helicobac
892	6	1.6	101	8	ADL30534	AdL30534 Human pro	965	6	1.6	114	3	AAK58274	Aak58274 Arabidops
893	6	1.6	102	3	AAK00612	Aak00612 Human pro	966	6	1.6	114	4	AAE11175	Aae11175 Clostridi
894	6	1.6	102	4	AAK95310	AbK95310 Human pro	967	6	1.6	114	4	AAU02563	Aau02563 Anti-adip
895	6	1.6	103	4	AAK88410	AbK88410 Human mem	968	6	1.6	114	5	AAE17793	Aae17793 Escherich
896	6	1.6	103	5	ABR40424	AbR40424 Human sec	969	6	1.6	114	8	ADK17087	AdK17087 Nanoarcha
897	6	1.6	103	5	ABR40500	AbR40500 Human sec	970	6	1.6	115	2	AAW04595	Aaw04595 Anti-DNA
898	6	1.6	103	6	ABO14011	AbO14011 Novel hum	971	6	1.6	115	4	ABG06719	AbG06719 Novel hum
899	6	1.6	103	7	ADP07339	AdP07339 Bacterial	972	6	1.6	115	5	ABP07259	AbP07259 Human ORF
900	6	1.6	103	8	ADN60708	AdN60708 Human sec	973	6	1.6	115	5	AAE29298	Aae29298 S. aureus
901	6	1.6	104	2	AAU27606	Aau27606 Human sec	974	6	1.6	115	7	ADF58686	Adf58686 Human pol

975 1.6 115 8 ADF77174
 976 1.6 116 2 AAR07322
 977 1.6 116 2 AAR28287
 978 1.6 116 2 AAR40951
 979 1.6 116 2 AAW14490
 980 1.6 116 2 AAR99877
 981 1.6 116 4 AAU07513
 982 1.6 116 5 ABP02834
 983 1.6 116 5 ABB79733
 984 1.6 116 6 ABO27162
 985 1.6 116 8 ADQ91072
 986 1.6 116 8 ADS12312
 987 1.6 117 3 AAB16448
 988 1.6 117 3 AAG38294
 989 1.6 117 4 AAB63651
 990 1.6 117 4 AAM94298
 991 1.6 117 5 ABB90352
 992 1.6 117 5 ABB90184
 993 1.6 117 6 ABJ18566
 994 1.6 117 7 ABR82773
 995 1.6 117 7 ABR82883
 996 1.6 117 7 ADC88400
 997 1.6 117 7 ADD41650
 998 1.6 117 8 ADG25836
 999 1.6 117 8 ADQ81963
 1000 1.6 118 2 AAY00292

ALIGNMENTS

RESULT 1
 AAW21965
 ID AAW21965 standard; protein; 377 AA.

XX AC AAW21965;
 DT 02-DEC-1997 (first entry)
 XX Human cyclin I.
 XX human; cyclin I; antisense; probe; neurone; cancer; antibody.
 XX Homo sapiens.
 XX WO9712973-A1.
 XX 10-APR-1997.
 XX 07-OCT-1996; 96WO-JP002905.
 XX 05-OCT-1995; 95JP-00284663.
 XX (SUME) SUMITOMO ELECTRIC IND CO.
 XX Nakamura T;
 XX WPI; 1997-226217/20.
 XX N-PSDB; AAT73937.

Human cyclin I protein and related (anti:sense) DNA - used for neuron labelling method and cancer cell detection.
 Claim 1; Fig 1; 45pp; Japanese.

This sequence is human cyclin I. Antisense polynucleotides are useful for as probes and can be labelled and used for detection of neurones by hybridisation with mRNA for cyclin I (contained in the neurones and arising by the expression of the cyclin I gene in these cells). The gene can be used for detection of cancer cells by detecting the expression of the cyclin I gene in these cells. Also antibodies specific for the fragments of the protein (especially AAW21966) can be used for detection

SQ Sequence 377 AA;

Query Match 100.0%; Score 377; DB 2; Length 377;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MKFPGLNORLSFLLLEKAITREAAQWKNVVRKMPNQNVSPQRDEVIQWLAKLKYQFN 60
 Db 1 MKFPGLNORLSFLLLEKAITREAAQWKNVVRKMPNQNVSPQRDEVIQWLAKLKYQFN 60
 Qy 61 LYPTETALASSILDRLFLATVKAHPKYLSCIAISCFPLAAKTVEDERIPLVKVLARDSF 120
 Db 61 LYPTETALASSILDRLFLATVKAHPKYLSCIAISCFPLAAKTVEDERIPLVKVLARDSF 120
 Qy 121 GCSSEILRMERIIIDKLNWDLHTATPLDPLHIFHAIIVSTRPQLLFSLPKLSPSOHLAV 180
 Db 121 GCSSEILRMERIIIDKLNWDLHTATPLDPLHIFHAIIVSTRPQLLFSLPKLSPSOHLAV 180
 Qy 181 LTKQLLHCMA CNQLQFRGSMALAMVSLMEKLIIPDWLSLTIELLOKAQMDSSQLIHCR 240
 Db 181 LTKQLLHCMA CNQLQFRGSMALAMVSLMEKLIIPDWLSLTIELLOKAQMDSSQLIHCR 240
 Qy 241 ELVAHHLSTLQSSLPNSVYVYRPLXHTLVTCDKGVFRLHPSSVPGDFSKDKSKPEVPV 300
 Db 241 ELVAHHLSTLQSSLPNSVYVYRPLXHTLVTCDKGVFRLHPSSVPGDFSKDKSKPEVPV 300
 Qy 301 RGTAAAFVHHLPAASGCKQTSTKRVKVEEMVDDFYDGIKRLYNEDNVSENVGSGTDLR 360
 Db 301 RGTAAAFVHHLPAASGCKQTSTKRVKVEEMVDDFYDGIKRLYNEDNVSENVGSGTDLR 360
 Qy 361 QEGHASPCLPQPVSV 377
 Db 361 QEGHASPCLPQPVSV 377

RESULT 2

AAW2185
 ID AAW2185 standard; protein; 377 AA.

XX AC AAW2185;
 DT 09-FEB-2000 (first entry)
 XX Human cyclin I amino acid sequence.

Cyclin-dependent kinase 2; CDK2; hsReg; hsReg*-1; hsReg*-2; cyclin I; E2H; cell cycle; proliferation; cancer; hyperproliferative disorder; atherosclerosis; tumour.

Homo sapiens.
 WO9925829-A2.
 27-MAY-1999.
 12-NOV-1998; 98WO-US024095.
 13-NOV-1997; 97US-00969106.

(CURA-) CURAGEN CORP.

Yang M, Nandabalan K, Schulz VP;
 WPI; 2000-061923/05.
 N-PSDB; AAZ37836.

New complexes of the cyclin-dependent kinase 2 protein with its interacting proteins, used to treat, e.g. atherosclerosis.

Example; Fig 2; 90pp; English.

This is the human Cyclin I amino acid sequence. Cyclin I is expressed at almost constant levels throughout the cell cycle, and is implicated in

controlling cell cycle progression and transcriptional control. Cyclins form complexes with cyclin-dependent kinases. CDK2, cyclin-dependent kinase 2, is used in the invention which relates to complexes of the CDK2 protein with other proteins, selected from cyclin I, ERH, hReg, hReg*-1 and hReg*-2 (AAV52185-V52188). CDK2 is expressed late in G1 or early in S phase of the cell cycle, and is pivotal for G1/S transition. Compositions containing a CDK2 complex, an antibody targeting the complex, and nucleotide sequences encoding CDK2 or its derivatives can be used therapeutically. The complexes and their nucleotide sequences can be used to treat diseases or disorders associated with increased or decreased levels of the complex. Screening the complex, or a derivative or a modulator of the complex for neoplastic activity by measuring the survival or proliferation of cells from a malignant cell line when in contact with the complex can be used to indicate if the complex has anti-neoplastic activity. Screening for molecules that modulate the formation of the complexes can be used for treating or preventing atherosclerosis or atherosclerosis-associated disease by contacting cells or using a test animal, in which tumour growth or regression is measured to test whether anti-neoplastic activity is displayed. Diseases which can be treated or prevented by molecule/s which modulate the function of the complex include cancer, hyperproliferative disorders and atherosclerosis

XX SQ Sequence 377 AA;

Query Match 100.0%; Score 377; DB 3; Length 377;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKFPGPLENQLSFLLEKAITREAQMKVNVKMPNSQNVSPSQRDEVIQWLAKLYQFN 60
Db 1 MKFPGPLENQLSFLLEKAITREAQMKVNVKMPNSQNVSPSQRDEVIQWLAKLYQFN 60

Qy 61 LYPETFALASSLLDRFLATVKAHPKYLSCIAISCFLLAAKTVEDEIPVLKVLARDSFC 120
Db 61 LYPETFALASSLLDRFLATVKAHPKYLSCIAISCFLLAAKTVEDEIPVLKVLARDSFC 120

Qy 121 GCSSEILRMERIIIDKLNWDLHTATPLDFLHIFHAIAVSTRPQLLSPLKSPSOHLAV 180
Db 121 GCSSEILRMERIIIDKLNWDLHTATPLDFLHIFHAIAVSTRPQLLSPLKSPSOHLAV 180

Qy 181 LTKQLLHMACNQLQFRGSMALAMVSLMEKLIIPWLSLTIELLOKQMDSSQLIHCR 240
Db 181 LTKQLLHMACNQLQFRGSMALAMVSLMEKLIIPWLSLTIELLOKQMDSSQLIHCR 240

Qy 241 ELVAHHLSTLQSSLPNSVYVYRPLKHTLVTCDKGVFRLHPSSVPGPDFSKDNSKPEVPV 300
Db 241 ELVAHHLSTLQSSLPNSVYVYRPLKHTLVTCDKGVFRLHPSSVPGPDFSKDNSKPEVPV 300

Qy 301 RGTAAFYHHLPAASGCKQTSTKRKVEEMEVDDFYDGIKRLYNEDNVSENVSGVCGTDLR 360
Db 301 RGTAAFYHHLPAASGCKQTSTKRKVEEMEVDDFYDGIKRLYNEDNVSENVSGVCGTDLR 360

Qy 361 QEGHASPCCPLQPVSV 377
Db 361 QEGHASPCCPLQPVSV 377

RESULT 3
ABR39934
ID ABR39934 standard; protein; 377 AA.
XX ABR39934;
XX AC ABR39934;
XX DT 11-AUG-2003 (first entry)
XX DE Human prostate selective polypeptide Pr325.
XX KW Prostate; molecular marker; cancer; cytostatic; gene therapy; human.
XX OS Homo sapiens.
XX WO2003014298-A2.

PD 20-FEB-2003.
XX 02-AUG-2002; 2002WO-US024431.
XX 03-AUG-2001; 2001US-0309470P.
XX 30-OCT-2001; 2001US-0330747P.
XX (ORIG-) ORIGENE TECHNOLOGIES INC.
XX Sun Z, Li X, Jay G, Kovacs KF, Shu Y, Fan W;
XX WPI: 2003-256562/25.
XX N-PSDB; ACC47339.
XX New polynucleotide, useful for preparing a composition for treating prostate disease, e.g., cancer.
XX Claim 5; Page 147-149; 212pp; English.
XX The invention relates to prostate selective polynucleotides and polypeptides. The polynucleotides are expressed in prostate and are useful as molecular markers, as drug targets, and for detecting, monitoring, preventing or treating diseases and conditions related to prostate, such as prostate cancers. The present sequence represents a prostate specific polypeptide

XX SQ Sequence 377 AA;

Query Match 100.0%; Score 377; DB 6; Length 377;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKFPGPLENQLSFLLEKAITREAQMKVNVKMPNSQNVSPSQRDEVIQWLAKLYQFN 60
Db 1 MKFPGPLENQLSFLLEKAITREAQMKVNVKMPNSQNVSPSQRDEVIQWLAKLYQFN 60

Qy 61 LYPETFALASSLLDRFLATVKAHPKYLSCIAISCFLLAAKTVEDEIPVLKVLARDSFC 120
Db 61 LYPETFALASSLLDRFLATVKAHPKYLSCIAISCFLLAAKTVEDEIPVLKVLARDSFC 120

Qy 121 GCSSEILRMERIIIDKLNWDLHTATPLDFLHIFHAIAVSTRPQLLSPLKSPSOHLAV 180
Db 121 GCSSEILRMERIIIDKLNWDLHTATPLDFLHIFHAIAVSTRPQLLSPLKSPSOHLAV 180

Qy 181 LTKQLLHMACNQLQFRGSMALAMVSLMEKLIIPWLSLTIELLOKQMDSSQLIHCR 240
Db 181 LTKQLLHMACNQLQFRGSMALAMVSLMEKLIIPWLSLTIELLOKQMDSSQLIHCR 240

Qy 241 ELVAHHLSTLQSSLPNSVYVYRPLKHTLVTCDKGVFRLHPSSVPGPDFSKDNSKPEVPV 300
Db 241 ELVAHHLSTLQSSLPNSVYVYRPLKHTLVTCDKGVFRLHPSSVPGPDFSKDNSKPEVPV 300

Qy 301 RGTAAFYHHLPAASGCKQTSTKRKVEEMEVDDFYDGIKRLYNEDNVSENVSGVCGTDLR 360
Db 301 RGTAAFYHHLPAASGCKQTSTKRKVEEMEVDDFYDGIKRLYNEDNVSENVSGVCGTDLR 360

Qy 361 QEGHASPCCPLQPVSV 377
Db 361 QEGHASPCCPLQPVSV 377

RESULT 4
ADP12615
ID ADP12615 standard; protein; 377 AA.
XX ADP12615;
XX AC ADP12615;
XX DT 12-AUG-2004 (first entry)
XX DE Protein encoded by mRNA of the invention #225.
XX KW transplacental rejection; immune system; rheumatoid arthritis; lupus; inflammatory bowel disease; multiple sclerosis; HIV; AIDS.

XX OS Homo sapiens.
 XX PN WO2004042346-A2.
 XX PD 21-MAY-2004.
 XX PF 24-APR-2003; 2003WO-US012946.
 XX PR 24-APR-2002; 2002US-00131831.
 XX PR 20-DEC-2002; 2002US-00325899.
 XX PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
 XX PI Wohlgenuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;
 XX PI Rosenberg S;
 XX PI WPI; 2004-400724/37.
 XX DR Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,
 XX PT pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
 XX PT rejection, in an individual, comprises detecting the expression level of
 XX PT the genes.
 XX PS Claim 65; SEQ ID NO 2624; 1762pp; English.
 XX CC The present invention relates to diagnosing or monitoring transplant
 XX CC rejection, e.g. cardiac or kidney transplant rejection, in an individual
 XX CC comprises detecting the expression level of one or more genes. The
 XX CC methods, system and kits are useful in diagnosing or monitoring
 XX CC transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
 XX CC islet, lung, bone marrow or stem cell transplant rejection,
 XX CC xenotransplant rejection or mechanical organ replacement rejection, in an
 XX CC individual. The method is also useful in assessing the immune status of
 XX CC an individual. The methods are also useful in diagnosing and monitoring
 XX CC diseases that involve the immune system, e.g. rheumatoid arthritis,
 XX CC lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
 XX CC viral, bacterial or fungal infection. The present sequence represents a
 XX CC protein that is encoded by the mRNA of the invention.
 XX SQ Sequence 377 AA;
 Query Match 100.0%; Score 377; DB 8; Length 377;
 Best Local Similarity, 100.0%; Pred. No. 0;
 Matches 377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKFPGPLENQLSFLEKAITREAQMKVYVRKMPNSQNVSPSORDEVIQWLAKLYQFN 60
 DB 1 MKFPGPLENQLSFLEKAITREAQMKVYVRKMPNSQNVSPSORDEVIQWLAKLYQFN 60
 QY 61 LYPETFALASSLLDRFLATVKAHPKYLSCIAISCFFLAAKTVEEDERIPVLKVLARDSPC 120
 DB 61 LYPETFALASSLLDRFLATVKAHPKYLSCIAISCFFLAAKTVEEDERIPVLKVLARDSPC 120
 QY 121 GCSSEILRMERIIIDKLNWDLHTATPLDFHIFHAIATVSTRPOLLPSLPKSPSQHLAV 180
 DB 121 GCSSEILRMERIIIDKLNWDLHTATPLDFHIFHAIATVSTRPOLLPSLPKSPSQHLAV 180
 QY 181 LTKQLLHMCACNQLLOFGSMLAMVLSLEKLIPOWLSLTIELLOKAQWDSQLTHCR 240
 DB 181 LTKQLLHMCACNQLLOFGSMLAMVLSLEKLIPOWLSLTIELLOKAQWDSQLTHCR 240
 QY 241 ELVAHLLSTLQSSPLNSVYVYRPLKHTLVTCDKGVFRLHPSSVPGPDFSKDMSKPEVPV 300
 DB 241 ELVAHLLSTLQSSPLNSVYVYRPLKHTLVTCDKGVFRLHPSSVPGPDFSKDMSKPEVPV 300
 QY 301 RGTAAFYHLLPAAGCKQTSTKRKVEVEVDFFDVGIKRLYNENNVENSGVCGTDLR 360
 DB 301 RGTAAFYHLLPAAGCKQTSTKRKVEVEVDFFDVGIKRLYNENNVENSGVCGTDLR 360
 QY 361 QEGHASPCPPLOPVSV 377
 DB 361 QEGHASPCPPLOPVSV 377

RESULT 5

AAE37938
 ID AAE37938 standard; protein; 334 AA.

XX AC AAE37938;

XX DT 06-NOV-2003 (first entry)

XX DE Human CGDD-27 protein.

XX KW Human; cell growth, differentiation and death protein; CGDD; leukaemia;
 KW neurodegenerative disorder; Parkinson's disease; Alzheimer's disease;
 KW muscular disorder; myotonic dystrophy; catatonia; endocrine disorder;
 KW diabetes; Grave's disease; cancer; immunological disorder; scleroderma;
 KW systemic lupus erythematosus; allergy; Crohn's disease; renal disorder;
 KW gastrointestinal disorder; Goodpasture's syndrome; infection; cirrhosis;
 KW cardiovascular disorder; atherosclerosis; hepatic disease; transgenic;
 KW transgenic animal; gene therapy; neuroprotective; relaxant; cytostatic;
 KW dermatological; immunosuppressive; cerebroprotective; anticonvulsant;
 KW antibacterial; antiparasitic; fungicide; virucide; uropathic; cardiant;
 KW protozoacide; nootropic.

XX OS Homo sapiens.

XX PN WO2003050253-A2.

XX PD 19-JUN-2003.

XX PF 04-DEC-2002; 2002WO-US039133.

XX PR 07-DEC-2001; 2001US-0340747P.

XX PR 20-DEC-2001; 2001US-0342761P.

XX PR 15-JAN-2002; 2002US-0349705P.

XX PR 06-FEB-2002; 2002US-0354764P.

XX PR 12-FEB-2002; 2002US-0356216P.

XX PA (INCY-) INCYTE GENOMICS INC.

XX PI Griffin JA, Runkumar J, Emerling BM, Kable AE, Elliott VS;
 PI Marquis JP, Baughn MR, Gorvad AE, Yue H, Lee EA, Becha SD, Tang YT;
 PI Tran UK, Swarnakar A, Lee S, Ison CH, Hafalia AJA, Tran B;
 PI Sprague WW, Lee SY, Khare R, Gandhi AR, Gietzen KJ, Bhatia U;
 PI Burriil JD, Blake JJ, Ho A, Zheng W;

XX WPI; 2003-532903/50.

XX DR N-PSDB; AAD57247.

XX PT New CGDD polypeptides, useful for diagnosing, preventing, and treating
 PT disorders associated with an abnormal expression or activity of CGDD,
 PT e.g. neuromuscular, immunological, cardiovascular disorders, cancer,
 PT and/or infections.

XX PS Claim 1; Page 250; 299pp; English.

XX CC The present invention relates to novel cell growth, differentiation and
 CC death (CGDD) proteins and polynucleotides encoding them. The sequences of
 CC the invention are useful in diagnosing, preventing and treating disorders
 CC associated with an abnormal expression or activity of CGDD such as
 CC neurodegenerative disorders (e.g. Parkinson's disease, Alzheimer's
 CC disease), muscular disorders (e.g. myotonic dystrophy, catatonia),
 CC endocrine disorders (e.g. diabetes, Grave's disease), cancers (e.g.
 CC leukaemia, cervical or breast cancers), immunological disorders (e.g.
 CC scleroderma, systemic lupus erythematosus; allergies), gastrointestinal
 CC disorders (e.g. Crohn's disease), renal disorders (e.g. Goodpasture's
 CC syndrome), infections (e.g. viral, bacterial, fungal, parasitic,
 CC protozoal, helminthic), cardiovascular disorders (e.g. atherosclerosis)
 CC and hepatic diseases (e.g. cirrhosis). The polynucleotides can be used to
 CC create humanised animals or transgenic animals to model human diseases.
 CC The invention is also used in gene therapy. The present sequence is human
 CC CGDD-27 protein

XX

SO	Sequence 334 AA;	
Query Match	78.5%; Score 296; DB 7; Length 334;	
Best Local Similarity	100.0%; Pred. No. 1.1e-283;	
Matches 296; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
QY	82 AHPKYLSCIAISCFPLAAKTVEEDERIPVLKVLARDSEFCSSSEILRMERIIIDKLNWD 141	
DB	39 AHPKYLSCIAISCFPLAAKTVEEDERIPVLKVLARDSEFCSSSEILRMERIIIDKLNWD 98	
QY	142 LHTATPLDPLHIFHAIAVSTRPQLLFSLPKLSPSOHLAVLKQLIHCACNQLLQFRGSM 201	
DB	99 LHTATPLDPLHIFHAIAVSTRPQLLFSLPKLSPSOHLAVLKQLIHCACNQLLQFRGSM 158	
QY	202 LALAMVSLMEKLIIPDWLSLTIELLOKAQMDSSQLIHCRELVAAHLSLTQSSLPVSVV 261	
DB	159 LALAMVSLMEKLIIPDWLSLTIELLOKAQMDSSQLIHCRELVAAHLSLTQSSLPVSVV 218	
QY	262 YRPLKHTLVTCDKGVRFLHPSSVPGPDFSKNSKPEVPVGTAAFYHHLPAASGCKQTST 321	
DB	219 YRPLKHTLVTCDKGVRFLHPSSVPGPDFSKNSKPEVPVGTAAFYHHLPAASGCKQTST 278	
QY	322 KRKVEEMEVDYFDGIKELYNEDNVSENVGVCCTDLRSQEGHASPCCPPLQPVSVM 377	
DB	279 KRKVEEMEVDYFDGIKELYNEDNVSENVGVCCTDLRSQEGHASPCCPPLQPVSVM 334	
RESULT 6		
ABM80569		
ID	ABM80569 standard; protein; 377 AA.	
XX	ABM80569;	
AC		
XX	18-NOV-2004 (first entry)	
DE	Tumour-associated antigenic target (TAT) polypeptide PRO4605, SEQ:1450.	
XX		
KW	Tumour-associated antigenic target; TAT; human; overexpression; cancer;	
KW	tumour; diagnosis; cell proliferative disorder; breast cancer;	
KW	colorectal cancer; lung cancer; ovarian cancer; liver cancer;	
KW	central nervous system cancer; bladder cancer; pancreatic cancer;	
KW	cervical cancer; melanoma; leukaemia; hybridisation probe;	
KW	chromosome identification; chromosome mapping; gene mapping;	
KW	gene therapy; cytostatic.	
XX		
OS	Homo sapiens.	
XX		
PN	WO2004030615-A2.	
XX		
PD	15-APR-2004.	
XX		
PF	29-SEP-2003; 2003WO-US028547.	
XX		
PR	02-OCT-2002; 2002US-0414971P.	
XX		
PA	(GETH) GENENTECH INC.	
XX		
PI	Wu TD, Zhang Z, Zhou Y;	
XX		
DR	WPI; 2004-347921/32.	
DR	N-PSDB; ACN38124.	
XX		
PT	New tumor-associated antigenic target polypeptides and nucleic acids,	
PT	useful in preparing a medicament for treating or detecting a	
PT	proliferative disorder, e.g. breast, lung, colorectal, ovarian or	
PT	prostate cancer or tumor.	
XX		
PS	Claim 12; SEQ ID NO 1450; 7273pp; English.	
XX		
CC	The invention relates to human tumour-associated antigenic target (TAT)	
CC	polypeptides, and their related nucleic acids. The TAT polypeptides are	
CC	overexpressed in cancer tissues compared to normal tissues, and may thus	
CC	serve as effective targets for the diagnosis and treatment of cancer in	
CC		
CC	mammals. The invention also relates to nucleic acid and polypeptide	
CC	sequences at least 80% identical to the TAT nucleic acids and	
CC	polypeptides; expression vectors and host cells comprising a TAT nucleic	
CC	acid; an antibody specific for a TAT polypeptide; a peptide or organic	
CC	molecule which binds to a TAT polypeptide; fusion proteins comprising a	
CC	TAT polypeptide; and methods and compositions for the treatment or	
CC	diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,	
CC	antibodies, antagonists, binding molecules and compositions are useful	
CC	for diagnosing or treating a cell proliferative disorder associated with	
CC	increased TAT expression, particularly cancers such as breast cancer,	
CC	colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder	
CC	cancer, pancreatic cancer, cervical cancer, cancers of the central	
CC	nervous system, melanoma and leukaemia. TAT nucleic acids may further be	
CC	used as hybridisation probes, in chromosome and gene mapping, in	
CC	chromosome identification and in gene therapy. The present sequence	
CC	represents a TAT polypeptide of the invention	
XX		
SQ	Sequence 377 AA;	
Query Match	73.2%; Score 276; DB 8; Length 377;	
Best Local Similarity	99.7%; Pred. No. 7.4e-264;	
Matches 376; Conservative	0; Mismatches 1; Indels 0; Gaps 0;	
QY	1 MKFPGPLENORLSFLLKAITREAOQMKVNVKMPNSQNVSPSORDEVIOWLAKLYQFN 60	
DB	1 MKFPGPLENORLSFLLKAITREAOQMKVNVKMPNSQNVSPSORDEVIOWLAKLYQFN 60	
QY	61 LYPETFALASSLLDRFLATVKAHPKYLSCIAISCFFLAAKTVEEDERIPVLKVLARDSFC 120	
DB	61 LYPETFALASSLLDRFLATVKAHPKYLSCIAISCFFLAAKTVEEDERIPVLKVLARDSFC 120	
QY	121 GCSSEILRMERIIIDKLNWDLHTATPLDPLHIFHAIAVSTRPQLLFSLPKLSPSOHLAV 180	
DB	121 GCSSEILRMERIIIDKLNWDLHTATPLDPLHIFHAIAVSTRPQLLFSLPKLSPSOHLAV 180	
QY	181 LTKQLLHCACNQLLQFRGSMIALAMVSLMEKLIIPDWLSLTIELLOKAQMDSSQLIHCR 240	
DB	181 LTKQLLHCACNQLLQFRGSMIALAMVSLMEKLIIPDWLSLTIELLOKAQMDSSQLIHCR 240	
QY	241 ELVAHLSTLQSSLPVSVVYRPLKHTLVTCDKGVRFLHPSSVPGPDFSKNSKPEVPV 300	
DB	241 ELVAHLSTLQSSLPVSVVYRPLKHTLVTCDKGVRFLHPSSVPGPDFSKNSKPEVPV 300	
QY	301 RGTAAFYHHLPAASGCKQTSTKRKVEEMEVDYFDGIKRLYNEDNVSENVGVCCTDLRS 360	
DB	301 RGTAAFYHHLPAASGCKQTSTKRKVEEMEVDYFDGIKRLYNEDNVSENVGVCCTDLRS 360	
QY	361 QEGHASPCCPPLQPVSVM 377	
DB	361 QEGHASPCCPPLQPVSVM 377	
RESULT 7		
ADN01131		
ID	ADN01131 standard; protein; 300 AA.	
XX		
AC	ADN01131;	
XX		
DT	01-JUL-2004 (first entry)	
XX		
DE	Human cell growth, differentiation, and death-associated protein #15.	
XX		
KW	human; cell growth; cell differentiation; cell death; CGDD;	
KW	cell proliferative disorder; arteriosclerosis; atherosclerosis; bursitis;	
KW	cirrhosis; hepatitis; polycythaemia vera; psoriasis; cancer;	
KW	developmental disorder; Cushing's syndrome; hypothyroidism;	
KW	neurological disorder; epilepsy; stroke; Alzheimer's disease;	
KW	Pick's disease; Huntington's disease; Parkinson's disease;	
KW	multiple sclerosis; autoimmune disorder; inflammatory disorder; AIDS;	
KW	allergy; anaemia; asthma; contact dermatitis; diabetes mellitus;	
KW	reproductive disorder; infertility; endometriosis; uterine fibroid.	
XX		
OS	Homo sapiens.	

XX WO2004031364-A2.
PN 15-APR-2004.
XX 03-OCT-2003; 2003WO-US0311441.
XX 03-OCT-2002; 2002US-0416205P.
PR 25-OCT-2002; 2002US-0421521P.
PR 21-NOV-2002; 2002US-0428376P.
PR 23-DEC-2002; 2002US-0436258P.
PR 10-JAN-2003; 2003US-0439292P.
PR 13-FEB-2003; 2003US-0447578P.
XX (INCY-) INCYTE CORP.
PA (BURR/) BURRILL J D.
XX Elliott VS, Swarnakar A, Tang YT, Yue H, Lu DAM, Khare R;
PI Chawla NK, Richardson TW, Marquis JP, Lal PG, Nguyen DB, Lee SY;
PI Tran UK, Bhatia UG, Lee S, Blake JU, Ho A, Zheng W, Gao J, Tran B;
PI Yang YG, Gietzen KJ, Hafalia AJA;
XX WPI: 2004-330172/30.
DR N-PSDB; ADN01156.
XX New isolated polypeptides associated with cell growth, differentiation
PT and death, useful for diagnosing, treating or preventing e.g.
PT atherosclerosis, psoriasis, cancers, Alzheimer's disease, AIDS, anemia,
PT diabetes mellitus or infertility.
XX Claim 1; SEQ ID NO 15; 213pp; English.
XX The invention comprises the amino acid and coding sequences of human
CC proteins that are associated with cell growth, differentiation, and death
CC (CGDD). The DNA and protein sequences of the invention are useful for
CC diagnosing, treating or preventing disorders associated with aberrant
CC expression of CGDD, such as: cell proliferative disorders (e.g.
CC arteriosclerosis, atherosclerosis, bursitis, cirrhosis, hepatitis,
CC polycythaemia vera, psoriasis and cancers), developmental disorders
CC Cushing's syndrome and hypothyroidism), neurological disorders (e.g.
CC epilepsy, stroke, Alzheimer's disease, Pick's disease, Huntington's
CC disease, Parkinson's disease and multiple sclerosis),
CC autoimmune/inflammatory disorders (e.g. AIDS, allergies, anaemia, asthma,
CC contact dermatitis and diabetes mellitus), and reproductive disorders
CC (e.g. infertility, endometriosis and uterine fibroid). The present amino
CC acid sequence represents a human CGDD-associated protein of the
CC invention.
XX Sequence 300 AA;
SQ Query Match 40.6%; Score 153; DB 8; Length 300;
Best Local Similarity 100.0%; Pred. No. 2.7e-142;
Matches 153; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MKFGPLENQLSFLLEKAITREAOQMKVNRKMPNSQNVSPQRDEVIQWLAKLYQFN 60
Db 1 MKFGPLENQLSFLLEKAITREAOQMKVNRKMPNSQNVSPQRDEVIQWLAKLYQFN 60
Qy 61 LYPETFALASSILDRFLATVKAHPKYLSCIALSCFFLAAKTVEDERIPVLKVLARDSPC 120
Db 61 LYPETFALASSILDRFLATVKAHPKYLSCIALSCFFLAAKTVEDERIPVLKVLARDSPC 120
Qy 121 GCSSEILRMERIIIDKLNWDLHTATPLDPLFI 153
Db 121 GCSSEILRMERIIIDKLNWDLHTATPLDPLFI 153
RESULT 8
AAG01903
ID AAG01903 standard; protein; 131 AA.
XX AAG01903;
XX

DT 06-OCT-2000 (first entry)
XX Human secreted protein, SEQ ID NO: 5984.
DE Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
XX gene therapy; chromosome mapping.
KW Homo sapiens.
OS EP1033401-A2.
XX 06-SEP-2000.
PD 21-FEB-2000; 2000EP-00200610.
PF 26-FEB-1999; 99US-0122487P.
PR (GEST) GENSET.
XX Dumas Milne Edwards J, Duclert A, Giordano J;
PI WPI: 2000-500381/45.
XX N-PSDB; AAC01909.
XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX Claim 13; SEQ ID NO 5984; 71pp + Sequence Listing; English.
XX The present sequence is a polypeptide encoded by one of a large number of
CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were
CC prepared from total human RNAs or polyA+ RNAs derived from 30 different
CC tissues. EST sequences usually correspond mainly to the 3' untranslated
CC region (UTR) of the mRNA because they are often obtained from oligo-dT
CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA
CC sequences derived from the 5' ends of mRNAs and even in those cases where
CC longer cDNA sequences have been obtained, the full 5' UTR is rarely
CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can
CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs
CC are also used in diagnostic, forensic, gene therapy and chromosome
CC mapping procedures. They are used to obtain upstream regulatory sequences
CC and to design expression and secretion vectors
XX Sequence 131 AA;
SQ Query Match 34.7%; Score 131; DB 3; Length 131;
Best Local Similarity 100.0%; Pred. No. 7.1e-121;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 130 MERIILDKLNWDLHTATPLDPLFIHFAIAVSTRPQLLFSLPKLSPSOHLAVLTQQLHLCM 189
Db 1 MERIILDKLNWDLHTATPLDPLFIHFAIAVSTRPQLLFSLPKLSPSOHLAVLTQQLHLCM 60
Qy 190 ACNOLLQFRGSMALAMVSLMEKLI PDWLSLTIELLOKQMDSSQLIHCRRELVHHLST 249
Db 61 ACNOLLQFRGSMALAMVSLMEKLI PDWLSLTIELLOKQMDSSQLIHCRRELVHHLST 120
Qy 250 LQSSPLNSVY 260
Db 121 LQSSPLNSVY 131
RESULT 9
AAO11635
ID AAO11635 standard; protein; 41 AA.
XX AAO11635;
XX 06-NOV-2001 (first entry)
DT Human polypeptide SEQ ID NO 25527.
DE
XX

KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation.
XX
XX OS Homo sapiens.
XX WO200164835-A2.
XX
XX PD 07-SEP-2001.
XX
XX PF 26-FEB-2001; 2001WO-US04927.
XX
XX PR 28-FEB-2000; 2000US-00515126.
XX PR 18-MAY-2000; 2000US-00577409.
XX
XX PA (HYSE-) HYSEQ INC.
XX
XX PI Tang YT, Liu C, Drmanac RT;
XX
XX DR WPI; 2001-514838/56.
XX DR N-PSDB; AA191566.
XX
XX PT Isolated nucleic acids and polypeptides, useful for preventing diagnosing
XX and treating e.g. leukemia, inflammation and immune disorders.
XX
XX PS Claim 20; SEQ ID NO 2527; 1399pp + Sequence Listing; English.
XX
XX CC The invention relates to human polynucleotides (AA179941-AA193841) and
XX the encoded proteins (AA00010-AA01310) that exhibit activity elating to
XX cytokine, cell proliferation or cell differentiation or which may induce
XX production of other cytokines in other cell populations. The
XX polynucleotides and polypeptides are useful in gene therapy, vaccines or
XX peptide therapy. The polypeptides have various cytokine-like activities,
XX e.g. stem cell growth factor activity, haematopoiesis regulating
XX activity, tissue growth factor activity, immunomodulatory activity and
XX activin/inhibin activity and may be useful in the diagnosis and/or
XX treatment of cancer, leukaemia, nervous system disorders, arthritis and
XX inflammation. Note: The sequence data for this patent did not form part
XX of the printed specification, but was obtained in electronic format
XX directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 41 AA;

Query Match 9.0%; Score 34; DB 4; Length 41;
Best Local Similarity 100.0%; Pred. No. 2.1e-25;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKFPGPLENQLSFLLEKAITREAOQWKVNVKRM 34
DB 8 MKFPGPLENQLSFLLEKAITREAOQWKVNVKRM 41

RESULT 10
AAW21966
ID AAW21966 standard; protein; 14 AA.
XX
XX AC AAW21966;
XX
XX DT 02-DEC-1997 (first entry)
XX
XX DE Human cyclin I peptide fragment.
XX
XX DE human; cyclin I; antisense; probe; neurone; cancer; antibody.
XX
XX KW Homo sapiens.
XX
XX OS WO9712973-A1.
XX
XX PD 10-APR-1997.
XX
XX PF 07-OCT-1996; 96WO-JP002905.
XX

PR 05-OCT-1995; 95JP-00284663.
XX
XX FA (SUME) SUMITOMO ELECTRIC IND CO.
XX
XX PI Nakamura T;
XX
XX DR WPI; 1997-226217/20.
XX
XX PT Human cyclin I protein and related (anti:sense) DNA - used for neuron
XX labelling method and cancer cell detection.
XX
XX PS Claim 7; Page 30; 45pp; Japanese.
XX
XX CC This peptide is a fragment of human cyclin I which can be specifically
XX recognised by antibodies of the invention. The antibodies are used to
XX detect the presence of cyclin I. Antisense cyclin I polynucleotides are
XX useful for as probes and can be labelled and used for detection of
XX neurones by hybridisation with mRNA for cyclin I (contained in the
XX neurones and arising by the expression of the cyclin I gene in these
XX cells). The gene can be used for detection of cancer cells by detecting
XX the expression of the cyclin I gene in these cells
XX
XX SQ Sequence 14 AA;

Query Match 3.7%; Score 14; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.6e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 343 EDNVSENVGSVCGT 356
DB 1 EDNVSENVGSVCGT 14

RESULT 11
ABJ20156
ID ABJ20156 standard; peptide; 10 AA.
XX
XX AC ABJ20156;
XX
XX DT 10-APR-2003 (first entry)
XX
XX DE MHC binding peptide SEQ ID No 321.
XX
XX KW Antirheumatic; antiallergic; antiarthritic; neurotropic; neuroprotective;
XX antiinflammatory; major histocompatibility complex; MHC;
XX autoimmune disease; T cell; B cell; allergic disease; multiple sclerosis;
XX rheumatoid arthritis; neurodegenerative disorder; Alzheimer's disease;
XX inflammation; gene therapy; MHC binding peptide.
XX
XX OS Synthetic.
XX
XX PN WO200294981-A2.
XX
XX PD 28-NOV-2002.
XX
XX PF 16-MAY-2002; 2002WO-IL000383.
XX
XX PR 16-MAY-2001; 2001US-0290958P.
XX PR 29-MAY-2001; 2001US-00865548.
XX
XX PA (TECR) TECHNION RES & DEV FOUND LTD.
XX
XX PI Barnea E, Beer I, Ziv T, Admon A, Dassau L, Buchsbaum S;
XX
XX DR WPI; 2003-210043/20.
XX
XX PT Identifying peptides that are capable of binding to major
XX histocompatibility complex (MHC) molecules of a particular haplotype by
XX analyzing peptides bound to the soluble and secreted form of the MHC
XX molecules of the particular haplotype.
XX
XX PS Claim 58; Page 225; 238pp; English.
XX

CC The invention relates to a novel method for identifying peptides
 CC originating from a particular cell type, which are capable of binding to
 CC major histocompatibility complex (MHC) molecules of a particular
 CC haplotype. The method comprises analysing peptides bound to the soluble
 CC and secreted form of the MHC molecules of the particular haplotype. The
 CC method is useful for identifying peptides for treating an autoimmune
 CC disease, such as T or B cell and/or allergic disease or condition,
 CC rheumatoid arthritis, or multiple sclerosis, neurodegenerative disorders,
 CC e.g. Alzheimer's disease, or diseases associated with inflammation. The
 CC sequences of the invention may be used in a gene therapy application.
 CC This sequence represents a peptide relating to the method for identifying
 CC MHC binding peptides of the invention

XX
 SQ Sequence 10 AA;
 Query Match 2.7%; Score 10; DB 6; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.03; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0;

Qy 71 SLDRFLATV 80
 |||||
 Db 1 SLDRFLATV 10

RESULT 12
 ABG32308
 ID ABG32308 standard; peptide; 9 AA.

XX AC ABG32308;

XX DT 05-NOV-2002 (first entry)

XX DE HLA-A2 associated immunogenic peptide from human Cyclin protein.

XX KW Human; immunogen; epitope; HLA-A1; human leukocyte antigen; CTL;
 KW cytotoxic Y lymphocyte; cytotoxic; cancer; colorectal carcinoma;
 KW ovarian carcinoma; lung carcinoma; prostate carcinoma; vaccine; tumour;
 KW HLA-2; passive immunotherapy; cyclin.

XX OS Homo sapiens.

XX PN WO200246416-A2.

XX PD 13-JUN-2002.

XX PF 04-DEC-2001; 2001WO-US047290.

XX PR 04-DEC-2000; 2000US-0251022P.

XX PR 20-DEC-2000; 2000US-0256824P.

XX PA (ARGO-) ARGONEX INC.

XX PI Ramakrishna V, Ross M, Philip R;

XX DR WPI; 2002-619021/66.

XX PT New immunogen useful as a vaccine for inducing cytotoxic T-lymphocyte,
 XX and for diagnosing, preventing or treating cancer e.g. ovarian carcinoma.

XX PS Claim 1; Page 50; 60pp; English.

XX
 CC The invention relates to an immunogen comprising an isolated polypeptide
 CC whose amino acid sequence comprises an epitopic peptide, does not include
 CC MAGE 4 or MFG-E8 proteins, or consists of MAGE D protein or its
 CC immunologically active fragment. Also included are a polynucleotide
 CC encoding the immunogen or its complement, a vector comprising the
 CC polynucleotide, a mammalian cell comprising the vector and expressing the
 CC polynucleotide, a vaccine composition comprising the immunogen and an
 CC antibody specific for the immunogen. The immunogen is useful for inducing
 CC a cytotoxic T lymphocyte (CTL) in vitro that is specific for a tumour
 CC cell expressing human leukocyte antigen (HLA)-A1 or A2. The immunogen is
 CC useful for inducing a CTL response when administered to a subject. A
 CC mammalian cell that can express the immunogen, is useful for inducing a

CC CTL response in vitro that is specific for a tumour cell expressing HLA-1
 CC or HLA-2. The immunogen or cell is useful for inducing CTL for treating a
 CC subject with cancer (carcinoma, preferably colorectal carcinoma, ovarian
 CC carcinoma, lung carcinoma and prostate carcinoma). The immunogen is also
 CC useful for screening and diagnostic agents, for gene screening in
 CC patients afflicted with cancer, for screening a sample for the presence
 CC of CRUs that specifically recognise the corresponding epitopes, as a
 CC diagnostic tool to evaluate the efficacy of the immunotherapeutic
 CC treatments, to prepare class I MHC (major histocompatibility class)
 CC tetramers which are utilised in conjunction with flow cytometry to
 CC quantitate the frequency of peptide-specific CTL that are present in a
 CC samples of lymphocytes from an individual, and for stimulating the
 CC production of antibodies for use in passive immunotherapy, for use as
 CC diagnostic reagents, and for use as reagents in other processes such as
 CC affinity chromatography. The present sequence is an immunogenic epitope
 CC of the invention derived from human cyclin

XX SQ Sequence 9 AA;

Query Match 2.4%; Score 9; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 72 LLDRFLATV 80

|||||
 Db 1 LLDRFLATV 9

RESULT 13

ABJ19986

ID ABJ19986 standard; peptide; 9 AA.

XX AC ABJ19986;

XX DT 10-APR-2003 (first entry)

XX DE MHC binding peptide SEQ ID No 151.

XX KW Antirheumatic; antiallergic; antiarthritic; nootropic; neuroprotective;
 KW antiinflammatory; major histocompatibility complex; MHC;
 KW autoimmune disease; T cell; B cell; allergic disease; multiple sclerosis;
 KW rheumatoid arthritis; neurodegenerative disorder; Alzheimer's disease;
 KW inflammation; gene therapy; MHC binding peptide.

XX OS Synthetic.

XX PN WO200294981-A2.

XX PD 28-NOV-2002.

XX PF 16-MAY-2002; 2002WO-IL000383.

XX PR 16-MAY-2001; 2001US-0290958P.

XX PR 29-MAY-2001; 2001US-00865548.

XX PA (TECR) TECHNION RES & DEV FOUND LTD.

XX PI Barnea E, Beer I, Ziv T, Admon A, Dassau L, Buchsbaum S;

XX DR WPI; 2003-210043/20.

XX
 CC Identifying peptides that are capable of binding to major
 CC histocompatibility complex (MHC) molecules of a particular haplotype by
 CC analysing peptides bound to the soluble and secreted form of the MHC
 CC molecules of the particular haplotype.

XX FS Claim 37; Page 183; 238pp; English.

XX
 CC The invention relates to a novel method for identifying peptides
 CC originating from a particular cell type, which are capable of binding to
 CC major histocompatibility complex (MHC) molecules of a particular
 CC haplotype. The method comprises analysing peptides bound to the soluble
 CC and secreted form of the MHC molecules of the particular haplotype. The

CC method is useful for identifying peptides for treating an autoimmune
 CC disease, such as T or B cell and/or allergic disease or condition,
 CC rheumatoid arthritis, or multiple sclerosis, neurodegenerative disorders,
 CC e.g. Alzheimer's disease, or diseases associated with inflammation. The
 CC sequences of the invention may be used in a gene therapy application.
 CC This sequence represents a peptide relating to the method for identifying
 CC MHC binding peptides of the invention

XX SQ Sequence 9 AA;

Query Match 2.4%; Score 9; DB 6; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 72 LLDRFLATV 80
 |||||
 Db 1 LLDRFLATV 9

RESULT 14
 AAU85684
 ID AAU85684 standard; protein; 462 AA.

XX AC AAU85684;

XX DT 19-JUL-1999 (first entry)

XX DE NBP46 root lectin.

XX KW NBP46; lectin; Rhizobium; leguminous plant; transgenic plant; nitrogen;
 XX KW nitrogen fixation; fertilizer.

XX OS Dolichos biflorus.

XX FH Key Location/Qualifiers

FT Region 52..73
 /label= Conserved region
 /note= "Conserved among various plant and animal
 FT pyrases"
 FT Region 128..144
 /label= Conserved region
 /note= "Conserved among various plant and animal
 FT pyrases"

FT Modified-site 139
 /note= "Potential N-glycosylation site"
 FT Region 153..175
 /label= Conserved region
 /note= "Conserved among various plant and animal
 FT pyrases"

FT Region 160..180
 /label= Conserved region
 /note= "Conserved among various plant and animal
 FT pyrases"

FT Modified-site 276
 /note= "Potential N-glycosylation site"

XX WO9907223-A1.

XX PD 18-FEB-1999.

XX PF 05-AUG-1998; 98WO-US016261.

XX PR 06-AUG-1997; 97US-00907226.

XX PA (REGC) UNIV CALIFORNIA.

XX PI Etzler ME, Murphy JB;

XX DR WPI; 1999-167136/14.

XX DR N-PSDB; AAX08522.

XX PT New polynucleotides encoding Nod factor binding lectins - useful for
 PT production of transgenic plants which are able to fix nitrogen.

XX PS Claim 7; Page 43; 57pp; English.

XX CC The NBP46 root lectin is instrumental in recognising and binding to
 CC nitrogen fixing rhizobial bacteria via a lectin-carbohydrate interaction.
 CC The production of transgenic plants comprising an expression cassette
 CC expressing the NBP46 root lectin is advantageous since it would mean that
 CC non-leguminous plants could fix nitrogen from the atmosphere, lessening
 CC the need for the addition of nitrogen containing fertilizer to soil. This
 CC would lead to higher crop yields where soil has been overplanted and
 CC replenishment of the depleted soil with usable nitrogen. Alternatively,
 CC expression of NBP46 can be used to modulate oligosaccharide signalling in
 CC the plant. The nucleic acid sequences can be used to inhibit expression
 CC of an endogenous gene and also to suppress endogenous NBP46 gene
 CC expression

XX SQ Sequence 462 AA;

Query Match 2.4%; Score 9; DB 2; Length 462;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 165 LLFSLPKLS 173
 |||||

Db 20 LLFSLPKLS 28

RESULT 15

AAU78818
 ID AAU78818 standard; protein; 462 AA.

XX AC AAU78818;

XX DT 18-JUN-2002 (first entry)

XX DE Dolichos biflorus lectin/nucleotide phosphohydrolase, LNP.

XX KW Lectin/nucleotide phosphohydrolase; LNP; mycorrhizal infection;
 XX KW carbohydrate binding protein; nucleotide dephosphorylation;
 XX KW oligosaccharide signalling; nutrient uptake; plant growth;
 XX KW plant development; antisense technology.

XX OS Dolichos biflorus.

XX FH Key Location/Qualifiers
 FT Peptide 1..48
 /label= Signal_peptide
 FT Protein 49..462
 /label= Mature LNP
 /note= "Lectin/nucleotide phosphohydrolase"

XX WO200220725-A2.

XX PD 14-MAR-2002.

XX PF 06-SEP-2001; 2001WO-US028165.

XX PR 06-SEP-2000; 2000US-00657631.

XX PA (REGC) UNIV CALIFORNIA.

XX PI Etzler ME, Roberts NJ;

XX DR WPI; 2002-304376/34.

XX DR N-PSDB; ABK11098.

XX PT Modulating mycorrhizal infection, useful for improving plant growth, by
 PT transforming plant cell with a sequence encoding lectin/nucleotide
 PT phosphohydrolase.

XX PS Claim 1; Page 31; 37pp; English.

XX PT The invention describes a method of modulating mycorrhizal infection by

CC introducing into a plant an expression cassette comprising a plant
CC promoter operably linked to a heterologous LNP (lectin/nucleotide
CC phosphohydrolase) polynucleotide, or its complement. The LNP's described
CC in the invention are involved in binding a variety of carbohydrates,
CC catalysing the dephosphorylation of nucleotide di- and tri-phosphates and
CC are suspected to be involved in oligosaccharide signalling, important for
CC the interaction of mycorrhizal fungi and plants. The method is useful to
CC increase mycorrhizal infection (by increasing expression of the
CC polynucleotide), resulting in increased uptake of nutrients by plants and
CC better growth/development, but antisense (or other methods of)
CC suppression of LNP expression is also contemplated. This is the amino
CC acid sequence of the Dolichos biflorus lectin/nucleotide phosphohydrolase
CC (LNP) that can be used to modulate mycorrhizal infection in plants
XX

SQ Sequence 462 AA;

Query Match 2.4%; Score 9; DB 5; Length 462;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 165 LLFSLPKLS 173
| | | | | | | |
Db 20 LLFSLPKLS 28

Search completed: February 11, 2005, 03:16:03
Job time : 162.061 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 11, 2005, 03:11:39 ; Search time 32.7826 Seconds
(without alignments)
858.464 Million cell updates/sec

Title: US-09-736-250-1

Perfect score: 377

Sequence: 1 MKFPGPLENQRSLFLEKAI.....LSRQEGHASPCLPQVSVM 377

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

Word size : 0

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Issued Patents AA.*

- 1: /cgm2_6/ptodata/1/iaa/5A-COMB.pep.*
- 2: /cgm2_6/ptodata/1/iaa/5B-COMB.pep.*
- 3: /cgm2_6/ptodata/1/iaa/6A-COMB.pep.*
- 4: /cgm2_6/ptodata/1/iaa/6B-COMB.pep.*
- 5: /cgm2_6/ptodata/1/iaa/PCTUS-COMB.pep.*
- 6: /cgm2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	377	100.0	377	2	US-08-969-106-6
2	377	100.0	377	3	US-09-054-492B-1
3	377	100.0	377	4	US-09-338-125-6
4	254	67.4	254	4	US-09-796-149B-4
5	131	34.7	131	4	US-09-513-999C-5984
6	14	3.7	14	3	US-09-054-492B-5
7	9	2.4	462	4	US-09-129-112-2
8	8	2.1	127	4	US-09-270-767-57798
9	8	2.1	170	4	US-09-270-767-39916
10	8	2.1	170	4	US-09-270-767-55133
11	7	1.9	21	3	US-09-128-155-12
12	7	1.9	52	3	US-09-128-155-8
13	7	1.9	63	3	US-09-128-155-4
14	7	1.9	70	4	US-09-270-767-34602
15	7	1.9	70	4	US-09-270-767-49819
16	7	1.9	78	4	US-09-248-796A-25813
17	7	1.9	85	4	US-09-543-681A-8234
18	7	1.9	136	3	US-09-128-155-11
19	7	1.9	146	2	US-08-788-943A-6
20	7	1.9	146	2	US-08-788-943A-10
21	7	1.9	146	2	US-08-788-943A-11
22	7	1.9	146	2	US-08-823-104-6
23	7	1.9	146	2	US-08-823-104-15
24	7	1.9	146	3	US-08-674-774-6
25	7	1.9	146	3	US-08-674-774-10
26	7	1.9	146	3	US-08-674-774-11
27	7	1.9	146	5	PCT-US96-00952-4
28	7	1.9	146	5	PCT-US96-00952-8
29	7	1.9	146	5	PCT-US96-00952-9
30	7	1.9	146	5	US-08-823-104-17
31	7	1.9	167	3	US-09-128-155-7
32	7	1.9	178	3	US-09-128-155-2
33	7	1.9	211	4	US-09-134-000C-4334
34	7	1.9	218	3	US-09-233-625-2
35	7	1.9	218	4	US-09-398-412B-2
36	7	1.9	218	4	US-09-398-412B-4
37	7	1.9	231	4	US-09-248-796A-15072
38	7	1.9	235	4	US-09-248-796A-15284
39	7	1.9	249	3	US-09-446-504-1
40	7	1.9	249	3	US-09-712-266-1
41	7	1.9	252	4	US-09-107-532A-6519
42	7	1.9	264	4	US-09-248-796A-15036
43	7	1.9	272	4	US-09-949-016-8863
44	7	1.9	274	4	US-09-328-352-5444
45	7	1.9	287	4	US-09-489-039A-10887
46	7	1.9	302	3	US-09-457-046B-8
47	7	1.9	302	3	US-09-457-046B-24
48	7	1.9	302	4	US-09-866-570B-8
49	7	1.9	302	4	US-09-866-570B-24
50	7	1.9	306	3	US-09-457-046B-2
51	7	1.9	306	4	US-09-866-570B-2
52	7	1.9	322	4	US-09-328-352-5489
53	7	1.9	328	4	US-09-252-991A-31963
54	7	1.9	350	4	US-09-800-729-91
55	7	1.9	350	4	US-09-800-729-127
56	7	1.9	354	4	US-09-328-352-7262
57	7	1.9	370	4	US-09-252-991A-24608
58	7	1.9	428	4	US-09-789-599A-2
59	7	1.9	437	3	US-08-757-230A-2
60	7	1.9	437	3	US-08-757-230A-9
61	7	1.9	437	4	US-08-700-393-2
62	7	1.9	437	5	PCT-US95-02315-2
63	7	1.9	439	3	US-09-457-046B-28
64	7	1.9	439	4	US-09-866-570B-28
65	7	1.9	441	4	US-09-949-016-10792
66	7	1.9	446	4	US-09-538-092-781
67	7	1.9	448	3	US-09-457-046B-56
68	7	1.9	448	4	US-09-866-570B-56
69	7	1.9	464	2	US-08-477-451-18
70	7	1.9	500	4	US-09-142-108C-4
71	7	1.9	508	4	US-09-142-108C-17
72	7	1.9	528	2	US-08-484-956-90
73	7	1.9	528	2	US-08-757-653-90
74	7	1.9	528	3	US-08-520-946-90
75	7	1.9	528	4	US-09-655-378A-90
76	7	1.9	560	4	US-09-949-016-6458
77	7	1.9	560	4	US-09-912-559-3
78	7	1.9	560	4	US-09-912-559-4
79	7	1.9	621	4	US-09-902-540-9744
80	7	1.9	626	4	US-09-248-796A-14855
81	7	1.9	739	4	US-09-489-039A-11874
82	7	1.9	752	4	US-09-252-991A-30127
83	7	1.9	789	3	US-08-727-308-1
84	7	1.9	833	2	US-08-484-956-85
85	7	1.9	833	2	US-08-757-653-85
86	7	1.9	833	3	US-08-520-946-85
87	7	1.9	833	4	US-08-758-282B-40
88	7	1.9	833	4	US-09-655-378A-85
89	7	1.9	833	4	US-09-577-304A-40
90	7	1.9	1045	2	US-08-553-436A-6
91	7	1.9	1045	4	US-09-394-272-7
92	7	1.9	1228	4	US-09-949-016-6805
93	7	1.9	1236	4	US-09-949-016-10398
94	6	1.6	13	1	US-08-324-301-5
95	6	1.6	14	1	US-08-182-967-23
96	6	1.6	23	4	US-09-149-476-621
97	6	1.6	23	4	US-09-618-304B-8
98	6	1.6	30	3	US-09-136-251-7
99	6	1.6	30	4	US-09-634-456-7
100	6	1.6	30	4	US-09-635-145A-7

Sequence 8, Appli
Sequence 9, Appli
Sequence 17, Appli
Sequence 2, Appli
Sequence 7, Appli
Sequence 4334, Ap
Sequence 2, Appli
Sequence 2, Appli
Sequence 4, Appli
Sequence 15072, A
Sequence 15284, A
Sequence 1, Appli
Sequence 6519, Ap
Sequence 15036, A
Sequence 8863, Ap
Sequence 5444, Ap
Sequence 10887, A
Sequence 8, Appli
Sequence 24, Appli
Sequence 8, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 5489, Ap
Sequence 31963, A
Sequence 91, Appli
Sequence 127, App
Sequence 127, App
Sequence 24608, A
Sequence 2, Appli
Sequence 2, Appli
Sequence 9, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 28, Appli
Sequence 28, Appli
Sequence 10792, A
Sequence 781, App
Sequence 56, Appli
Sequence 56, Appli
Sequence 18, Appli
Sequence 4, Appli
Sequence 17, Appli
Sequence 90, Appli
Sequence 90, Appli
Sequence 90, Appli
Sequence 6458, Ap
Sequence 4, Appli
Sequence 9744, Ap
Sequence 14855, A
Sequence 11874, A
Sequence 30127, A
Sequence 1, Appli
Sequence 85, Appli
Sequence 85, Appli
Sequence 85, Appli
Sequence 85, Appli
Sequence 40, Appli
Sequence 6, Appli
Sequence 7, Appli
Sequence 6805, Ap
Sequence 10398, A
Sequence 23, Appli
Sequence 621, App
Sequence 8, Appli
Sequence 7, Appli
Sequence 7, Appli

101	6	1.6	31	2	US-08-526-583-15	Sequence 15, Appl	174	4	US-09-543-681A-7624	Sequence 7624, Ap
102	6	1.6	32	2	US-08-526-583-13	Sequence 13, Appl	175	4	US-09-902-540-11774	Sequence 11774, A
103	6	1.6	32	2	US-08-526-583-14	Sequence 14, Appl	176	4	US-09-134-000C-4513	Sequence 4513, Ap
104	6	1.6	32	2	US-08-526-583-16	Sequence 16, Appl	177	4	US-09-583-110-4875	Sequence 4875, Ap
105	6	1.6	38	4	US-09-203-258-721	Sequence 721, App	178	1	US-08-122-546-12	Sequence 12, Appl
106	6	1.6	40	4	US-09-902-540-15209	Sequence 15209, A	179	1	US-07-942-245-14	Sequence 14, Appl
107	6	1.6	43	1	US-07-745-206A-30	Sequence 30, Appl	180	1	US-08-764-938-12	Sequence 12, Appl
108	6	1.6	43	1	US-08-455-543A-57	Sequence 57, Appl	181	2	US-09-111-052-12	Sequence 12, Appl
109	6	1.6	43	2	US-08-223-305C-57	Sequence 57, Appl	182	3	US-09-131-053A-12	Sequence 12, Appl
110	6	1.6	43	2	US-08-311-363-30	Sequence 30, Appl	183	4	US-09-248-796A-24843	Sequence 24843, A
111	6	1.6	48	2	US-08-460-890A-49	Sequence 49, Appl	184	4	US-09-252-991A-21351	Sequence 21351, A
112	6	1.6	48	3	US-08-167-641C-49	Sequence 49, Appl	185	1	US-08-467-420A-15	Sequence 15, Appl
113	6	1.6	48	3	US-08-460-971A-49	Sequence 49, Appl	186	1	US-08-470-110A-15	Sequence 15, Appl
114	6	1.6	48	3	US-08-462-040-49	Sequence 49, Appl	187	2	US-08-940-371-15	Sequence 15, Appl
115	6	1.6	48	3	US-08-460-890A-48	Sequence 48, Appl	188	2	US-08-637-647-15	Sequence 15, Appl
116	6	1.6	49	3	US-08-167-641C-48	Sequence 48, Appl	189	4	US-09-270-767-59367	Sequence 59367, A
117	6	1.6	49	3	US-08-460-971A-48	Sequence 48, Appl	190	4	US-09-270-767-54584	Sequence 54584, A
118	6	1.6	49	3	US-08-462-040-48	Sequence 48, Appl	191	4	US-09-902-540-13065	Sequence 13065, A
119	6	1.6	50	4	US-09-621-976-7723	Sequence 7723, Ap	192	2	US-08-795-868-18	Sequence 18, Appl
120	6	1.6	51	3	US-08-630-916A-117	Sequence 117, App	193	3	US-09-303-069-18	Sequence 18, Appl
121	6	1.6	52	3	US-09-330-330-12	Sequence 12, Appl	194	4	US-09-134-250-18	Sequence 18, Appl
122	6	1.6	52	3	US-09-621-976-5568	Sequence 5568, Ap	195	4	US-09-726-219A-218	Sequence 218, App
123	6	1.6	58	4	US-09-270-767-35469	Sequence 35469, A	196	4	US-09-865-483-8	Sequence 8, Appli
124	6	1.6	58	4	US-09-270-767-50686	Sequence 50686, A	197	6	US-08-881-037-22	Sequence 22, Appl
125	6	1.6	60	4	US-09-248-796A-23846	Sequence 23846, A	198	6	US-08-122-546-8	Sequence 8, Appli
126	6	1.6	61	4	US-09-583-110-4730	Sequence 4730, Ap	199	6	US-08-764-938-8	Sequence 18, Appl
127	6	1.6	61	4	US-09-270-767-43046	Sequence 43046, A	200	6	US-08-308-494A-21	Sequence 21, Appl
128	6	1.6	61	4	US-09-270-767-58375	Sequence 58375, A	201	6	US-09-131-052-8	Sequence 8, Appli
129	6	1.6	61	4	US-09-248-796A-21236	Sequence 21236, A	202	6	US-08-397-411-4	Sequence 4, Appli
130	6	1.6	61	4	US-09-248-796A-25070	Sequence 25070, A	203	6	US-09-131-053A-8	Sequence 8, Appli
131	6	1.6	63	4	US-08-828-683A-28	Sequence 28, Appl	204	6	US-09-232-290-36	Sequence 36, Appl
132	6	1.6	63	4	US-09-543-681A-5520	Sequence 5520, Ap	205	6	US-09-615-192A-400	Sequence 400, App
133	6	1.6	65	1	US-08-123-343A-2	Sequence 2, Appli	206	6	US-09-732-210-653	Sequence 60, Appl
134	6	1.6	65	1	US-09-513-999C-6589	Sequence 6589, Ap	207	6	US-08-477-728-60	Sequence 60, Appl
135	6	1.6	66	4	US-09-621-976-5772	Sequence 5772, Ap	208	6	US-08-474-040-60	Sequence 60, Appl
136	6	1.6	68	4	US-09-248-796A-22651	Sequence 22651, A	209	6	US-08-487-200-60	Sequence 60, Appl
137	6	1.6	68	4	US-09-513-999C-4893	Sequence 4893, Ap	210	6	US-08-667-769A-15	Sequence 15, Appl
138	6	1.6	69	4	US-09-205-258-439	Sequence 439, Ap	211	6	US-08-752-844-16	Sequence 16, Appl
139	6	1.6	69	4	US-09-205-258-439	Sequence 439, Ap	212	6	US-08-591-196-16	Sequence 16, Appl
140	6	1.6	70	3	US-08-851-843A-200	Sequence 200, App	213	6	US-08-484-537-60	Sequence 60, Appl
141	6	1.6	70	3	US-08-974-549A-319	Sequence 319, App	214	6	US-09-293-533-16	Sequence 16, Appl
142	6	1.6	70	3	US-08-854-050-200	Sequence 200, App	215	6	PCT-US95-17082A-15	Sequence 15, Appl
143	6	1.6	70	3	US-09-430-323-200	Sequence 320, App	216	6	US-09-252-991A-24595	Sequence 24595, A
144	6	1.6	70	3	US-09-402-181B-319	Sequence 319, App	217	6	US-08-652-558-8	Sequence 8, Appli
145	6	1.6	76	3	US-09-721-456-319	Sequence 319, App	218	6	US-08-652-558-38	Sequence 38, Appl
146	6	1.6	76	3	US-09-134-001C-4287	Sequence 4287, Ap	219	6	US-09-254-189-5	Sequence 5, Appli
147	6	1.6	77	4	US-09-248-796A-27483	Sequence 27483, A	220	6	US-08-881-037-67	Sequence 67, Appl
148	6	1.6	78	4	US-09-270-767-42639	Sequence 42639, A	221	6	US-09-732-210-733	Sequence 733, App
149	6	1.6	84	4	US-09-543-681A-5717	Sequence 5717, Ap	222	6	US-09-461-325-355	Sequence 355, App
150	6	1.6	85	4	US-09-513-999C-7654	Sequence 7654, Ap	223	6	US-09-198-452A-1225	Sequence 1225, Ap
151	6	1.6	86	4	US-09-621-976-7127	Sequence 7127, Ap	224	6	US-10-012-542-355	Sequence 355, App
152	6	1.6	86	4	US-09-583-110-2919	Sequence 2919, Ap	225	6	US-10-115-123-355	Sequence 355, App
153	6	1.6	88	4	US-09-107-433-4102	Sequence 4102, Ap	226	6	US-09-232-290-41	Sequence 41, Appl
154	6	1.6	89	4	US-09-107-532A-6179	Sequence 6179, Ap	227	6	US-09-328-352-5925	Sequence 5925, Ap
155	6	1.6	94	4	US-09-902-540-12396	Sequence 12396, A	228	6	US-09-248-796A-21935	Sequence 21935, A
156	6	1.6	94	4	US-10-014-269-6	Sequence 6, Appli	229	6	US-09-716-129-173	Sequence 173, App
157	6	1.6	95	4	US-09-205-258-314	Sequence 314, App	230	6	US-09-513-999C-4892	Sequence 4892, App
158	6	1.6	95	4	US-09-471-276-1419	Sequence 1419, Ap	231	6	US-09-949-016-11072	Sequence 11072, A
159	6	1.6	96	4	US-09-270-767-40163	Sequence 40163, A	232	6	US-09-248-796A-19032	Sequence 19032, A
160	6	1.6	96	4	US-09-270-767-55379	Sequence 55379, A	233	6	US-09-252-991A-23430	Sequence 23430, A
161	6	1.6	97	3	US-08-881-037-66	Sequence 66, Appl	234	6	US-09-270-767-42781	Sequence 42781, A
162	6	1.6	98	2	US-08-752-844-5	Sequence 5, Appli	235	6	US-09-248-796A-14793	Sequence 14793, A
163	6	1.6	98	2	US-09-591-196-5	Sequence 5, Appli	236	6	US-09-513-999C-7977	Sequence 7977, Ap
164	6	1.6	98	4	US-09-543-681A-5462	Sequence 5462, Ap	237	6	US-09-774-639-114	Sequence 114, App
165	6	1.6	98	4	US-09-293-533-5	Sequence 533-5	238	6	US-09-513-999C-7872	Sequence 7872, Ap
166	6	1.6	99	4	US-09-732-210-980	Sequence 980, App	239	6	US-08-621-751A-4	Sequence 4, Appli
167	6	1.6	99	4	US-09-270-767-57896	Sequence 57896, A	240	6	US-07-634-278-33	Sequence 33, Appl
168	6	1.6	100	4	US-09-328-352-6731	Sequence 6731, Ap	241	6	US-08-477-728-33	Sequence 33, Appl
169	6	1.6	100	4	US-09-248-796A-19747	Sequence 19747, A	242	6	US-08-474-040-33	Sequence 33, Appl
170	6	1.6	100	4	US-09-248-796A-20216	Sequence 20216, A	243	6	US-08-487-200-33	Sequence 33, Appl
171	6	1.6	102	4	US-09-621-976-4820	Sequence 4820, Ap	244	6	US-09-438-185A-859	Sequence 859, App
172	6	1.6	102	4	US-09-513-999C-4693	Sequence 4693, Ap	245	6		
173	6	1.6	102	4	US-09-513-999C-4693	Sequence 4693, Ap	246	6		

247	6	1.6	139	4	US-09-640-211A-887	Sequence 887, App	320	6	1.6	206	4	US-09-394-142B-18	Sequence 18, Appl
248	6	1.6	141	4	US-09-248-796A-26930	Sequence 26930, A	321	6	1.6	208	4	US-09-107-532A-5399	Sequence 5399, Ap
249	6	1.6	142	4	US-09-248-796A-27617	Sequence 27617, A	322	6	1.6	210	4	US-09-710-279-708	Sequence 708, App
250	6	1.6	142	4	US-09-252-991A-21626	Sequence 21626, A	323	6	1.6	210	4	US-09-248-796A-15470	Sequence 15470, A
251	6	1.6	142	4	US-09-270-767-32362	Sequence 32362, A	324	6	1.6	210	4	US-09-949-016-7162	Sequence 7162, Ap
252	6	1.6	142	4	US-09-902-540-12459	Sequence 12459, A	325	6	1.6	212	1	US-08-353-341-1	Sequence 1, Appli
253	6	1.6	145	4	US-09-270-767-39030	Sequence 39030, A	326	6	1.6	212	4	US-09-270-767-42586	Sequence 42586, A
254	6	1.6	145	4	US-09-270-767-54247	Sequence 54247, A	327	6	1.6	214	4	US-09-270-767-41374	Sequence 41374, A
255	6	1.6	147	4	US-09-489-039A-12992	Sequence 12992, A	328	6	1.6	214	4	US-09-270-767-56590	Sequence 56590, A
256	6	1.6	152	2	US-08-752-844-4	Sequence 4, Appli	329	6	1.6	216	4	US-09-902-540-12039	Sequence 12039, A
257	6	1.6	152	2	US-08-591-196-4	Sequence 4, Appli	330	6	1.6	218	4	US-09-1320-13220	Sequence 13220, A
258	6	1.6	152	3	US-09-192-838B-4	Sequence 4, Appli	331	6	1.6	218	4	US-09-489-039A-10574	Sequence 10574, A
259	6	1.6	152	4	US-09-293-533-4	Sequence 4, Appli	332	6	1.6	219	4	US-09-538-092-499	Sequence 499, App
260	6	1.6	152	4	US-09-324-131-4	Sequence 4, Appli	333	6	1.6	220	4	US-09-949-016-11039	Sequence 11039, A
261	6	1.6	152	4	US-09-732-210-872	Sequence 872, App	334	6	1.6	221	4	US-09-270-767-60149	Sequence 60149, A
262	6	1.6	154	4	US-09-732-210-871	Sequence 871, App	335	6	1.6	222	1	US-08-336-257A-5	Sequence 5, Appli
263	6	1.6	154	4	US-09-732-210-873	Sequence 873, App	336	6	1.6	222	2	US-08-190-199A-67	Sequence 67, Appl
264	6	1.6	157	4	US-09-270-767-33063	Sequence 33063, A	337	6	1.6	222	4	US-09-270-767-40120	Sequence 40120, A
265	6	1.6	157	4	US-09-270-767-48280	Sequence 48280, A	338	6	1.6	222	4	US-09-270-767-55336	Sequence 55336, A
266	6	1.6	158	2	US-08-414-938A-2	Sequence 2, Appli	339	6	1.6	222	4	US-09-949-016-5983	Sequence 5983, Ap
267	6	1.6	159	4	US-09-270-767-38167	Sequence 38167, A	340	6	1.6	222	6	5386025-2	Patent No. 5386025
268	6	1.6	159	4	US-09-270-767-53384	Sequence 53384, A	341	6	1.6	222	6	5386025-2	Patent No. 5386025
269	6	1.6	160	4	US-09-394-142B-10	Sequence 10, Appl	342	6	1.6	224	3	US-08-871-572B-13	Sequence 13, Appl
270	6	1.6	160	4	US-09-902-540-13231	Sequence 13231, A	343	6	1.6	224	3	US-09-134-001C-4608	Sequence 4608, Ap
271	6	1.6	161	4	US-09-252-991A-23037	Sequence 23037, A	344	6	1.6	224	4	US-09-482-273-174	Sequence 174, App
272	6	1.6	161	4	US-09-583-110-5057	Sequence 5057, App	345	6	1.6	225	1	US-08-462-169B-22	Sequence 22, Appl
273	6	1.6	166	4	US-09-252-991A-19472	Sequence 19472, A	346	6	1.6	225	2	US-08-951-822-25	Sequence 25, Appl
274	6	1.6	167	4	US-09-270-767-46834	Sequence 46834, A	347	6	1.6	225	3	US-09-103-079-22	Sequence 22, Appl
275	6	1.6	167	4	US-09-198-452A-72	Sequence 72, Appl	348	6	1.6	225	3	US-08-705-245-3	Sequence 3, Appli
276	6	1.6	168	4	US-09-902-540-12311	Sequence 12311, A	349	6	1.6	225	3	US-08-705-245-10	Sequence 10, Appl
277	6	1.6	169	4	US-09-107-433-2609	Sequence 2609, App	350	6	1.6	225	3	US-08-368-951-25	Sequence 25, Appl
278	6	1.6	170	4	US-09-107-433-2609	Sequence 2609, App	351	6	1.6	225	4	US-09-425-021-22	Sequence 22, Appl
279	6	1.6	173	4	US-09-585-228-2	Sequence 2, Appli	352	6	1.6	225	4	US-09-229-947-25	Sequence 25, Appl
280	6	1.6	173	4	US-09-252-991A-23656	Sequence 23656, A	353	6	1.6	225	4	US-09-564-829-16	Sequence 16, Appl
281	6	1.6	174	4	US-09-270-767-44914	Sequence 44914, A	354	6	1.6	225	4	US-09-490-714-3	Sequence 3, Appli
282	6	1.6	174	4	US-09-673-395A-304	Sequence 304, App	355	6	1.6	225	4	US-09-490-714-10	Sequence 10, Appl
283	6	1.6	174	4	US-09-270-767-36870	Sequence 36870, A	356	6	1.6	225	4	US-08-462-159B-2	Sequence 2, Appli
284	6	1.6	174	4	US-09-270-767-52087	Sequence 52087, A	357	6	1.6	226	3	US-09-949-016-10966	Sequence 10966, A
285	6	1.6	176	4	US-09-270-767-39416	Sequence 39416, A	358	6	1.6	226	3	US-09-134-001C-5486	Sequence 5486, Ap
286	6	1.6	176	4	US-09-270-767-54633	Sequence 54633, A	359	6	1.6	228	4	US-09-543-681A-5259	Sequence 5259, Ap
287	6	1.6	176	4	US-09-248-796A-19842	Sequence 19842, A	360	6	1.6	229	4	US-09-583-110-4946	Sequence 4946, Ap
288	6	1.6	177	3	US-08-748-506-21	Sequence 21, Appl	361	6	1.6	230	4	US-09-602-787A-472	Sequence 472, App
289	6	1.6	177	3	US-09-082-920-3	Sequence 3, Appli	362	6	1.6	231	4	US-09-248-796A-15033	Sequence 15033, A
290	6	1.6	177	4	US-09-543-681A-5159	Sequence 5159, App	363	6	1.6	235	2	US-08-190-199A-61	Sequence 61, Appl
291	6	1.6	177	4	US-09-603-472A-62	Sequence 62, Appl	364	6	1.6	235	4	US-09-580-235-2	Sequence 2, Appli
292	6	1.6	181	4	US-09-489-039A-9684	Sequence 9684, App	365	6	1.6	235	4	US-09-580-235-6	Sequence 6, Appli
293	6	1.6	182	4	US-09-270-767-41975	Sequence 41975, A	366	6	1.6	235	4	US-09-580-181-2	Sequence 2, Appli
294	6	1.6	183	4	US-09-248-796A-19228	Sequence 19228, A	367	6	1.6	235	4	US-09-580-181-6	Sequence 6, Appli
295	6	1.6	184	4	US-09-252-991A-29270	Sequence 29270, A	368	6	1.6	235	4	US-09-102-530-2	Sequence 2, Appli
296	6	1.6	187	3	US-09-134-001C-4780	Sequence 4780, App	369	6	1.6	235	4	US-09-102-530-6	Sequence 6, Appli
297	6	1.6	188	4	US-09-543-681A-8022	Sequence 8022, App	370	6	1.6	235	4	US-09-107-433-4367	Sequence 4367, Ap
298	6	1.6	189	2	US-08-464-517-21	Sequence 21, Appl	371	6	1.6	236	2	US-08-464-517-22	Sequence 22, Appl
299	6	1.6	189	2	US-08-246-361A-21	Sequence 21, Appl	372	6	1.6	236	2	US-08-246-361A-22	Sequence 22, Appl
300	6	1.6	189	3	US-08-463-772-21	Sequence 21, Appl	373	6	1.6	236	3	US-08-463-772-22	Sequence 22, Appl
301	6	1.6	189	5	PCT-US93-05000-21	Sequence 21, Appl	374	6	1.6	236	3	US-09-634-137-32	Sequence 32, Appl
302	6	1.6	190	4	US-09-543-681A-8168	Sequence 8168, App	375	6	1.6	236	4	US-09-248-796A-23590	Sequence 23590, A
303	6	1.6	191	4	US-09-640-211A-1080	Sequence 1080, App	376	6	1.6	236	5	PCT-US93-05000-22	Sequence 22, Appl
304	6	1.6	193	4	US-09-792-024-103	Sequence 103, App	377	6	1.6	237	2	US-08-576-626A-56	Sequence 56, Appl
305	6	1.6	195	4	US-09-270-767-44051	Sequence 44051, A	378	6	1.6	237	3	US-09-320-878-11	Sequence 11, Appl
306	6	1.6	196	4	US-09-328-352-5445	Sequence 5445, App	379	6	1.6	237	3	US-09-105-537-18	Sequence 18, Appl
307	6	1.6	196	4	US-09-583-110-4152	Sequence 4152, App	380	6	1.6	237	4	US-09-657-440-11	Sequence 11, Appl
308	6	1.6	197	4	US-09-252-991A-28165	Sequence 28165, A	381	6	1.6	239	2	US-08-860-174A-2	Sequence 2, Appli
309	6	1.6	200	4	US-09-252-991A-29135	Sequence 29135, A	382	6	1.6	239	4	US-09-949-016-9708	Sequence 9708, Ap
310	6	1.6	200	4	US-09-540-236-3005	Sequence 3005, App	383	6	1.6	239	6	5455030-13	Patent No. 5455030
311	6	1.6	201	1	US-08-240-124-4	Sequence 4, Appli	384	6	1.6	239	6	5455030-13	Patent No. 5455030
312	6	1.6	201	2	US-08-453-943-4	Sequence 4, Appli	385	6	1.6	240	4	US-09-270-767-40675	Sequence 40675, A
313	6	1.6	201	2	US-09-057-121-4	Sequence 4, Appli	386	6	1.6	240	4	US-09-270-767-55891	Sequence 55891, A
314	6	1.6	201	3	US-09-358-734-4	Sequence 4, Appli	387	6	1.6	241	4	US-09-554-765-13	Sequence 13, Appl
315	6	1.6	201	4	US-09-615-192A-391	Sequence 391, App	388	6	1.6	241	4	US-09-248-796A-21751	Sequence 21751, A
316	6	1.6	201	4	US-09-214-631-8	Sequence 8, Appli	389	6	1.6	241	4	US-10-101-464A-698	Sequence 698, App
317	6	1.6	203	4	US-09-134-000C-5644	Sequence 5644, App	390	6	1.6	241	4	US-09-726-219A-187	Sequence 187, App
318	6	1.6	204	4	US-09-328-352-6580	Sequence 6580, App	391	6	1.6	242	6	5455030-15	Patent No. 5455030
319	6	1.6	204	4	US-09-302-540-15674	Sequence 15674, A	392	6	1.6	242	6	5455030-15	Patent No. 5455030

333	6	1.6	246	4	US-09-270-767-39204	Sequence 39204, A	466	1.6	302	4	US-09-107-433-4911	Sequence 4911, Ap
334	6	1.6	246	4	US-09-270-767-39204	Sequence 54421, A	467	1.6	302	4	US-09-949-016-10213	Sequence 10213, A
335	6	1.6	247	1	US-08-353-341-2	Sequence 2, Appli	468	1.6	303	4	US-09-198-452A-904	Sequence 904, App
336	6	1.6	247	3	US-08-858-207A-300	Sequence 300, App	469	1.6	303	4	US-09-107-532A-5585	Sequence 5585, Ap
337	6	1.6	247	4	US-09-252-991A-32400	Sequence 32400, A	470	1.6	303	4	US-09-543-681A-7946	Sequence 7946, Ap
338	6	1.6	247	4	US-09-583-110-3069	Sequence 3069, Ap	471	1.6	305	4	US-09-674-529B-14	Sequence 14, Appl
339	6	1.6	248	4	US-09-270-767-38407	Sequence 38407, A	472	1.6	306	4	US-09-328-352-8079	Sequence 8079, Ap
340	6	1.6	248	4	US-09-270-767-53624	Sequence 53624, A	473	1.6	309	2	US-08-464-517-4	Sequence 4, Appli
341	6	1.6	249	4	US-09-673-395A-586	Sequence 586, App	474	1.6	309	3	US-08-463-772-4	Sequence 4, Appli
342	6	1.6	249	4	US-09-796-149B-3	Sequence 3, Appli	475	1.6	309	4	US-09-655-908-12	Sequence 12, Appli
343	6	1.6	249	4	US-09-796-149B-7	Sequence 7, Appli	476	1.6	309	4	US-09-710-279-936	Sequence 936, App
344	6	1.6	251	4	US-09-489-039A-5020	Sequence 9020, Ap	477	1.6	310	4	US-09-438-185A-841	Sequence 841, App
345	6	1.6	251	4	US-09-107-433-4204	Sequence 4204, Ap	478	1.6	311	4	US-09-252-991A-16719	Sequence 16719, A
346	6	1.6	253	4	US-09-796-149B-8	Sequence 8, Appli	479	1.6	311	4	US-09-270-767-44261	Sequence 44261, A
347	6	1.6	253	4	US-09-902-540-9969	Sequence 9969, Ap	480	1.6	314	4	US-09-270-767-46010	Sequence 46010, A
348	6	1.6	254	3	US-09-449-437A-4	Sequence 4, Appli	481	1.6	315	1	US-08-253-155A-34	Sequence 34, Appl
349	6	1.6	254	3	US-09-449-437A-6	Sequence 6, Appli	482	1.6	317	4	US-09-270-767-40937	Sequence 40937, A
350	6	1.6	254	3	US-09-195-106-2	Sequence 2, Appli	483	1.6	317	4	US-09-270-767-56153	Sequence 56153, A
351	6	1.6	256	4	US-09-489-039A-8086	Sequence 8086, Ap	484	1.6	318	4	US-09-902-540-10733	Sequence 10733, A
352	6	1.6	256	4	US-09-270-767-39978	Sequence 39978, A	485	1.6	320	3	US-09-134-001C-4439	Sequence 4439, Ap
353	6	1.6	256	4	US-09-270-767-39978	Sequence 55195, A	486	1.6	325	4	US-09-651-200-20	Sequence 20, Appl
354	6	1.6	257	4	US-09-252-991A-26120	Sequence 26120, A	487	1.6	325	3	US-08-748-506-14	Sequence 14, Appl
355	6	1.6	258	3	US-09-134-001C-4806	Sequence 4806, Ap	488	1.6	327	3	US-08-748-506-22	Sequence 22, Appl
356	6	1.6	260	4	US-09-270-767-33511	Sequence 33511, A	489	1.6	327	3	US-08-748-506-23	Sequence 23, Appl
357	6	1.6	260	4	US-09-902-540-14188	Sequence 14188, A	490	1.6	327	3	US-08-748-506-24	Sequence 24, Appl
358	6	1.6	262	4	US-09-252-991A-18779	Sequence 18779, A	491	1.6	331	4	US-09-489-039A-9306	Sequence 9306, Ap
359	6	1.6	262	4	US-09-270-767-43745	Sequence 43745, A	492	1.6	331	4	US-09-328-352-6400	Sequence 6400, Ap
360	6	1.6	262	4	US-09-809-920-13	Sequence 13, Appl	493	1.6	332	4	US-09-949-016-10159	Sequence 10159, A
361	6	1.6	263	2	US-08-752-844-66	Sequence 66, Appl	494	1.6	332	4	US-09-902-540-12515	Sequence 12515, A
362	6	1.6	263	4	US-09-293-533-86	Sequence 66, Appl	495	1.6	333	4	US-09-543-681A-6874	Sequence 6874, Ap
363	6	1.6	264	4	US-09-710-279-388	Sequence 388, App	496	1.6	336	4	US-09-543-681A-5330	Sequence 5330, Ap
364	6	1.6	266	2	US-07-857-224B-43	Sequence 43, Appl	497	1.6	336	4	US-09-902-540-16045	Sequence 16045, A
365	6	1.6	266	2	US-07-857-224B-44	Sequence 44, Appl	498	1.6	337	4	US-09-252-991A-18558	Sequence 18558, A
366	6	1.6	266	4	US-09-328-352-4705	Sequence 4705, Ap	499	1.6	337	4	US-09-705-534-2	Sequence 2, Appli
367	6	1.6	269	3	US-09-134-001C-4919	Sequence 4919, Ap	500	1.6	337	4	US-09-949-016-6825	Sequence 6825, Ap
368	6	1.6	269	4	US-09-252-991A-30515	Sequence 30515, A	501	1.6	338	3	US-08-561-536-2	Sequence 2, Appli
369	6	1.6	270	4	US-09-540-236-2797	Sequence 2797, Ap	502	1.6	338	4	US-09-583-110-4275	Sequence 4275, Ap
370	6	1.6	271	4	US-09-252-991A-24319	Sequence 24319, A	503	1.6	338	4	US-09-432-682-2	Sequence 2, Appli
371	6	1.6	272	4	US-08-756-416-39	Sequence 39, Appl	504	1.6	342	4	US-09-489-039A-12340	Sequence 12340, A
372	6	1.6	272	4	US-09-270-767-59048	Sequence 59048, A	505	1.6	344	3	US-09-393-554-3	Sequence 3, Appli
373	6	1.6	272	4	US-09-726-219A-183	Sequence 183, App	506	1.6	345	4	US-09-248-796A-25189	Sequence 25189, A
374	6	1.6	272	4	US-09-949-016-6331	Sequence 6331, App	507	1.6	346	4	US-09-107-433-4305	Sequence 4305, Ap
375	6	1.6	272	4	US-09-949-016-10996	Sequence 10996, A	508	1.6	349	4	US-09-398-858-22	Sequence 22, Appl
376	6	1.6	275	4	US-09-252-991A-29459	Sequence 29459, A	509	1.6	351	4	US-08-311-731A-28	Sequence 28, Appl
377	6	1.6	275	4	US-09-270-767-57677	Sequence 57677, A	510	1.6	351	4	US-09-902-540-13214	Sequence 13214, A
378	6	1.6	275	4	US-09-270-767-61549	Sequence 61549, A	511	1.6	353	4	US-09-949-016-7157	Sequence 7157, Ap
379	6	1.6	280	4	US-09-252-991A-31168	Sequence 31168, A	512	1.6	357	4	US-09-489-039A-13443	Sequence 13443, A
380	6	1.6	281	4	US-09-583-110-2802	Sequence 2802, Ap	513	1.6	360	4	US-09-328-352-7879	Sequence 7879, Ap
381	6	1.6	281	4	US-09-902-540-16177	Sequence 16177, A	514	1.6	360	4	US-09-602-787A-150	Sequence 150, App
382	6	1.6	282	1	US-08-324-301-15	Sequence 15, Appl	515	1.6	361	4	US-09-252-991A-25005	Sequence 25005, A
383	6	1.6	282	4	US-09-270-767-41601	Sequence 41601, A	516	1.6	362	4	US-09-248-796A-20105	Sequence 20105, A
384	6	1.6	284	4	US-09-248-796A-19213	Sequence 19213, A	517	1.6	363	1	US-08-530-950-6	Sequence 6, Appli
385	6	1.6	286	4	US-09-328-352-6975	Sequence 6975, Ap	518	1.6	363	3	US-08-888-429A-6	Sequence 6, Appli
386	6	1.6	287	4	US-09-107-433-4368	Sequence 4368, Ap	519	1.6	363	3	US-09-149-879-6	Sequence 6, Appli
387	6	1.6	289	2	US-08-246-361A-4	Sequence 4, Appli	520	1.6	363	4	US-09-057-009-6	Sequence 6, Appli
388	6	1.6	289	4	US-09-328-352-6027	Sequence 6027, Ap	521	1.6	363	4	US-09-593-653-6	Sequence 6, Appli
389	6	1.6	289	4	US-09-919-497-54	Sequence 54, Appl	522	1.6	363	4	US-09-142-108C-25	Sequence 25, Appl
390	6	1.6	289	4	US-09-949-016-6127	Sequence 6127, Ap	523	1.6	369	4	US-09-252-991A-18905	Sequence 18905, A
391	6	1.6	289	5	PCT-US93-05000-4	Sequence 4, Appli	524	1.6	369	4	US-09-252-991A-28650	Sequence 28650, A
392	6	1.6	291	4	US-09-328-352-4678	Sequence 4678, Ap	525	1.6	369	4	US-09-902-540-10817	Sequence 10817, A
393	6	1.6	292	3	US-08-858-207A-391	Sequence 391, App	526	1.6	370	2	US-08-341-538A-2	Sequence 2, Appli
394	6	1.6	292	4	US-09-543-681A-6495	Sequence 6495, Ap	527	1.6	370	2	US-08-725-518-2	Sequence 2, Appli
395	6	1.6	292	4	US-09-583-110-3607	Sequence 3607, Ap	528	1.6	371	4	US-09-636-215-708	Sequence 708, App
396	6	1.6	292	4	US-09-583-110-3607	Sequence 3607, Ap	529	1.6	371	4	US-09-685-166A-708	Sequence 708, App
397	6	1.6	293	4	US-09-252-991A-23471	Sequence 23471, A	530	1.6	371	4	US-09-679-426-708	Sequence 708, App
398	6	1.6	293	4	US-09-270-767-46006	Sequence 46006, A	531	1.6	371	4	US-09-759-143-708	Sequence 708, App
399	6	1.6	295	4	US-09-949-016-6449	Sequence 6449, Ap	532	1.6	371	4	US-09-651-236-708	Sequence 708, App
400	6	1.6	298	4	US-09-270-767-41588	Sequence 41588, A	533	1.6	371	4	US-09-651-236-708	Sequence 708, App
401	6	1.6	299	4	US-09-134-000C-4703	Sequence 4703, Ap	534	1.6	372	3	US-08-120-601B-7	Sequence 7, Appli
402	6	1.6	299	4	US-09-902-540-9930	Sequence 9930, Ap	535	1.6	372	4	US-09-252-991A-21179	Sequence 21179, A
403	6	1.6	301	4	US-09-252-991A-26242	Sequence 26242, A	536	1.6	373	4	US-09-252-991A-20254	Sequence 20254, A
404	6	1.6	302	4	US-09-482-273-105	Sequence 105, App	537	1.6	374	4	US-09-543-681A-7631	Sequence 7631, Ap
405	6	1.6	302	4	US-09-252-991A-24353	Sequence 24353, A	538	1.6	374	4	US-09-489-039A-10660	Sequence 10660, A
	6	1.6	302	4	US-08-426-630-40	Sequence 40, Appl	539	1.6	376	4	US-09-248-796A-14887	Sequence 14887, A

539	6	1.6	378	4	US-09-248-796A-15663	Sequence 15663, A	612	6	1.6	420	4	US-09-168-595-142	Sequence 142, App
540	6	1.6	378	4	US-09-349-016-8020	Sequence 8020, Ap	613	6	1.6	420	4	US-09-684-855-120	Sequence 120, App
541	6	1.6	379	4	US-09-252-991A-19597	Sequence 19597, A	614	6	1.6	420	4	US-09-543-681A-6289	Sequence 6289, Ap
542	6	1.6	384	4	US-09-502-540-10126	Sequence 10126, A	615	6	1.6	420	4	US-09-488-265B-19	Sequence 19, Appl
543	6	1.6	388	4	US-09-489-039A-9580	Sequence 9580, Ap	616	6	1.6	423	4	US-09-253-991A-26714	Sequence 26714, A
544	6	1.6	389	4	US-09-949-016-7723	Sequence 7723, Ap	617	6	1.6	423	4	US-09-976-594-19	Sequence 19, Appl
545	6	1.6	392	3	US-08-861-774B-24	Sequence 24, Appl	618	6	1.6	423	4	US-09-913-039-19	Sequence 19, Appl
546	6	1.6	393	1	US-08-530-950-8	Sequence 8, Appl	619	6	1.6	423	4	US-09-248-796A-20238	Sequence 20238, A
547	6	1.6	393	3	US-08-888-429A-8	Sequence 8, Appl	620	6	1.6	424	3	US-09-087-134-8	Sequence 8, Appl
548	6	1.6	393	3	US-09-149-879-8	Sequence 8, Appl	621	6	1.6	424	3	US-09-253-991A-16822	Sequence 16822, A
549	6	1.6	393	4	US-08-178-257-13	Sequence 13, Appl	622	6	1.6	424	4	US-09-252-991A-32935	Sequence 32935, A
550	6	1.6	393	4	US-09-057-009-8	Sequence 8, Appl	623	6	1.6	424	4	US-09-198-452A-45	Sequence 45, Appl
551	6	1.6	393	4	US-09-593-653-8	Sequence 8, Appl	624	6	1.6	424	4	US-09-538-092-881	Sequence 881, App
552	6	1.6	393	6	52329279-6	Patent No. 52329279	625	6	1.6	425	2	US-09-096-776B-8	Sequence 8, Appl
553	6	1.6	393	6	5512669-6	Patent No. 5512669	626	6	1.6	425	2	US-08-732-028-2	Sequence 2, Appl
554	6	1.6	393	6	52329279-6	Patent No. 52329279	627	6	1.6	425	3	US-09-183-228-2	Sequence 8, Appl
555	6	1.6	393	6	5512669-6	Patent No. 5512669	628	6	1.6	425	3	US-09-923-923-8	Sequence 8, Appl
556	6	1.6	394	2	US-08-646-590B-40	Sequence 40, Appl	629	6	1.6	425	4	US-09-949-016-6670	Sequence 6670, Ap
557	6	1.6	394	3	US-09-412-184-40	Sequence 40, Appl	630	6	1.6	426	4	US-09-904-540-11847	Sequence 11847, A
558	6	1.6	394	4	US-09-134-000C-4332	Sequence 4332, Ap	631	6	1.6	430	4	US-09-903-540-14448	Sequence 14448, A
559	6	1.6	394	4	US-09-949-016-9565	Sequence 9565, Ap	632	6	1.6	433	4	US-09-252-991A-23726	Sequence 23726, A
560	6	1.6	396	1	US-08-769-309A-15	Sequence 15, Appl	633	6	1.6	436	3	US-08-840-767-6	Sequence 6, Appl
561	6	1.6	396	3	US-08-994-570-15	Sequence 15, Appl	634	6	1.6	436	3	US-09-150-213-4	Sequence 4, Appl
562	6	1.6	399	1	US-08-530-950-10	Sequence 10, Appl	635	6	1.6	437	1	US-08-176-427B-8	Sequence 8, Appl
563	6	1.6	399	2	US-08-874-186-92	Sequence 92, Appl	636	6	1.6	437	2	US-08-356-060A-11	Sequence 11, Appl
564	6	1.6	399	3	US-08-888-429A-10	Sequence 10, Appl	637	6	1.6	437	3	US-08-946-359A-20	Sequence 20, Appl
565	6	1.6	399	3	US-09-149-879-10	Sequence 10, Appl	638	6	1.6	437	3	US-08-567-379A-20	Sequence 20, Appl
566	6	1.6	399	4	US-09-057-009-10	Sequence 10, Appl	639	6	1.6	437	3	US-08-460-900C-11	Sequence 11, Appl
567	6	1.6	399	4	US-09-593-653-10	Sequence 10, Appl	640	6	1.6	437	3	US-08-729-743A-20	Sequence 20, Appl</

685	1	1.6	453	1	US-08-769-309A-14	Sequence 14, Appl	758	1	US-08-245-500A-3	Sequence 3, Appl
686	3	1.6	453	3	US-08-994-570-14	Sequence 14, Appl	759	1	US-08-390-546-3	Sequence 3, Appl
687	4	1.6	458	4	US-09-252-991A-25185	Sequence 25185, A	760	1	US-08-390-479A-3	Sequence 3, Appl
688	4	1.6	459	4	US-09-328-352-8095	Sequence 8095, Ap	761	1	US-08-557-393-3	Sequence 3, Appl
689	4	1.6	459	4	US-09-902-540-16639	Sequence 16639, A	762	1	US-08-390-516C-3	Sequence 3, Appl
690	1	1.6	461	1	US-08-186-222-2	Sequence 2, Appl	763	1	US-08-390-517A-3	Sequence 3, Appl
691	4	1.6	463	4	US-09-907-794A-285	Sequence 285, App	764	1	US-08-390-515A-3	Sequence 3, Appl
692	4	1.6	463	4	US-09-905-125A-285	Sequence 285, App	765	1	US-08-801-718-3	Sequence 3, Appl
693	4	1.6	463	4	US-09-902-770A-285	Sequence 285, App	766	1	US-09-170-159A-3	Sequence 3, Appl
694	4	1.6	463	4	US-09-906-700A-285	Sequence 285, App	767	1	US-09-480-718-44	Sequence 44, Appl
695	4	1.6	463	4	US-09-903-603A-285	Sequence 285, App	768	1	US-09-949-016-8486	Sequence 8486, Ap
696	4	1.6	463	4	US-09-904-920A-285	Sequence 285, App	769	1	US-10-237-551-204	Sequence 204, App
697	4	1.6	463	4	US-09-909-064A-285	Sequence 285, App	770	1	US-09-949-016-7790	Sequence 7790, Ap
698	4	1.6	463	4	US-09-905-381A-285	Sequence 285, App	771	1	US-09-902-540-14215	Sequence 14215, A
699	4	1.6	463	4	US-09-906-618-285	Sequence 285, App	772	1	US-09-710-279-1558	Sequence 1558, Ap
700	4	1.6	466	4	US-09-252-991A-32781	Sequence 32781, A	773	1	US-09-134-000C-4863	Sequence 4863, Ap
701	3	1.6	467	3	US-08-701-582D-2	Sequence 2, Appl	774	1	US-09-252-991A-27888	Sequence 27888, A
702	3	1.6	467	3	US-09-087-134-2	Sequence 4, Appl	775	1	US-09-988-863A-2	Sequence 2, Appl
703	3	1.6	467	3	US-09-082-039A-2	Sequence 2, Appl	776	1	US-09-130-337A-25	Sequence 25, Appl
704	3	1.6	467	3	US-09-082-039A-15	Sequence 15, Appl	777	1	US-09-107-532A-5470	Sequence 5470, Ap
705	3	1.6	467	3	US-08-840-767-42	Sequence 42, Appl	778	1	US-09-252-991A-18691	Sequence 18691, A
706	3	1.6	467	3	US-08-840-767-50	Sequence 50, Appl	779	1	US-09-142-108C-2	Sequence 2, Appl
707	3	1.6	467	3	US-09-086-776B-7	Sequence 7, Appl	780	1	US-09-142-108C-6	Sequence 6, Appl
708	3	1.6	467	3	US-09-087-134-2	Sequence 2, Appl	781	1	US-09-252-991A-32774	Sequence 32774, Ap
709	3	1.6	467	3	US-09-087-134-5	Sequence 5, Appl	782	1	US-09-134-000C-51277	Sequence 5127, A
710	3	1.6	467	3	US-09-552-138-2	Sequence 2, Appl	783	1	US-09-142-108C-15	Sequence 15, Appl
711	3	1.6	467	3	US-09-552-138-15	Sequence 15, Appl	784	1	US-09-902-540-16127	Sequence 15127, A
712	4	1.6	467	4	US-08-580-031A-15	Sequence 15, Appl	785	1	US-09-142-108C-21	Sequence 21, Appl
713	4	1.6	467	4	US-08-580-031A-15	Sequence 15, Appl	786	1	US-09-693-746-10	Sequence 10, Appl
714	4	1.6	468	4	US-09-248-796A-17308	Sequence 7, Appl	787	1	US-09-328-352-5423	Sequence 5423, Ap
715	4	1.6	470	4	US-09-134-001C-4610	Sequence 4610, Ap	788	1	US-09-693-746-12	Sequence 12, Appl
716	4	1.6	471	4	US-09-270-767-60488	Sequence 60488, A	789	1	US-08-853-659A-35	Sequence 35, Appl
717	3	1.6	472	3	US-08-492-459-22	Sequence 22, Appl	790	1	US-08-852-401-3	Sequence 3, Appl
718	3	1.6	472	3	US-08-423-752-22	Sequence 22, Appl	791	1	US-09-107-532A-6562	Sequence 6562, Ap
719	3	1.6	472	3	US-08-716-873-36	Sequence 36, Appl	792	1	US-09-949-016-7125	Sequence 7125, Ap
720	3	1.6	472	3	US-09-368-431-36	Sequence 36, Appl	793	1	US-09-949-016-7126	Sequence 7126, Ap
721	3	1.6	472	3	US-09-414-006-22	Sequence 22, Appl	794	1	US-09-949-016-7127	Sequence 7127, Ap
722	4	1.6	472	4	US-09-447-223-22	Sequence 22, Appl	795	1	US-09-949-016-7128	Sequence 7128, Ap
723	4	1.6	472	4	US-09-328-352-6296	Sequence 6296, Ap	796	1	US-09-949-016-7129	Sequence 7129, Ap
724	4	1.6	472	4	US-09-951-217-36	Sequence 36, Appl	797	1	US-09-252-991A-26641	Sequence 26641, A
725	4	1.6	474	4	US-09-489-039A-14147	Sequence 14147, A	798	1	US-09-310-174B-13	Sequence 13, Appl
726	4	1.6	476	4	US-09-142-108C-23	Sequence 23, Appl	799	1	US-09-620-461-13	Sequence 13, Appl
727	3	1.6	477	3	US-09-113-309-3	Sequence 3, Appl	800	1	US-09-949-016-8028	Sequence 8028, Ap
728	3	1.6	477	3	US-09-521-109-3	Sequence 3, Appl	801	1	US-09-540-236-3343	Sequence 3343, Ap
729	3	1.6	477	3	US-08-840-767-2	Sequence 2, Appl	802	1	US-09-328-352-7300	Sequence 7300, Ap
730	3	1.6	477	3	US-09-562-332-3	Sequence 3, Appl	803	1	US-09-134-001C-4091	Sequence 4091, Ap
731	4	1.6	478	4	US-09-770-916-2	Sequence 2, Appl	804	1	US-10-037-667-1	Sequence 1, Appl
732	4	1.6	478	4	US-09-902-540-14070	Sequence 14070, A	805	1	US-09-710-279-3134	Sequence 3134, Ap
733	1	1.6	479	1	US-08-278-635B-2	Sequence 2, Appl	806	1	US-09-248-796A-15935	Sequence 15935, A
734	3	1.6	479	3	US-08-464-258B-2	Sequence 2, Appl	807	1	US-09-252-991A-21132	Sequence 21132, A
735	3	1.6	479	3	US-08-471-961-2	Sequence 2, Appl	808	1	US-09-252-991A-18055	Sequence 18055, A
736	3	1.6	479	3	US-09-345-109C-2	Sequence 2, Appl	809	1	US-09-543-681A-7663	Sequence 7663, Ap
737	4	1.6	480	4	US-09-543-681A-4680	Sequence 4680, Ap	810	1	US-09-270-767-42391	Sequence 42391, A
738	4	1.6	480	4	US-09-248-796A-15701	Sequence 15701, A	811	1	US-09-252-991A-16984	Sequence 16984, A
739	4	1.6	480	4	US-09-949-016-8233	Sequence 8233, Ap	812	1	US-09-248-796A-17366	Sequence 17366, A
740	4	1.6	481	4	US-09-252-991A-27157	Sequence 27157, A	813	1	US-08-309-341-2	Sequence 2, Appl
741	4	1.6	482	4	US-09-248-796A-18796	Sequence 18796, A	814	1	US-08-309-341-4	Sequence 4, Appl
742	3	1.6	485	3	US-08-930-894-2	Sequence 2, Appl	815	1	US-08-608-267-2	Sequence 2, Appl
743	4	1.6	485	4	US-09-248-796A-18473	Sequence 18473, A	816	1	US-08-608-267-4	Sequence 4, Appl
744	4	1.6	485	4	US-09-949-016-7633	Sequence 7633, Ap	817	1	US-08-608-452-2	Sequence 2, Appl
745	4	1.6	490	4	US-09-461-325-250	Sequence 250, App	818	1	US-08-608-452-4	Sequence 4, Appl
746	4	1.6	490	4	US-09-461-325-518	Sequence 518, App	819	1	US-08-608-224-2	Sequence 2, Appl
747	4	1.6	490	4	US-09-252-991A-30355	Sequence 30355, A	820	1	US-08-608-224-4	Sequence 4, Appl
748	4	1.6	490	4	US-10-012-542-250	Sequence 250, App	821	1	US-08-967-149-2	Sequence 2, Appl
749	4	1.6	490	4	US-10-012-542-518	Sequence 518, App	822	1	US-08-967-149-4	Sequence 4, Appl
750	4	1.6	490	4	US-09-270-767-40737	Sequence 40737, A	823	1	US-09-538-092-278	Sequence 278, App
751	4	1.6	490	4	US-09-270-767-55953	Sequence 55953, A	824	1	US-09-364-206-47	Sequence 47, Appl
752	4	1.6	490	4	US-10-115-123-250	Sequence 250, App	825	1	US-09-252-991A-229263	Sequence 229263, A
753	4	1.6	490	4	US-10-115-123-518	Sequence 518, App	826	1	US-09-252-991A-22037	Sequence 22037, A
754	4	1.6	490	4	US-10-053-510-19	Sequence 19, Appl	827	1	US-09-543-681A-6918	Sequence 6918, Ap
755	1	1.6	491	1	US-07-903-103-2	Sequence 2, Appl	828	1	US-09-270-767-39217	Sequence 39217, A
756	1	1.6	491	1	US-08-044-619A-2	Sequence 2, Appl	829	1	US-09-270-767-54434	Sequence 54434, A
757	1	1.6	491	1	US-08-283-911-2	Sequence 2, Appl	830	1	US-09-815-923-14	Sequence 14, Appl

831	6	1.6	601	2	US-08-795-868-16	Sequence 16, Appl	904	4	US-09-854-845-45	Sequence 45, Appl
832	6	1.6	602	3	US-09-303-069-16	Sequence 16, Appl	905	4	US-09-835-145A-2	Sequence 2, Appl
833	6	1.6	603	3	US-09-134-250-16	Sequence 16, Appl	906	4	US-09-489-039A-11310	Sequence 11310, A
834	6	1.6	604	4	US-09-107-532A-3809	Sequence 3809, Ap	907	4	US-09-854-845-43	Sequence 43, Appl
835	6	1.6	605	4	US-09-902-540-12446	Sequence 12446, A	908	4	US-09-362-336A-14	Sequence 14, Appl
836	6	1.6	606	4	US-09-543-681A-5181	Sequence 5181, Ap	909	4	US-09-252-911A-21696	Sequence 21696, A
837	6	1.6	607	4	US-08-207-954-5	Sequence 5, Appl	910	4	US-09-688-188B-24	Sequence 24, Appl
838	6	1.6	608	3	US-09-134-001C-2994	Sequence 2994, Ap	911	4	US-09-291-417D-24	Sequence 24, Appl
839	6	1.6	609	4	US-09-252-991A-20596	Sequence 20596, A	912	4	US-09-949-016-7201	Sequence 7201, Ap
840	6	1.6	610	4	US-09-328-352-5752	Sequence 5752, Ap	913	4	US-09-949-016-7202	Sequence 7202, Ap
841	6	1.6	611	3	US-08-968-563-13	Sequence 13, Appl	914	4	US-09-252-991A-29893	Sequence 29893, A
842	6	1.6	612	3	US-08-969-683A-13	Sequence 13, Appl	915	4	US-08-942-686-2	Sequence 2, Appl
843	6	1.6	613	3	US-09-297-928-9	Sequence 9, Appl	916	4	US-08-444-818-70	Sequence 70, Appl
844	6	1.6	614	3	US-09-275-252A-4	Sequence 4, Appl	917	4	US-09-854-845-49	Sequence 49, Appl
845	6	1.6	615	4	US-09-331-568A-2	Sequence 2, Appl	918	4	US-08-789-078-1	Sequence 1, Appl
846	6	1.6	616	4	US-09-331-568A-26	Sequence 26, Appl	919	4	US-08-752-633-1	Sequence 1, Appl
847	6	1.6	617	1	US-08-653-740-7	Sequence 7, Appl	920	4	US-08-476-062A-45	Sequence 45, Appl
848	6	1.6	618	2	US-09-073-594-7	Sequence 7, Appl	921	4	US-07-728-215-31	Sequence 31, Appl
849	6	1.6	619	3	US-09-275-925-7	Sequence 7, Appl	922	4	US-08-938-085A-31	Sequence 31, Appl
850	6	1.6	620	3	US-09-252-991A-21205	Sequence 21205, A	923	4	US-09-252-991A-26777	Sequence 26777, A
851	6	1.6	621	4	US-09-949-016-6530	Sequence 6530, Ap	924	4	US-10-072-844-31	Sequence 31, Appl
852	6	1.6	622	4	US-09-252-991A-31696	Sequence 31696, A	925	4	US-10-072-838-31	Sequence 31, Appl
853	6	1.6	623	4	US-10-101-464A-927	Sequence 927, App	926	4	US-10-072-841A-31	Sequence 31, Appl
854	6	1.6	624	4	US-09-538-092-226	Sequence 226, App	927	4	US-10-219-631A-31	Sequence 31, Appl
855	6	1.6	625	4	US-09-360-545-59	Sequence 69, Appl	928	5	PCT-US95-04886-1	Sequence 1, Appl
856	6	1.6	626	4	US-09-949-016-7565	Sequence 7565, Ap	929	5	PCT-US96-01314-45	Sequence 45, Appl
857	6	1.6	627	4	US-09-653-274-13	Sequence 13, Appl	930	5	US-09-543-681A-4291	Sequence 4291, Ap
858	6	1.6	628	4	US-10-461-791-13	Sequence 13, Appl	931	4	US-09-854-845-47	Sequence 47, Appl
859	6	1.6	629	4	US-09-489-039A-10943	Sequence 10943, A	932	4	US-09-252-991A-32892	Sequence 32892, A
860	6	1.6	630	3	US-09-328-501-1	Sequence 1, Appl	933	4	US-09-738-946-8	Sequence 8, Appl
861	6	1.6	631	4	US-09-777-710A-1	Sequence 1, Appl	934	4	US-09-688-188B-23	Sequence 23, Appl
862	6	1.6	632	1	US-08-769-309A-17	Sequence 17, Appl	935	4	US-09-291-417D-23	Sequence 23, Appl
863	6	1.6	633	3	US-08-650-766-6	Sequence 6, Appl	936	4	US-09-688-188B-151	Sequence 151, App
864	6	1.6	634	3	US-08-922-635-5	Sequence 5, Appl	937	4	US-09-291-417D-151	Sequence 151, App
865	6	1.6	635	3	US-08-994-570-17	Sequence 17, Appl	938	3	US-09-134-001C-4917	Sequence 4917, Ap
866	6	1.6	636	4	US-09-252-991A-19760	Sequence 19760, A	939	4	US-09-252-991A-21975	Sequence 21975, A
867	6	1.6	637	4	US-09-389-487-6	Sequence 6, Appl	940	4	US-09-248-796A-18375	Sequence 18375, A
868	6	1.6	638	4	US-09-252-991A-27682	Sequence 27682, Ap	941	4	US-09-489-039A-12742	Sequence 12742, A
869	6	1.6	639	3	US-09-134-001C-5039	Sequence 5039, A	942	4	US-09-583-110-3214	Sequence 3214, Ap
870	6	1.6	640	4	US-09-538-092-442	Sequence 442, App	943	4	US-09-107-433-4642	Sequence 4642, Ap
871	6	1.6	641	4	US-09-270-767-45005	Sequence 45005, A	944	4	US-09-489-039A-11547	Sequence 11547, A
872	6	1.6	642	3	US-09-328-501-15	Sequence 15, Appl	945	4	US-08-785-310A-8	Sequence 8, Appl
873	6	1.6	643	4	US-09-777-710A-15	Sequence 15, Appl	946	4	US-08-816-693A-53	Sequence 53, Appl
874	6	1.6	644	3	US-09-121-321-16	Sequence 16, Appl	947	4	US-08-885-291-53	Sequence 53, Appl
875	6	1.6	645	3	US-09-933-803A-16	Sequence 16, Appl	948	4	US-09-496-672-53	Sequence 53, Appl
876	6	1.6	646	3	US-08-630-172-10	Sequence 10, Appl	949	4	US-09-489-039A-8184	Sequence 8184, Ap
877	6	1.6	647	3	US-09-375-419-10	Sequence 10, Appl	950	4	US-09-248-796A-19161	Sequence 19161, A
878	6	1.6	648	4	US-09-248-796A-16453	Sequence 16453, A	951	4	US-08-684-932A-38	Sequence 38, Appl
879	6	1.6	649	4	US-09-252-991A-29396	Sequence 29396, A	952	4	US-09-489-039A-13920	Sequence 13920, A
880	6	1.6	650	4	US-08-380-403A-2	Sequence 2, Appl	953	4	US-09-618-304B-2	Sequence 2, Appl
881	6	1.6	651	2	US-08-380-403A-5	Sequence 5, Appl	954	4	US-09-438-185A-29	Sequence 29, Appl
882	6	1.6	652	2	US-08-895-628-2	Sequence 2, Appl	955	4	US-09-107-532A-5709	Sequence 5709, Ap
883	6	1.6	653	2	US-08-895-628-5	Sequence 5, Appl	956	4	US-09-854-845-29	Sequence 29, Appl
884	6	1.6	654	2	US-08-895-628-5	Sequence 5, Appl	957	4	US-09-489-039A-13252	Sequence 13252, A
885	6	1.6	655	4	US-08-895-810D-2	Sequence 2, Appl	958	4	US-09-949-016-6569	Sequence 6569, Ap
886	6	1.6	656	4	US-08-895-810D-5	Sequence 5, Appl	959	4	US-09-854-845-27	Sequence 27, Appl
887	6	1.6	657	4	US-09-248-796A-26144	Sequence 26144, Ap	960	4	US-09-538-092-932	Sequence 932, App
888	6	1.6	658	4	US-09-949-016-7806	Sequence 7806, Ap	961	4	US-09-949-016-8846	Sequence 8846, Ap
889	6	1.6	659	4	US-09-489-039A-13463	Sequence 13463, A	962	4	US-09-949-016-8847	Sequence 8847, Ap
890	6	1.6	660	3	US-08-968-563-18	Sequence 18, Appl	963	4	US-09-949-016-8276	Sequence 8276, Ap
891	6	1.6	661	3	US-08-968-563A-18	Sequence 18, Appl	964	4	US-09-538-092-206	Sequence 206, App
892	6	1.6	662	3	US-09-297-928-15	Sequence 15, Appl	965	4	US-09-949-016-7553	Sequence 7553, Ap
893	6	1.6	663	4	US-09-902-540-15419	Sequence 15419, A	966	4	US-08-620-694A-2	Sequence 2, Appl
894	6	1.6	664	4	US-09-417-197-75	Sequence 75, Appl	967	4	US-09-022-355-2	Sequence 2, Appl
895	6	1.6	665	4	US-09-417-197-51	Sequence 51, Appl	968	4	US-09-022-355-2	Sequence 2, Appl
896	6	1.6	666	4	US-08-914-999-4	Sequence 4, Appl	969	4	US-08-978-773-2	Sequence 2, Appl
897	6	1.6	667	3	US-08-914-999-4	Sequence 4, Appl	970	4	US-09-022-453-2	Sequence 2, Appl
898	6	1.6	668	4	US-09-252-991A-24201	Sequence 24201, A	971	4	US-09-022-453-2	Sequence 2, Appl
899	6	1.6	669	4	US-09-350-457A-4	Sequence 4, Appl	972	4	US-09-022-359-2	Sequence 2, Appl
900	6	1.6	670	4	US-09-252-991A-30569	Sequence 30569, A	973	4	US-09-022-359-2	Sequence 2, Appl
901	6	1.6	671	3	US-09-102-528-29	Sequence 29, Appl	974	4	US-09-022-357-2	Sequence 2, Appl
902	6	1.6	672	3	US-09-136-251-2	Sequence 2, Appl	975	4	US-09-549-679-2	Sequence 2, Appl
903	6	1.6	673	4	US-09-634-496-2	Sequence 2, Appl	976	4	US-09-854-845-33	Sequence 33, Appl

977 6 1.6 867 4 US-09-248-796A-19207
978 6 1.6 870 4 US-09-602-787A-578
979 6 1.6 870 4 US-09-854-845-31
980 6 1.6 871 4 US-09-328-352-7076
981 6 1.6 874 4 US-09-543-681A-6958
982 6 1.6 883 4 US-09-252-991A-16929
983 6 1.6 901 4 US-09-714-767A-4
984 6 1.6 901 4 US-09-538-092-826
985 6 1.6 916 4 US-09-949-016-8291
986 6 1.6 916 4 US-09-949-016-8292
987 6 1.6 919 4 US-09-949-016-7873
988 6 1.6 943 4 US-09-583-110-4794
989 6 1.6 945 4 US-09-107-433-3340
990 6 1.6 959 4 US-09-543-681A-6879
991 6 1.6 965 4 US-09-538-092-650
992 6 1.6 966 4 US-09-606-312-2
993 6 1.6 983 4 US-09-252-991A-21667
994 6 1.6 995 4 US-09-252-991A-22297
995 6 1.6 995 4 US-09-252-991A-32802
996 6 1.6 997 1 US-08-232-540-1
997 6 1.6 997 1 US-08-428-949A-1
998 6 1.6 997 1 US-08-428-948A-1
999 6 1.6 997 2 US-08-428-946-1
1000 6 1.6 997 4 US-09-198-452A-602

ALIGNMENTS

RESULT 1
US-08-969-106-6
; Sequence 6, Application US/08969106
; Patent No. 5986055
; GENERAL INFORMATION:
; APPLICANT: Yang, M.
; APPLICANT: Nandabalan, K.
; APPLICANT: Schulz, V.
; TITLE OF INVENTION: CPK2 INTERACTIONS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US-08-969,106
; FILING DATE: 13-NOV-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7934-057
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 377 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-969-106-6

Query Match 100.0%; Score 377; DB 2; Length 377;

Sequence 19207, A
Sequence 578, App
Sequence 31, Appl
Sequence 7076, Ap
Sequence 6958, Ap
Sequence 16929, A
Sequence 4, Appl
Sequence 826, App
Sequence 8291, Ap
Sequence 8292, Ap
Sequence 7873, Ap
Sequence 4794, Ap
Sequence 3340, Ap
Sequence 6879, Ap
Sequence 650, App
Sequence 2, Appl
Sequence 21667, A
Sequence 22297, A
Sequence 32802, A
Sequence 1, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 602, App

Best Local Similarity 100.0%; Pred. No. 0;
Matches 377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MKPFGPLENORLSFLLKAITREAOQWKVNRKMPNSQNVSPSQORDVIOWLAKLKYQFN 60
Db 1 MKPFGPLENORLSFLLKAITREAOQWKVNRKMPNSQNVSPSQORDVIOWLAKLKYQFN 60
Qy 61 LYPTFALASLLDRFLATVKAHPKYLSCIAISCFFLAAKTVEDEIRIPVLKVLARDSFC 120
Db 61 LYPTFALASLLDRFLATVKAHPKYLSCIAISCFFLAAKTVEDEIRIPVLKVLARDSFC 120
Qy 121 GCSSEILRMERIILDKLNWDLHTATPLDPLHIFAHAVSTRPQLLSFKLSPSOHLAV 180
Db 121 GCSSEILRMERIILDKLNWDLHTATPLDPLHIFAHAVSTRPQLLSFKLSPSOHLAV 180
Qy 181 LTKQLLHCMAQNQLQFRGSMALAMVLSLEMEKLIIPDWLSLTIELLOKAQWDSQLIHC 240
Db 181 LTKQLLHCMAQNQLQFRGSMALAMVLSLEMEKLIIPDWLSLTIELLOKAQWDSQLIHC 240
Qy 241 ELVAHLSTLQSSLPNSVYVYRPLKHTLVTCDKGVFRLHPSSVPGDFKDNKSKPEVPV 300
Db 241 ELVAHLSTLQSSLPNSVYVYRPLKHTLVTCDKGVFRLHPSSVPGDFKDNKSKPEVPV 300
Qy 301 RGTAAFYHLLPAASGCKQTSTKRKVEEMVEDDFYDGIKRLYNEDNVSENVGSGVCGTDL 360
Db 301 RGTAAFYHLLPAASGCKQTSTKRKVEEMVEDDFYDGIKRLYNEDNVSENVGSGVCGTDL 360
Qy 361 QEGHASPCLPQVSV 377
Db 361 QEGHASPCLPQVSV 377

RESULT 2
US-09-054-492B-1
; Sequence 1, Application US/09054492B
; Patent No. 6218115
; GENERAL INFORMATION:
; APPLICANT: TAKESHI NAKAMURA
; TITLE OF INVENTION: HUMAN CYCLIN I AND GENES ENCODING SAME
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY, MADISON & SUTRO
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/054,492B
; FILING DATE: APRIL 3, 1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: PAUL E. WHITE, JR.
; REGISTRATION NUMBER: 32,011
; REFERENCE/DOCKET NUMBER: 7898/252159
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; TELEX: 6714627CUSH
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 377
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-054-492B-1

Query Match 100.0%; Score 377; DB 3; Length 377;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Matches 377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MKFPGPLENQRSLFLEKAITREAOQMKVNRKMPNSQNSPSQORDEVIQWLAKLKYQFN 60
Db 1 MKFPGPLENQRSLFLEKAITREAOQMKVNRKMPNSQNSPSQORDEVIQWLAKLKYQFN 60
Qy 61 LYPETPALASSLLDRFLATVKAHPKYLSCIAISCFFLAAKTVEDEDERIPVLKVLARDSFC 120
Db 61 LYPETPALASSLLDRFLATVKAHPKYLSCIAISCFFLAAKTVEDEDERIPVLKVLARDSFC 120
Qy 121 GCSSEILRMERIILDKLNWDLHTATPLDFLHIFHAIAVSTRPOLLFSLPKLSPSOHLAV 180
Db 121 GCSSEILRMERIILDKLNWDLHTATPLDFLHIFHAIAVSTRPOLLFSLPKLSPSOHLAV 180
Qy 181 LTKQLLHMACNQLQFRGSMALAMVLSLEMEKLIIPDWLSITIELLOKQAMDSQLIHC 240
Db 181 LTKQLLHMACNQLQFRGSMALAMVLSLEMEKLIIPDWLSITIELLOKQAMDSQLIHC 240
Qy 241 ELVAHHLSTLQSSPLNSVYVYRPLKHTLVTCDKGVFRLHPSSVPGPDFSKDNSKPEVPV 300
Db 241 ELVAHHLSTLQSSPLNSVYVYRPLKHTLVTCDKGVFRLHPSSVPGPDFSKDNSKPEVPV 300
Qy 301 RGTAAFYHHLPAASGCKQTSTKRVEMEVDVDFDGIKRLYNEDNVSENVSVCCTDLSR 360
Db 301 RGTAAFYHHLPAASGCKQTSTKRVEMEVDVDFDGIKRLYNEDNVSENVSVCCTDLSR 360
Qy 361 QEGHASPCLPPLQPVSV 377
Db 361 QEGHASPCLPPLQPVSV 377

RESULT 3

US-09-736-125-6
; Sequence 6, Application US/09338125
; Patent No. 6521412
; GENERAL INFORMATION:
; APPLICANT: Yang, M.
; APPLICANT: Nandabalan, K.
; APPLICANT: Schulz, V.
; TITLE OF INVENTION: CDK2 INTERACTIONS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA: US/09/338,125
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: US/08/969,106
; FILING DATE: 13-NOV-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7934-057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 377 amino acids
; TYPE: amino acid

STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-09-736-125-6

Query Match 100.0%; Score 377; DB 4; Length 377;
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Matches 377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKFPGPLENQRSLFLEKAITREAOQMKVNRKMPNSQNSPSQORDEVIQWLAKLKYQFN 60
Db 1 MKFPGPLENQRSLFLEKAITREAOQMKVNRKMPNSQNSPSQORDEVIQWLAKLKYQFN 60
Qy 61 LYPETPALASSLLDRFLATVKAHPKYLSCIAISCFFLAAKTVEDEDERIPVLKVLARDSFC 120
Db 61 LYPETPALASSLLDRFLATVKAHPKYLSCIAISCFFLAAKTVEDEDERIPVLKVLARDSFC 120
Qy 121 GCSSEILRMERIILDKLNWDLHTATPLDFLHIFHAIAVSTRPOLLFSLPKLSPSOHLAV 180
Db 121 GCSSEILRMERIILDKLNWDLHTATPLDFLHIFHAIAVSTRPOLLFSLPKLSPSOHLAV 180
Qy 181 LTKQLLHMACNQLQFRGSMALAMVLSLEMEKLIIPDWLSITIELLOKQAMDSQLIHC 240
Db 181 LTKQLLHMACNQLQFRGSMALAMVLSLEMEKLIIPDWLSITIELLOKQAMDSQLIHC 240
Qy 241 ELVAHHLSTLQSSPLNSVYVYRPLKHTLVTCDKGVFRLHPSSVPGPDFSKDNSKPEVPV 300
Db 241 ELVAHHLSTLQSSPLNSVYVYRPLKHTLVTCDKGVFRLHPSSVPGPDFSKDNSKPEVPV 300
Qy 301 RGTAAFYHHLPAASGCKQTSTKRVEMEVDVDFDGIKRLYNEDNVSENVSVCCTDLSR 360
Db 301 RGTAAFYHHLPAASGCKQTSTKRVEMEVDVDFDGIKRLYNEDNVSENVSVCCTDLSR 360
Qy 361 QEGHASPCLPPLQPVSV 377
Db 361 QEGHASPCLPPLQPVSV 377

RESULT 4

US-09-796-149B-4
; Sequence 4, Application US/09796149B
; Patent No. 6825033
; GENERAL INFORMATION:
; APPLICANT: Univ. of Southern California
; TITLE OF INVENTION: Mutated cyclin G1 protein
; FILE REFERENCES: 4-31342A/USC
; CURRENT APPLICATION NUMBER: US/09/796,149B
; CURRENT FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-796-149B-4

Query Match 67.4%; Score 254; DB 4; Length 254;
Best Local Similarity 100.0%; Pred. No. 4.5e-242;
Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 40 VSPSORDEVIQWLAKLKYQFNLYPETPALASSLLDRFLATVKAHPKYLSCIAISCFFLAA 99
Db 1 VSPSORDEVIQWLAKLKYQFNLYPETPALASSLLDRFLATVKAHPKYLSCIAISCFFLAA 60
Qy 100 KTVDEDERIPVLKVLARDSFCGSSSEILRMERIILDKLNWDLHTATPLDFLHIFHAIAV 159
Db 61 KTVDEDERIPVLKVLARDSFCGSSSEILRMERIILDKLNWDLHTATPLDFLHIFHAIAV 120
Qy 160 STRPQLLFSPLKSPSOHLAVLTKQLLHMACNQLQFRGSMALAMVLSLEMEKLIIPDWL 219
Db 121 STRPQLLFSPLKSPSOHLAVLTKQLLHMACNQLQFRGSMALAMVLSLEMEKLIIPDWL 180
Qy 220 SLTIELLOKQAMDSQLIHCRLVAHLSTLQSSPLNSVYVYRPLKHTLVTCDKGVFRL 279

Db 181 SLTIELLQKQWSSQLHCHRELVAHLSTLQSSLPNSVYVRPLKHTLVTCCKGVRL 240
Qy 280 HPSSVPGPDFSKDN 293
Db 241 HPSSVPGPDFSKDN 254

RESULT 5
US-09-513-999C-5984
; Sequence 5984, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59-US2-REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 5984
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-513-999C-5984

Query Match 34.7%; Score 131; DB 4; Length 131;
Best Local Similarity 100.0%; Pred. No. 4.3e-121;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 130 MERILDKLNDIATATPLDPLHIFHAIVSTRPQLFSLPKLSPSOHLAVITKQLHCM 189
Db 1 MERILDKLNDLHTATPLDPLHIFHAIVSTRPQLFSLPKLSPSOHLAVITKQLHCM 60
Qy 190 ACNQLQPRGSMALAMVLSLEMEKLPDWSLTTLIELLQKQWSSQLHCHRELVAHLST 249
Db 61 ACNQLQPRGSMALAMVLSLEMEKLPDWSLTTLIELLQKQWSSQLHCHRELVAHLST 120
Qy 250 LQSSLPNSVY 260
Db 121 LQSSLPNSVY 131

RESULT 6
US-09-054-492B-5
; Sequence 5, Application US/09054492B
; Patent No. 6218115
; GENERAL INFORMATION:
; APPLICANT: TAKESHI NAKAMURA
; TITLE OF INVENTION: HUMAN CYCLIN I AND GENES ENCODING SAME
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY, MADISON & SUTRO
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/054,492B
; FILING DATE: APRIL 3, 1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:

; NAME: PAUL E. WHITE, JR.
; REGISTRATION NUMBER: 32,011
; REFERENCE/DOCKET NUMBER: 7898/252159
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; TELEX: 6714627CUSH
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-054-492B-5

Query Match 3.7%; Score 14; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 343 EDNVSENVGSVCGT 356
Db 1 EDNVSENVGSVCGT 14

RESULT 7
US-09-129-112-2
; Sequence 2, Application US/09129112
; Patent No. 6465716
; GENERAL INFORMATION:
; APPLICANT: Etzler, Marilyn E.
; APPLICANT: Murphy, Judith B.
; TITLE OF INVENTION: The Regents of the University of California
; FILE REFERENCE: 023070-079810US
; CURRENT APPLICATION NUMBER: US/09/129,112
; CURRENT FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: US 08/907,226
; PRIOR FILING DATE: 1997-08-06
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Dolichos biflorus
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (52)..(73)
; OTHER INFORMATION: motif identified as conserved region among a
; OTHER INFORMATION: variety of plant and animal apyrases
; NAME/KEY: PEPTIDE
; LOCATION: (128)..(144)
; OTHER INFORMATION: motif identified as conserved region among a
; OTHER INFORMATION: variety of plant and animal apyrases
; NAME/KEY: PEPTIDE
; LOCATION: (173)..(195)
; OTHER INFORMATION: motif identified as conserved region among a
; OTHER INFORMATION: variety of plant and animal apyrases
; NAME/KEY: PEPTIDE
; LOCATION: (200)..(220)
; OTHER INFORMATION: motif identified as conserved region among a
; OTHER INFORMATION: variety of plant and animal apyrases
US-09-129-112-2

Query Match 2.4%; Score 9; DB 4; Length 462;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 165 LLFSLPKLS 173
Db 20 LLFSLPKLS 28

RESULT 8

```
US-09-270-767-57798
; Sequence 57798, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 57798
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-57798
Query Match      2.1%; Score 8; DB 4; Length 127;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      180 VLTQQLH 187
Db      79 VLTQQLH 86
|||||
RESULT 9
US-09-270-767-39916
; Sequence 39916, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39916
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-39916
Query Match      2.1%; Score 8; DB 4; Length 170;
Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      219 LSLTIELL 226
Db      72 LSLTIELL 79
|||||
RESULT 10
US-09-270-767-55133
; Sequence 55133, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55133
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-55133
Query Match      2.1%; Score 8; DB 4; Length 170;
Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      219 LSLTIELL 226
Db      72 LSLTIELL 79
|||||
RESULT 11
US-09-128-155-12
; Sequence 12, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; CURRENT FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-128-155-12
Query Match      1.9%; Score 7; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      66 FALASSL 72
Db      10 FALASSL 16
|||||
RESULT 12
US-09-128-155-8
; Sequence 8, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; CURRENT FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-128-155-8
Query Match      1.9%; Score 7; DB 3; Length 52;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      66 FALASSL 72
```

```
Db      41 FALASSL 47
|||||
RESULT 13
US-09-128-155-4
; Sequence 4, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; CURRENT FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-128-155-4

Query Match      1.9%; Score 7; DB 3; Length 63;
Best Local Similarity 100.0%; Pred.No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      66 FALASSL 72
|||||
Db      52 FALASSL 58

RESULT 14
US-09-270-767-34602
; Sequence 34602, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34602
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-34602

Query Match      1.9%; Score 7; DB 4; Length 70;
Best Local Similarity 100.0%; Pred.No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      11 RLSFLL 17
|||||
Db      58 RLSFLL 64

RESULT 15
US-09-270-767-49819
; Sequence 49819, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 49819
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-49819

Query Match      1.9%; Score 7; DB 4; Length 70;
Best Local Similarity 100.0%; Pred.No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      11 RLSFLL 17
|||||
Db      58 RLSFLL 64

; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 49819
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-49819

Query Match      1.9%; Score 7; DB 4; Length 70;
Best Local Similarity 100.0%; Pred.No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      11 RLSFLL 17
|||||
Db      58 RLSFLL 64

Search completed: February 11, 2005, 03:18:29
Job time : 47.7826 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 11, 2005, 03:16:44 ; Search time 86.7775 Seconds
(without alignments)
1419.543 Million cell updates/sec

Title: US-09-736-250-1

Perfect score: 377

Sequence: 1 MKFPGPLENORLSFILEKAI.....LSRQGHASCPPLQPVSM 377

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 1376875 seqs, 326749119 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1376875

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	377	100.0	377	12	US-09-736-250-1
2	254	67.4	254	9	US-09-796-149-4
3	14	3.7	14	12	US-09-736-250-5
4	9	2.4	9	10	US-09-865-548A-151
5	9	2.4	9	14	US-10-006-177-8
6	9	2.4	462	9	US-09-123-112-2
7	8	2.1	83	15	US-10-425-114-42971
8	2.1	99	15	US-10-424-599-245711	
9	8	2.1	216	15	US-10-424-599-196677
10	8	2.1	289	15	US-10-424-599-196680
11	8	2.1	379	16	US-10-437-963-145582
12	8	2.1	391	9	US-09-866-562-62
13	8	2.1	416	15	US-10-236-392-92
					Sequence 1, Appli
					Sequence 4, Appli
					Sequence 5, Appli
					Sequence 151, App
					Sequence 8, Appli
					Sequence 2, Appli
					Sequence 42971, A
					Sequence 245711, A
					Sequence 196677, A
					Sequence 196680, A
					Sequence 145582, A
					Sequence 62, Appli
					Sequence 92, Appli

14	8	2.1	418	15	US-10-425-114-51949	Sequence 51949, A
15	8	2.1	514	16	US-10-767-701-44456	Sequence 44456, A
16	8	2.1	589	15	US-10-425-114-69696	Sequence 69696, A
17	8	2.1	1931	16	US-10-437-963-138321	Sequence 138321, A
18	7	1.9	21	13	US-10-095-407-12	Sequence 12, Appli
19	7	1.9	45	16	US-10-716-029-211	Sequence 211, App
20	7	1.9	50	15	US-10-424-599-219329	Sequence 219329, A
21	7	1.9	52	13	US-10-095-407-8	Sequence 8, Appli
22	7	1.9	56	15	US-10-424-599-161917	Sequence 161917, A
23	7	1.9	58	9	US-09-925-301-1162	Sequence 1162, Ap
24	7	1.9	62	14	US-10-156-761-13291	Sequence 13291, A
25	7	1.9	63	13	US-10-095-407-4	Sequence 4, Appli
26	7	1.9	68	10	US-09-764-891-4938	Sequence 4938, Ap
27	7	1.9	71	14	US-10-205-428-417	Sequence 417, App
28	7	1.9	78	16	US-10-437-963-157984	Sequence 157984, A
29	7	1.9	80	15	US-10-424-599-224197	Sequence 224197, A
30	7	1.9	83	16	US-10-767-701-62088	Sequence 62088, A
31	7	1.9	85	16	US-10-437-963-111076	Sequence 111076, A
32	7	1.9	93	15	US-10-424-599-190556	Sequence 190556, A
33	7	1.9	98	9	US-09-764-869-1104	Sequence 1104, Ap
34	7	1.9	98	14	US-10-091-504-1104	Sequence 1104, Ap
35	7	1.9	98	15	US-10-227-577-1104	Sequence 1104, Ap
36	7	1.9	110	9	US-09-864-761-45514	Sequence 45514, A
37	7	1.9	123	16	US-10-437-963-166119	Sequence 166119, A
38	7	1.9	128	15	US-10-425-114-42724	Sequence 42724, A
39	7	1.9	134	16	US-10-437-963-137857	Sequence 137857, A
40	7	1.9	136	13	US-10-095-407-11	Sequence 11, Appli
41	7	1.9	143	15	US-10-424-599-170638	Sequence 170638, A
42	7	1.9	154	15	US-10-424-599-173129	Sequence 173129, A
43	7	1.9	157	10	US-09-876-790-10	Sequence 10, Appli
44	7	1.9	157	14	US-10-302-554-9	Sequence 9, Appli
45	7	1.9	157	14	US-10-302-554-10	Sequence 10, Appli
46	7	1.9	157	14	US-10-302-554-12	Sequence 12, Appli
47	7	1.9	157	14	US-10-302-554-15	Sequence 15, Appli
48	7	1.9	157	17	US-10-888-779-10	Sequence 10, Appli
49	7	1.9	157	17	US-10-888-867-10	Sequence 10, Appli
50	7	1.9	157	17	US-10-888-780-10	Sequence 10, Appli
51	7	1.9	157	17	US-10-888-931-10	Sequence 10, Appli
52	7	1.9	158	16	US-10-437-963-189349	Sequence 189349, A
53	7	1.9	160	15	US-10-425-114-43681	Sequence 43681, A
54	7	1.9	162	15	US-10-425-114-40890	Sequence 40890, A
55	7	1.9	167	13	US-10-095-407-7	Sequence 7, Appli
56	7	1.9	176	9	US-09-965-528-25	Sequence 25, Appli
57	7	1.9	176	11	US-09-969-984-25	Sequence 25, Appli
58	7	1.9	178	13	US-10-095-407-2	Sequence 2, Appli
59	7	1.9	178	14	US-10-139-833-11	Sequence 11, Appli
60	7	1.9	178	16	US-10-767-701-59743	Sequence 59743, A
61	7	1.9	192	10	US-09-876-790-3	Sequence 3, Appli
62	7	1.9	192	14	US-10-139-833-13	Sequence 13, Appli
63	7	1.9	192	17	US-10-888-779-3	Sequence 3, Appli
64	7	1.9	192	17	US-10-888-867-3	Sequence 3, Appli
65	7	1.9	192	17	US-10-888-780-3	Sequence 3, Appli
66	7	1.9	192	17	US-10-888-931-3	Sequence 3, Appli
67	7	1.9	193	13	US-10-006-867-142	Sequence 142, App
68	7	1.9	193	13	US-10-063-547-142	Sequence 142, App
69	7	1.9	193	13	US-10-063-551-142	Sequence 142, App
70	7	1.9	193	14	US-10-063-616-142	Sequence 142, App
71	7	1.9	193	14	US-10-063-569-142	Sequence 142, App
72	7	1.9	193	14	US-10-063-513-142	Sequence 142, App
73	7	1.9	193	14	US-10-063-515-142	Sequence 142, App
74	7	1.9	193	14	US-10-063-512-142	Sequence 142, App
75	7	1.9	193	14	US-10-063-502-142	Sequence 142, App
76	7	1.9	193	14	US-10-063-549-142	Sequence 142, App
77	7	1.9	193	14	US-10-063-554-142	Sequence 142, App
78	7	1.9	193	14	US-10-063-553-142	Sequence 142, App
79	7	1.9	193	14	US-10-063-518-142	Sequence 142, App
80	7	1.9	193	14	US-10-063-598-142	Sequence 142, App
81	7	1.9	193	14	US-10-227-693-142	Sequence 142, App
82	7	1.9	193	14	US-10-063-563-142	Sequence 142, App
83	7	1.9	193	14	US-10-063-555-142	Sequence 142, App
84	7	1.9	193	14	US-10-063-594-142	Sequence 142, App
85	7	1.9	193	14	US-10-063-567-142	Sequence 142, App
86	7	1.9	193	14	US-10-063-538-142	Sequence 142, App

233	7	1.9	218	15	US-10-694-978-4	Sequence 4, Appli	306	7	1.9	437	15	US-10-414-267-6	Sequence 6, Appli
234	7	1.9	218	16	US-10-679-201-6	Sequence 6, Appli	307	7	1.9	439	9	US-09-866-572A-28	Sequence 28, Appl
235	7	1.9	218	17	US-10-888-779-8	Sequence 8, Appli	308	7	1.9	439	9	US-09-866-570A-28	Sequence 28, Appl
236	7	1.9	218	17	US-10-888-867-8	Sequence 8, Appli	309	7	1.9	439	14	US-10-167-984-28	Sequence 28, Appl
237	7	1.9	218	17	US-10-888-780-8	Sequence 8, Appli	310	7	1.9	439	15	US-10-167-603C-12	Sequence 12, Appl
238	7	1.9	218	17	US-10-888-931-8	Sequence 8, Appli	311	7	1.9	439	15	US-10-166-984-28	Sequence 28, Appl
239	7	1.9	238	16	US-10-437-963-171439	Sequence 171439, A	312	7	1.9	446	15	US-10-149-310-280	Sequence 280, Appl
240	7	1.9	235	15	US-10-282-122A-57350	Sequence 57350, A	313	7	1.9	448	9	US-09-866-572A-56	Sequence 56, Appl
241	7	1.9	239	14	US-10-156-761-9042	Sequence 9042, Ap	314	7	1.9	448	9	US-09-866-570A-56	Sequence 56, Appl
242	7	1.9	244	15	US-10-424-599-237463	Sequence 237463, A	315	7	1.9	448	14	US-10-166-984-56	Sequence 56, Appl
243	7	1.9	245	15	US-10-424-599-180015	Sequence 180015, A	316	7	1.9	448	15	US-10-166-984-56	Sequence 56, Appl
244	7	1.9	249	9	US-09-971-309-1	Sequence 1, Appli	317	7	1.9	451	15	US-10-424-599-265555	Sequence 265555, A
245	7	1.9	249	16	US-10-702-400-68	Sequence 68, Appl	318	7	1.9	467	15	US-10-424-599-223383	Sequence 223383, A
246	7	1.9	249	16	US-10-828-924-60	Sequence 60, Appl	319	7	1.9	510	15	US-10-369-493-3993	Sequence 3993, Ap
247	7	1.9	256	14	US-10-156-761-13846	Sequence 13846, A	320	7	1.9	511	15	US-10-424-599-253543	Sequence 253543, A
248	7	1.9	260	16	US-10-437-963-133492	Sequence 133492, A	321	7	1.9	513	14	US-10-134-102-10	Sequence 10, Appl
249	7	1.9	266	15	US-10-434-599-173128	Sequence 173128, A	322	7	1.9	513	14	US-09-940-925A-90	Sequence 90, Appl
250	7	1.9	271	15	US-10-282-122A-45041	Sequence 45041, A	323	7	1.9	528	10	US-09-941-193A-90	Sequence 90, Appl
251	7	1.9	274	16	US-10-437-963-173780	Sequence 173780, A	324	7	1.9	537	16	US-10-437-963-142350	Sequence 142350, A
252	7	1.9	285	15	US-10-282-122A-74796	Sequence 74796, A	325	7	1.9	559	15	US-10-425-114-68937	Sequence 68937, A
253	7	1.9	289	15	US-10-424-599-173670	Sequence 173670, A	326	7	1.9	560	9	US-09-912-559-3	Sequence 3, Appli
254	7	1.9	298	15	US-10-389-566-536	Sequence 536, App	327	7	1.9	560	9	US-09-912-559-4	Sequence 4, Appli
255	7	1.9	298	15	US-10-425-114-52930	Sequence 52930, A	328	7	1.9	560	14	US-10-172-712-32	Sequence 32, Appl
256	7	1.9	302	9	US-09-866-572A-8	Sequence 8, Appli	329	7	1.9	560	15	US-10-391-215-5	Sequence 5, Appli
257	7	1.9	302	9	US-09-866-572A-24	Sequence 24, Appl	330	7	1.9	560	15	US-10-391-215-6	Sequence 6, Appli
258	7	1.9	302	9	US-09-866-570A-8	Sequence 8, Appli	331	7	1.9	560	15	US-10-391-215-7	Sequence 7, Appli
259	7	1.9	302	9	US-09-866-570A-24	Sequence 24, Appl	332	7	1.9	560	15	US-10-391-215-8	Sequence 8, Appli
260	7	1.9	302	14	US-10-166-984-8	Sequence 8, Appli	333	7	1.9	573	15	US-10-369-493-22865	Sequence 22865, A
261	7	1.9	302	14	US-10-166-984-24	Sequence 24, Appl	334	7	1.9	578	15	US-10-369-493-10208	Sequence 10208, A
262	7	1.9	302	15	US-10-166-984-8	Sequence 8, Appli	335	7	1.9	603	15	US-10-425-114-68922	Sequence 68922, A
263	7	1.9	302	15	US-10-166-984-24	Sequence 24, Appl	336	7	1.9	610	15	US-10-425-114-58388	Sequence 58388, A
264	7	1.9	306	9	US-09-866-572A-2	Sequence 2, Appli	337	7	1.9	622	14	US-10-032-585-7890	Sequence 7890, Ap
265	7	1.9	306	9	US-09-866-570A-2	Sequence 2, Appli	338	7	1.9	628	15	US-10-425-114-66875	Sequence 66875, A
266	7	1.9	306	14	US-10-166-984-2	Sequence 2, Appli	339	7	1.9	639	15	US-10-360-937-39	Sequence 39, Appl
267	7	1.9	306	15	US-10-166-984-2	Sequence 2, Appli	340	7	1.9	651	16	US-10-437-963-182057	Sequence 182057, A
268	7	1.9	317	15	US-10-282-122A-55956	Sequence 55956, A	341	7	1.9	652	9	US-09-815-242-13695	Sequence 13695, A
269	7	1.9	322	15	US-10-425-114-37377	Sequence 37377, A	342	7	1.9	656	15	US-10-425-114-53846	Sequence 53846, A
270	7	1.9	327	15	US-10-425-114-43516	Sequence 43516, A	343	7	1.9	673	15	US-10-755-889-4480	Sequence 4480, App
271	7	1.9	331	14	US-10-214-473-50	Sequence 50, Appl	344	7	1.9	673	15	US-10-425-114-64380	Sequence 64380, A
272	7	1.9	331	14	US-10-214-473-50	Sequence 50, Appl	345	7	1.9	685	10	US-09-877-843-59	Sequence 59, Appl
273	7	1.9	332	16	US-10-437-963-171440	Sequence 171440, A	346	7	1.9	730	11	US-09-939-853A-40	Sequence 40, Appl
274	7	1.9	339	15	US-10-282-122A-45100	Sequence 45100, A	347	7	1.9	737	16	US-10-437-963-203756	Sequence 203756, A
275	7	1.9	350	9	US-09-800-729-91	Sequence 91, Appl	348	7	1.9	772	15	US-10-369-493-16014	Sequence 16014, A
276	7	1.9	350	9	US-09-800-729-127	Sequence 127, App	349	7	1.9	789	15	US-10-041-018-395	Sequence 395, App
277	7	1.9	350	11	US-09-284-320-6	Sequence 6, Appli	350	7	1.9	833	10	US-09-940-925A-85	Sequence 85, Appl
278	7	1.9	350	11	US-09-833-245-2215	Sequence 2215, Ap	351	7	1.9	833	10	US-09-864-636A-239	Sequence 239, App
279	7	1.9	350	11	US-09-833-245-2216	Sequence 2216, Ap	352	7	1.9	833	10	US-09-941-193A-85	Sequence 85, Appl
280	7	1.9	356	15	US-10-284-237-1530	Sequence 1530, Ap	353	7	1.9	833	10	US-09-758-282-40	Sequence 40, Appl
281	7	1.9	356	16	US-10-437-963-171441	Sequence 171441, A	354	7	1.9	833	11	US-09-864-426A-239	Sequence 239, App
282	7	1.9	357	15	US-10-376-397A-44	Sequence 44, Appl	355	7	1.9	833	14	US-10-084-839-239	Sequence 239, App
283	7	1.9	367	15	US-10-282-122A-47588	Sequence 47588, A	356	7	1.9	895	14	US-10-345-092-5	Sequence 5, Appli
284	7	1.9	368	10	US-09-866-050A-670	Sequence 670, App	357	7	1.9	1008	16	US-10-437-963-181880	Sequence 181880, A
285	7	1.9	369	15	US-10-369-493-22377	Sequence 22377, A	358	7	1.9	1045	14	US-10-217-700-7	Sequence 7, Appli
286	7	1.9	370	14	US-10-021-955-78	Sequence 78, Appl	359	7	1.9	1190	15	US-10-369-493-18546	Sequence 18546, A
287	7	1.9	370	14	US-10-021-955-83	Sequence 83, Appl	360	7	1.9	1216	15	US-10-028-248A-72	Sequence 72, Appl
288	7	1.9	370	14	US-10-021-955-90	Sequence 90, Appl	361	7	1.9	1216	15	US-10-107-782-72	Sequence 72, Appl
289	7	1.9	379	15	US-10-425-114-60718	Sequence 60718, A	362	7	1.9	1228	14	US-10-021-660-129	Sequence 129, App
290	7	1.9	379	14	US-10-156-761-8561-	Sequence 8561, Ap	363	7	1.9	1228	15	US-10-211-462-101	Sequence 101, App
291	7	1.9	385	15	US-10-425-114-64567	Sequence 64567, A	364	7	1.9	1228	17	US-10-741-600-1577	Sequence 1577, Ap
292	7	1.9	391	15	US-10-425-114-68619	Sequence 68619, A	365	7	1.9	1236	15	US-10-334-143-38	Sequence 38, Appl
293	7	1.9	394	9	US-09-738-626-4690	Sequence 4690, Ap	366	7	1.9	1274	16	US-10-415-615-3	Sequence 3, Appli
294	7	1.9	399	15	US-10-108-260A-2891	Sequence 2891, Ap	367	7	1.9	1282	16	US-10-437-963-110654	Sequence 110654, A
295	7	1.9	403	15	US-10-369-493-2119	Sequence 2119, Ap	368	7	1.9	1371	16	US-10-437-963-128341	Sequence 128341, A
296	7	1.9	409	14	US-10-156-761-10839	Sequence 10839, A	369	7	1.9	1435	16	US-10-437-963-174801	Sequence 174801, A
297	7	1.9	414	14	US-10-156-761-13568	Sequence 13568, A	370	7	1.9	1554	16	US-10-383-930-38	Sequence 38, Appl
298	7	1.9	420	15	US-10-310-154-414	Sequence 414, App	371	7	1.9	1579	16	US-10-437-963-172638	Sequence 172638, A
299	7	1.9	424	10	US-09-496-444-2	Sequence 2, Appli	372	7	1.9	3700	14	US-10-329-079-4	Sequence 4, Appli
300	7	1.9	424	15	US-10-310-154-418	Sequence 418, App	373	7	1.9	6291	14	US-10-329-079-41	Sequence 41, Appl
301	7	1.9	427	15	US-10-424-599-209873	Sequence 209873, A	374	6	1.6	9	14	US-10-281-478-33	Sequence 33, Appl
302	7	1.9	428	9	US-09-789-599A-2	Sequence 2, Appli	375	6	1.6	10	10	US-09-572-404B-2795	Sequence 2795, Ap
303	7	1.9	428	9	US-09-816-079-2	Sequence 2, Appli	376	6	1.6	10	10	US-09-572-404B-3069	Sequence 3069, Ap
304	7	1.9	437	15	US-10-411-927-2	Sequence 2, Appli	377	7	1.9	12	14	US-10-225-301-5	Sequence 5, Appli
305	7	1.9	437	15	US-10-456-954-6	Sequence 6, Appli	378	6	1.6	12	15	US-10-264-309-35	Sequence 35, Appl

379	6	1.6	16	14	US-10-225-567A-1535	Sequence 1535, App	452	6	1.6	62	15	US-10-424-599-253050	Sequence 253050, A
380	6	1.6	23	10	US-09-809-391-621	Sequence 621, App	453	6	1.6	62	15	US-10-425-114-71256	Sequence 11256, A
381	6	1.6	23	10	US-09-882-171-621	Sequence 621, App	454	6	1.6	62	15	US-10-437-963-109872	Sequence 109872, A
382	6	1.6	23	15	US-10-164-861-621	Sequence 621, App	455	6	1.6	62	16	US-10-437-963-15236	Sequence 15236, A
383	6	1.6	31	15	US-10-424-599-239402	Sequence 239402, App	456	6	1.6	62	16	US-10-437-963-173614	Sequence 173614, A
384	6	1.6	32	9	US-09-828-708-69	Sequence 69, App	457	6	1.6	63	13	US-10-112-793-28	Sequence 28, App
385	6	1.6	32	9	US-09-828-708-71	Sequence 71, App	458	6	1.6	63	13	US-10-424-599-221760	Sequence 221760, A
386	6	1.6	32	16	US-10-467-513-12	Sequence 12, App	459	6	1.6	63	15	US-10-437-963-193019	Sequence 193019, A
387	6	1.6	34	9	US-09-864-761-38444	Sequence 38444, A	460	6	1.6	63	16	US-10-437-963-193019	Sequence 193019, A
388	6	1.6	34	10	US-09-942-024-36	Sequence 36, App	461	6	1.6	63	16	US-10-767-701-33346	Sequence 33346, A
389	6	1.6	34	10	US-09-942-024-36	Sequence 36, App	462	6	1.6	64	9	US-09-864-761-34896	Sequence 34896, A
390	6	1.6	34	14	US-10-218-102-127	Sequence 127, App	463	6	1.6	64	9	US-09-864-761-34896	Sequence 34896, A
391	6	1.6	34	15	US-10-261-161-58	Sequence 58, App	464	6	1.6	64	15	US-10-424-599-150897	Sequence 150897, A
392	6	1.6	34	16	US-10-437-963-126146	Sequence 126146, App	465	6	1.6	64	15	US-10-424-599-220265	Sequence 220265, A
393	6	1.6	34	16	US-09-864-761-33420	Sequence 33420, A	466	6	1.6	64	16	US-10-437-963-148408	Sequence 148408, A
394	6	1.6	35	10	US-09-986-480-319	Sequence 319, App	467	6	1.6	65	9	US-09-864-761-48443	Sequence 48443, A
395	6	1.6	35	16	US-10-168-804B-20	Sequence 20, App	468	6	1.6	65	9	US-09-924-102-1	Sequence 1, App
396	6	1.6	37	9	US-09-864-761-48546	Sequence 48546, A	469	6	1.6	65	14	US-10-203-081-1	Sequence 1, App
397	6	1.6	38	10	US-09-933-767-721	Sequence 721, App	470	6	1.6	65	14	US-10-156-761-13535	Sequence 13535, A
398	6	1.6	38	14	US-10-004-860-721	Sequence 721, App	471	6	1.6	66	14	US-10-437-963-133003	Sequence 133003, A
399	6	1.6	38	14	US-10-023-282-721	Sequence 721, App	472	6	1.6	66	14	US-10-012-140-21	Sequence 21, App
400	6	1.6	38	14	US-10-029-386-28020	Sequence 28020, A	473	6	1.6	66	15	US-10-424-599-159226	Sequence 159226, A
401	6	1.6	39	9	US-09-864-761-48726	Sequence 48726, A	474	6	1.6	66	15	US-10-424-599-190626	Sequence 190626, A
402	6	1.6	39	15	US-10-236-115-1024	Sequence 1024, App	475	6	1.6	67	11	US-09-833-245-254	Sequence 254, App
403	6	1.6	39	16	US-10-168-804B-21	Sequence 21, App	476	6	1.6	67	11	US-09-833-245-255	Sequence 255, App
404	6	1.6	40	9	US-09-864-761-35683	Sequence 35683, A	477	6	1.6	67	15	US-10-424-599-279518	Sequence 279518, A
405	6	1.6	40	16	US-10-767-701-49319	Sequence 49319, A	478	6	1.6	67	16	US-10-437-963-131974	Sequence 131974, A
406	6	1.6	42	9	US-09-864-761-33592	Sequence 33592, A	479	6	1.6	68	16	US-10-767-701-32826	Sequence 32826, A
407	6	1.6	42	9	US-09-864-761-37920	Sequence 37920, A	480	6	1.6	68	16	US-10-437-963-135157	Sequence 135157, A
408	6	1.6	42	14	US-10-163-198-11	Sequence 11, App	481	6	1.6	69	10	US-09-933-767-439	Sequence 439, App
409	6	1.6	43	15	US-10-375-253-24	Sequence 24, App	482	6	1.6	69	14	US-10-004-860-439	Sequence 439, App
410	6	1.6	43	16	US-10-437-963-158129	Sequence 158129, A	483	6	1.6	69	14	US-10-023-282-439	Sequence 439, App
411	6	1.6	45	16	US-10-424-599-164119	Sequence 164119, A	484	6	1.6	69	14	US-10-106-698-7334	Sequence 7334, App
412	6	1.6	45	16	US-10-437-963-111147	Sequence 111147, A	485	6	1.6	69	15	US-10-424-599-149679	Sequence 149679, A
413	6	1.6	46	10	US-09-974-879-226	Sequence 226, App	486	6	1.6	69	15	US-10-424-599-152230	Sequence 152230, A
414	6	1.6	46	15	US-10-424-599-143885	Sequence 143885, A	487	6	1.6	69	15	US-10-424-599-181599	Sequence 181599, A
415	6	1.6	46	15	US-10-424-599-246989	Sequence 246989, A	488	6	1.6	69	15	US-10-424-599-257426	Sequence 257426, A
416	6	1.6	46	16	US-10-621-401-226	Sequence 226, App	489	6	1.6	69	16	US-10-276-774-2603	Sequence 2603, App
417	6	1.6	46	16	US-10-437-963-127744	Sequence 127744, A	490	6	1.6	70	9	US-10-437-963-106289	Sequence 106289, A
418	6	1.6	47	10	US-09-305-736-226	Sequence 226, App	491	6	1.6	70	9	US-09-729-674-116	Sequence 116, App
419	6	1.6	47	10	US-09-818-683-226	Sequence 226, App	492	6	1.6	70	9	US-09-843-676-200	Sequence 200, App
420	6	1.6	47	11	US-09-818-683-226	Sequence 226, App	493	6	1.6	70	11	US-09-438-486-200	Sequence 200, App
421	6	1.6	49	14	US-10-029-386-31703	Sequence 31703, A	494	6	1.6	70	11	US-09-978-360A-502	Sequence 502, App
422	6	1.6	49	16	US-10-437-963-118184	Sequence 118184, A	495	6	1.6	70	14	US-10-053-758-200	Sequence 200, App
423	6	1.6	51	14	US-10-185-050-117	Sequence 117, App	496	6	1.6	70	14	US-10-054-295-200	Sequence 200, App
424	6	1.6	51	15	US-10-424-599-197112	Sequence 197112, A	497	6	1.6	70	15	US-10-054-611-200	Sequence 200, App
425	6	1.6	51	15	US-10-767-701-53206	Sequence 53206, A	498	6	1.6	70	15	US-10-325-810-319	Sequence 319, App
426	6	1.6	53	15	US-10-424-599-212230	Sequence 212230, A	499	6	1.6	70	15	US-10-264-049-3008	Sequence 3008, App
427	6	1.6	54	16	US-10-437-963-180832	Sequence 180832, A	500	6	1.6	70	15	US-10-424-599-183183	Sequence 183183, A
428	6	1.6	55	15	US-10-424-599-229366	Sequence 229366, A	501	6	1.6	70	15	US-10-424-599-261515	Sequence 261515, A
429	6	1.6	55	16	US-10-767-701-45316	Sequence 45316, A	502	6	1.6	70	16	US-10-425-114-43696	Sequence 43696, A
430	6	1.6	56	15	US-10-424-599-159749	Sequence 159749, A	503	6	1.6	70	16	US-10-913-553-116	Sequence 116, App
431	6	1.6	57	10	US-09-948-783-207	Sequence 207, App	504	6	1.6	70	17	US-10-877-146-319	Sequence 319, App
432	6	1.6	57	15	US-10-424-599-252463	Sequence 252463, A	505	6	1.6	71	9	US-10-472-928-1056	Sequence 1056, App
433	6	1.6	57	16	US-10-311-174A-65	Sequence 65, App	506	6	1.6	71	9	US-09-864-761-48254	Sequence 48254, A
434	6	1.6	57	16	US-10-311-174A-76	Sequence 76, App	507	6	1.6	71	14	US-10-083-357-739	Sequence 739, App
435	6	1.6	57	16	US-10-437-963-166513	Sequence 166513, A	508	6	1.6	72	14	US-10-106-698-6518	Sequence 6518, App
436	6	1.6	57	16	US-10-767-701-48417	Sequence 48417, A	509	6	1.6	72	14	US-10-029-386-27450	Sequence 27450, A
437	6	1.6	58	10	US-09-892-877-206	Sequence 206, App	510	6	1.6	72	15	US-10-424-599-176892	Sequence 176892, A
438	6	1.6	58	15	US-10-424-599-247908	Sequence 247908, App	511	6	1.6	72	15	US-10-424-599-213151	Sequence 213151, A
439	6	1.6	58	16	US-10-437-963-109006	Sequence 109006, A	512	6	1.6	73	9	US-10-424-599-227819	Sequence 227819, A
440	6	1.6	59	9	US-09-864-761-39074	Sequence 39074, A	513	6	1.6	73	15	US-09-764-877-1730	Sequence 1730, App
441	6	1.6	59	15	US-10-424-599-180812	Sequence 180812, A	514	6	1.6	73	15	US-10-242-515-1730	Sequence 1730, App
442	6	1.6	59	15	US-10-424-599-254089	Sequence 254089, A	515	6	1.6	73	15	US-10-424-599-212040	Sequence 212040, A
443	6	1.6	60	14	US-10-097-065-370	Sequence 370, App	516	6	1.6	73	16	US-10-437-963-177023	Sequence 177023, A
444	6	1.6	60	15	US-10-372-876-370	Sequence 370, App	517	6	1.6	74	15	US-10-424-599-154932	Sequence 154932, A
445	6	1.6	60	15	US-10-424-599-174447	Sequence 174447, A	518	6	1.6	74	15	US-10-424-599-165862	Sequence 165862, A
446	6	1.6	60	16	US-10-437-963-114678	Sequence 114678, A	519	6	1.6	74	15	US-10-424-599-171170	Sequence 171170, A
447	6	1.6	61	16	US-10-437-963-119090	Sequence 119090, A	520	6	1.6	74	15	US-10-424-599-236639	Sequence 236639, A
448	6	1.6	61	16	US-10-424-599-205644	Sequence 205644, A	521	6	1.6	74	15	US-10-424-599-177318	Sequence 177318, A
449	6	1.6	61	16	US-10-767-701-59078	Sequence 59078, A	522	6	1.6	74	15	US-10-424-599-274773	Sequence 274773, A
450	6	1.6	61	16	US-10-767-701-59078	Sequence 59078, A	523	6	1.6	74	16	US-10-311-174A-45	Sequence 45, App
451	6	1.6	62	11	US-09-864-408A-2376	Sequence 2376, App	524	6	1.6	74	16	US-10-437-963-152170	Sequence 152170, A

525	6	1.6	75	15	US-10-424-599-183618	Sequence 183618,	598	6	1.6	91	16	US-10-767-701-42778	Sequence 42778, A
526	6	1.6	75	15	US-10-424-599-225545	Sequence 225545,	599	6	1.6	91	16	US-10-767-701-59309	Sequence 59309, A
527	6	1.6	75	15	US-10-424-599-225469	Sequence 225469,	600	6	1.6	92	15	US-10-424-599-148202	Sequence 148202,
528	6	1.6	75	16	US-10-424-599-158823	Sequence 58823, A	601	6	1.6	92	15	US-10-424-599-189027	Sequence 189027,
529	6	1.6	76	15	US-10-424-599-176817	Sequence 176817,	602	6	1.6	92	16	US-10-437-963-187327	Sequence 187327,
530	6	1.6	76	15	US-10-424-599-199695	Sequence 199695,	603	6	1.6	93	15	US-10-424-599-275089	Sequence 275089,
531	6	1.6	77	9	US-09-925-301-1464	Sequence 1464, Ap	604	6	1.6	93	16	US-10-767-701-47340	Sequence 47340, A
532	6	1.6	77	15	US-10-029-020-190	Sequence 190, App	605	6	1.6	94	13	US-10-014-269-6	Sequence 6, Appli
533	6	1.6	77	15	US-10-425-114-36990	Sequence 36990, A	606	6	1.6	94	13	US-10-002-974-6	Sequence 6, Appli
534	6	1.6	77	16	US-10-437-963-118108	Sequence 118108,	607	6	1.6	94	14	US-10-314-506-6	Sequence 6, Appli
535	6	1.6	77	16	US-10-437-963-175941	Sequence 175941,	608	6	1.6	94	15	US-10-424-599-152960	Sequence 152960,
536	6	1.6	78	15	US-10-051-874-84	Sequence 84, Appl	609	6	1.6	94	16	US-10-437-963-130164	Sequence 130164,
537	6	1.6	78	15	US-10-042-865-71	Sequence 71, Appl	610	6	1.6	94	16	US-10-437-963-167269	Sequence 167269,
538	6	1.6	80	13	US-10-114-893-56	Sequence 56, Appl	611	6	1.6	94	16	US-10-466-531-141	Sequence 141, App
539	6	1.6	80	15	US-10-015-115-122	Sequence 122, App	612	6	1.6	95	10	US-09-933-767-314	Sequence 314, App
540	6	1.6	80	15	US-10-051-874-77	Sequence 77, Appl	613	6	1.6	95	14	US-10-004-860-314	Sequence 314, App
541	6	1.6	80	15	US-10-051-874-146	Sequence 146, App	614	6	1.6	95	14	US-10-023-282-314	Sequence 314, App
542	6	1.6	80	15	US-10-424-599-221452	Sequence 221452,	615	6	1.6	95	15	US-10-363-616-353	Sequence 353, App
543	6	1.6	80	16	US-10-311-1748-50	Sequence 50, Appl	616	6	1.6	95	16	US-10-437-963-179908	Sequence 179908,
544	6	1.6	80	16	US-10-437-963-114598	Sequence 114598,	617	6	1.6	95	16	US-10-767-701-39219	Sequence 39219, A
545	6	1.6	80	16	US-10-437-963-174243	Sequence 174243,	618	6	1.6	96	14	US-10-317-833-82	Sequence 82, Appl
546	6	1.6	81	9	US-09-925-300-1641	Sequence 1641, Ap	619	6	1.6	96	15	US-10-424-599-215384	Sequence 215384,
547	6	1.6	81	9	US-09-864-921-172	Sequence 172, App	620	6	1.6	97	9	US-09-764-869-1055	Sequence 1055, Ap
548	6	1.6	81	10	US-09-948-783-134	Sequence 134, App	621	6	1.6	97	14	US-10-091-504-1055	Sequence 1055, Ap
549	6	1.6	81	15	US-10-264-049-3886	Sequence 3886, Ap	622	6	1.6	97	15	US-10-227-577-1055	Sequence 1055, Ap
550	6	1.6	81	15	US-10-424-599-153018	Sequence 153018,	623	6	1.6	97	16	US-10-437-963-115369	Sequence 115369,
551	6	1.6	81	15	US-10-424-599-186385	Sequence 186385,	624	6	1.6	97	16	US-10-437-963-134225	Sequence 134225,
552	6	1.6	81	15	US-10-424-599-206427	Sequence 206427,	625	6	1.6	97	16	US-10-437-963-193790	Sequence 193790,
553	6	1.6	82	10	US-09-892-877-132	Sequence 132, App	626	6	1.6	97	17	US-10-472-928-2286	Sequence 2286, Ap
554	6	1.6	82	15	US-10-424-599-190374	Sequence 190374,	627	6	1.6	98	14	US-10-240-730-2	Sequence 2, Appli
555	6	1.6	83	14	US-10-156-761-11667	Sequence 11667, A	628	6	1.6	98	14	US-10-153-401-5	Sequence 5, Appli
556	6	1.6	83	15	US-10-424-599-185540	Sequence 185540,	629	6	1.6	98	15	US-10-424-599-243891	Sequence 243891,
557	6	1.6	83	15	US-10-424-599-250483	Sequence 250483,	630	6	1.6	98	15	US-10-424-599-244020	Sequence 244020,
558	6	1.6	83	16	US-10-437-963-184334	Sequence 184334,	631	6	1.6	98	16	US-10-437-963-144302	Sequence 144302,
559	6	1.6	84	15	US-10-424-599-271907	Sequence 271907,	632	6	1.6	99	14	US-10-317-833-44	Sequence 44, Appl
560	6	1.6	84	16	US-10-437-963-130740	Sequence 130740,	633	6	1.6	99	15	US-10-424-599-264649	Sequence 264649,
561	6	1.6	84	16	US-10-437-963-161451	Sequence 161451,	634	6	1.6	99	16	US-10-437-963-141270	Sequence 141270,
562	6	1.6	84	16	US-10-767-701-58899	Sequence 58899, A	635	6	1.6	99	16	US-10-437-963-152930	Sequence 152930,
563	6	1.6	85	11	US-09-864-408A-250	Sequence 250, App	636	6	1.6	99	16	US-10-767-701-44721	Sequence 44721, A
564	6	1.6	85	15	US-10-424-599-208916	Sequence 208916,	637	6	1.6	100	11	US-09-864-408A-8622	Sequence 119862,
565	6	1.6	85	15	US-10-424-599-240185	Sequence 240185,	638	6	1.6	100	16	US-10-437-963-119862	Sequence 119862,
566	6	1.6	85	15	US-10-424-599-241996	Sequence 241996,	639	6	1.6	100	16	US-10-437-963-151047	Sequence 151047,
567	6	1.6	85	16	US-10-437-963-143579	Sequence 143579,	640	6	1.6	100	9	US-09-828-708-10	Sequence 10, Appl
568	6	1.6	86	14	US-10-080-254-65	Sequence 65, Appl	641	6	1.6	101	15	US-10-424-599-205133	Sequence 205133,
569	6	1.6	86	15	US-10-242-355-609	Sequence 609, App	642	6	1.6	101	15	US-10-424-599-205134	Sequence 205134,
570	6	1.6	86	15	US-10-424-599-245019	Sequence 245019,	643	6	1.6	101	15	US-10-424-599-275269	Sequence 275269,
571	6	1.6	86	15	US-10-001-885-166	Sequence 166, App	644	6	1.6	102	15	US-10-424-599-217908	Sequence 217908,
572	6	1.6	86	16	US-10-437-963-104144	Sequence 104144,	645	6	1.6	103	15	US-09-974-879-178	Sequence 178, App
573	6	1.6	87	9	US-09-867-550-996	Sequence 996, App	646	6	1.6	103	15	US-10-424-599-197474	Sequence 197474,
574	6	1.6	87	15	US-10-424-599-201905	Sequence 201905,	647	6	1.6	103	15	US-10-424-599-267511	Sequence 267511,
575	6	1.6	87	15	US-10-638-210-7	Sequence 7, Appli	648	6	1.6	103	15	US-10-621-401-178	Sequence 178, App
576	6	1.6	87	15	US-10-638-210-45	Sequence 45, Appl	649	6	1.6	103	16	US-10-437-963-125644	Sequence 125644,
577	6	1.6	87	16	US-10-789-378-12	Sequence 12, Appl	650	6	1.6	104	9	US-09-815-242-5168	Sequence 5168, Ap
578	6	1.6	88	9	US-09-764-887-217	Sequence 217, App	651	6	1.6	104	10	US-09-305-736-178	Sequence 178, App
579	6	1.6	88	14	US-10-073-961-217	Sequence 217, App	652	6	1.6	104	10	US-09-818-683-178	Sequence 178, App
580	6	1.6	88	15	US-10-424-599-198594	Sequence 198594,	653	6	1.6	104	11	US-09-818-683-178	Sequence 178, App
581	6	1.6	88	15	US-10-424-599-232362	Sequence 232362,	654	6	1.6	104	15	US-10-108-260A-3928	Sequence 3928, Ap
582	6	1.6	88	15	US-10-425-114-53154	Sequence 53154, A	655	6	1.6	104	15	US-10-282-122A-43483	Sequence 43483, A
583	6	1.6	88	16	US-10-767-701-60463	Sequence 60463, A	656	6	1.6	104	15	US-10-282-122A-67824	Sequence 67824, A
584	6	1.6	89	15	US-10-424-599-238357	Sequence 238357,	657	6	1.6	104	15	US-10-282-122A-69234	Sequence 69234, A
585	6	1.6	89	16	US-10-437-963-108179	Sequence 108179,	658	6	1.6	104	15	US-10-424-599-203898	Sequence 203898,
586	6	1.6	90	14	US-10-083-357-741	Sequence 741, App	659	6	1.6	104	15	US-10-424-599-216327	Sequence 216327,
587	6	1.6	90	15	US-10-424-599-195600	Sequence 195600,	660	6	1.6	104	16	US-10-437-963-135545	Sequence 135545,
588	6	1.6	90	15	US-10-424-599-233485	Sequence 233485,	661	6	1.6	104	16	US-10-437-963-204622	Sequence 204622,
589	6	1.6	90	15	US-10-424-599-289419	Sequence 289419,	662	6	1.6	105	9	US-09-864-761-42752	Sequence 42752, A
590	6	1.6	90	16	US-10-437-963-128220	Sequence 128220,	663	6	1.6	105	15	US-10-424-599-215170	Sequence 215170,
591	6	1.6	90	16	US-10-437-963-138206	Sequence 138206,	664	6	1.6	105	15	US-10-424-599-278225	Sequence 278225,
592	6	1.6	91	11	US-09-864-408A-1904	Sequence 1904, Ap	665	6	1.6	105	16	US-10-437-963-139789	Sequence 139789,
593	6	1.6	91	14	US-10-029-386-34100	Sequence 34100, A	666	6	1.6	106	15	US-10-424-599-235720	Sequence 235720,
594	6	1.6	91	15	US-10-282-122A-46443	Sequence 46443, A	667	6	1.6	106	15	US-10-424-599-258137	Sequence 258137,
595	6	1.6	91	15	US-10-424-599-165858	Sequence 165858,	668	6	1.6	106	15	US-10-424-599-273183	Sequence 273183,
596	6	1.6	91	15	US-10-335-977-6836	Sequence 6836, Ap	669	6	1.6	106	16	US-10-767-701-59987	Sequence 59987, A
597	6	1.6	91	16	US-10-437-963-155786	Sequence 155786,	670	6	1.6	107	16	US-10-437-963-111994	Sequence 111994,

671	6	1.6	107	16	US-10-437-963-191176	Sequence 191176,	744	14	US-10-012-543-355	Sequence 355, App
672	6	1.6	108	15	US-10-264-237-1506	Sequence 1506, Ap	745	14	US-10-115-123-355	Sequence 355, App
673	6	1.6	109	15	US-10-424-599-175617	Sequence 175617,	746	15	US-10-289-762-1225	Sequence 1225, Ap
674	6	1.6	108	16	US-10-767-701-49690	Sequence 49690, A	747	15	US-10-425-114-61655	Sequence 61655, A
675	6	1.6	108	16	US-10-767-701-59593	Sequence 59593, A	748	16	US-10-437-963-139692	Sequence 139692,
676	6	1.6	109	15	US-10-424-599-154412	Sequence 154412,	749	6	US-09-984-245-169	Sequence 169, App
677	6	1.6	109	15	US-10-424-599-271737	Sequence 271737,	750	6	US-09-984-245-169	Sequence 169, App
678	6	1.6	110	9	US-09-864-761-46752	Sequence 46752, A	751	6	US-10-424-599-251992	Sequence 251992,
679	6	1.6	110	15	US-10-369-493-12685	Sequence 12685, A	752	6	US-10-424-599-251992	Sequence 251992,
680	6	1.6	110	16	US-10-437-963-146902	Sequence 146902,	753	6	US-10-059-395-169	Sequence 169, App
681	6	1.6	111	14	US-10-156-761-8026	Sequence 8026, Ap	754	6	US-10-143-090-169	Sequence 169, App
682	6	1.6	111	15	US-10-424-599-172044	Sequence 172044,	755	6	US-10-767-701-47346	Sequence 47346, A
683	6	1.6	111	15	US-10-424-599-205630	Sequence 205630,	756	6	US-10-424-599-206300	Sequence 206300,
684	6	1.6	111	15	US-10-424-599-257944	Sequence 257944,	757	6	US-10-424-599-223727	Sequence 223727,
685	6	1.6	111	16	US-10-437-963-165536	Sequence 165536,	758	6	US-10-424-599-251992	Sequence 251992,
686	6	1.6	112	9	US-09-828-708-8	Sequence 8, Appli	759	6	US-10-335-977-5125	Sequence 5125, Ap
687	6	1.6	112	11	US-09-978-3608-507	Sequence 507, App	760	6	US-10-632-983-173	Sequence 173, App
688	6	1.6	112	15	US-10-424-599-191335	Sequence 191335,	761	6	US-10-471-115-4	Sequence 4, Appli
689	6	1.6	112	15	US-10-424-599-236211	Sequence 236211,	762	6	US-10-818-068-2	Sequence 2, Appli
690	6	1.6	112	15	US-10-425-114-42211	Sequence 42211, A	763	6	US-10-818-068-3	Sequence 3, Appli
691	6	1.6	112	15	US-10-425-114-53352	Sequence 53352, A	764	6	US-10-818-068-5	Sequence 5, Appli
692	6	1.6	112	15	US-10-425-114-57383	Sequence 57383, A	765	6	US-10-818-068-6	Sequence 6, Appli
693	6	1.6	112	15	US-10-425-114-59445	Sequence 59445, A	766	6	US-09-764-864-1419	Sequence 1419, Ap
694	6	1.6	112	15	US-10-425-114-59445	Sequence 59445, A	767	6	US-10-424-599-167136	Sequence 167136,
695	6	1.6	113	13	US-10-160-865-18	Sequence 18, Appl	768	6	US-10-437-963-195607	Sequence 195607,
696	6	1.6	113	14	US-10-097-111-344	Sequence 344, App	769	6	US-10-104-047-2610	Sequence 2610, Ap
697	6	1.6	113	15	US-10-424-599-223450	Sequence 223450,	770	6	US-10-282-122A-45640	Sequence 45640, A
698	6	1.6	113	16	US-10-803-622-218	Sequence 218, App	771	6	US-10-282-122A-52394	Sequence 52394, A
699	6	1.6	113	16	US-10-803-653-218	Sequence 218, App	772	6	US-10-425-114-41476	Sequence 41476, A
700	6	1.6	114	9	US-09-865-483-8	Sequence 8, Appli	773	6	US-10-408-768A-1250	Sequence 1250, Ap
701	6	1.6	114	14	US-10-012-819-140	Sequence 140, App	774	6	US-10-437-963-102732	Sequence 102732,
702	6	1.6	114	15	US-10-424-599-146860	Sequence 146860,	775	6	US-10-767-701-33544	Sequence 33544, A
703	6	1.6	114	15	US-10-425-114-54750	Sequence 54750, A	776	6	US-10-106-698-6272	Sequence 6272, Ap
704	6	1.6	114	15	US-10-425-114-71072	Sequence 71072, A	777	6	US-10-424-599-150153	Sequence 150153,
705	6	1.6	114	16	US-10-726-555-8	Sequence 8, Appli	778	6	US-10-424-599-273120	Sequence 273120,
706	6	1.6	115	15	US-10-424-599-148792	Sequence 148792,	779	6	US-10-437-963-181637	Sequence 181637,
707	6	1.6	116	9	US-09-881-823-18	Sequence 18, Appl	780	6	US-10-767-701-52116	Sequence 52116, A
708	6	1.6	116	14	US-10-194-975-100	Sequence 100, App	781	6	US-10-424-599-236587	Sequence 236587,
709	6	1.6	116	14	US-10-169-351-108	Sequence 108, App	782	6	US-10-424-599-258512	Sequence 258512,
710	6	1.6	116	15	US-10-424-599-176186	Sequence 176186,	783	6	US-10-424-599-281027	Sequence 281027,
711	6	1.6	116	15	US-10-424-599-225567	Sequence 225567,	784	6	US-10-437-963-203303	Sequence 203303,
712	6	1.6	116	15	US-10-435-299-4	Sequence 4, Appli	785	6	US-10-424-599-280176	Sequence 280176,
713	6	1.6	116	16	US-10-437-963-182706	Sequence 182706,	786	6	US-10-424-599-280176	Sequence 280176,
714	6	1.6	116	16	US-10-682-845-53	Sequence 53, Appl	787	6	US-10-437-963-121228	Sequence 121228,
715	6	1.6	117	10	US-09-764-891-2956	Sequence 2956, Ap	788	6	US-10-437-963-129295	Sequence 129295,
716	6	1.6	117	14	US-10-174-693-400	Sequence 400, App	789	6	US-09-864-408A-1970	Sequence 1970, Ap
717	6	1.6	117	15	US-10-372-481-11	Sequence 11, Appl	790	6	US-10-437-963-138858	Sequence 138858,
718	6	1.6	117	15	US-10-371-797-11	Sequence 11, Appl	791	6	US-10-437-963-174401	Sequence 174401,
719	6	1.6	117	15	US-10-264-237-2560	Sequence 2560, Ap	792	6	US-10-767-701-60523	Sequence 60523, A
720	6	1.6	117	15	US-10-264-237-2728	Sequence 2728, Ap	793	6	US-10-437-963-184319	Sequence 184319,
721	6	1.6	117	16	US-10-767-701-56500	Sequence 56500, A	794	6	US-10-437-963-197861	Sequence 197861,
722	6	1.6	118	10	US-09-820-649-136	Sequence 136, App	795	6	US-09-925-297-581	Sequence 581, App
723	6	1.6	118	14	US-10-056-052-8	Sequence 8, Appli	796	6	US-09-746-783-214	Sequence 214, App
724	6	1.6	118	14	US-10-160-162-136	Sequence 136, App	797	6	US-09-969-730-114	Sequence 114, App
725	6	1.6	119	13	US-10-140-555-2	Sequence 2, Appli	798	6	US-09-969-730-139	Sequence 139, App
726	6	1.6	119	14	US-10-144-644-15	Sequence 15, Appl	799	6	US-09-764-891-3761	Sequence 3761, Ap
727	6	1.6	119	14	US-10-232-187-2	Sequence 2, Appli	800	6	US-10-621-363-114	Sequence 114, App
728	6	1.6	119	14	US-10-153-401-16	Sequence 16, Appl	801	6	US-10-621-363-199	Sequence 199, App
729	6	1.6	119	15	US-10-389-155-19	Sequence 19, Appl	802	6	US-10-282-122A-76411	Sequence 76411, A
730	6	1.6	119	15	US-10-389-656-23	Sequence 23, Appl	803	6	US-10-424-599-181076	Sequence 181076,
731	6	1.6	119	15	US-10-389-417-19	Sequence 19, Appl	804	6	US-10-276-774-1601	Sequence 1601, Ap
732	6	1.6	119	16	US-10-452-357-60	Sequence 60, Appl	805	6	US-10-437-963-130448	Sequence 130448,
733	6	1.6	119	16	US-10-700-740-15	Sequence 15, Appl	806	6	US-10-437-963-161425	Sequence 161425,
734	6	1.6	120	14	US-10-194-975-112	Sequence 112, App	807	6	US-10-767-701-61151	Sequence 61151, A
735	6	1.6	120	15	US-10-239-656-33	Sequence 33, Appl	808	6	US-09-774-638-114	Sequence 114, App
736	6	1.6	120	15	US-10-239-656-43	Sequence 43, Appl	809	6	US-10-010-729-68	Sequence 68, Appl
737	6	1.6	120	16	US-10-437-963-158380	Sequence 158380,	810	6	US-10-108-260A-2614	Sequence 2614, Ap
738	6	1.6	120	16	US-10-767-701-39909	Sequence 39909, A	811	6	US-10-309-290-80	Sequence 80, Appl
739	6	1.6	121	13	US-10-078-929-118	Sequence 118, App	812	6	US-10-437-963-151630	Sequence 151630,
740	6	1.6	121	14	US-10-056-052-12	Sequence 12, Appl	813	6	US-10-437-963-203106	Sequence 203106,
741	6	1.6	121	15	US-10-056-052-20	Sequence 20, Appl	814	6	US-10-470-390A-8	Sequence 8, Appli
742	6	1.6	121	15	US-10-424-599-201530	Sequence 201530,	815	6	US-10-351-748-31	Sequence 31, Appl
743	6	1.6	121	16	US-10-437-963-141451	Sequence 141451,	816	6	US-10-767-701-61121	Sequence 61121, A

817	6	1.6	135	16	US-10-351-748-31	Sequence 31, Appl	890	6	1.6	160	10	US-09-394-142B-10	Sequence 10, Appl
818	6	1.6	136	15	US-10-094-749-2334	Sequence 2334, Ap	891	6	1.6	160	15	US-10-425-114-69519	Sequence 69519, A
819	6	1.6	137	16	US-10-437-963-150496	Sequence 150496,	892	6	1.6	160	15	US-10-210-172-30	Sequence 30, Appl
820	6	1.6	137	16	US-10-437-963-198795	Sequence 198795,	893	6	1.6	160	16	US-10-782-627-10	Sequence 10, Appl
821	6	1.6	137	16	US-10-767-701-36077	Sequence 36077, A	894	6	1.6	160	16	US-10-767-701-41173	Sequence 41173, A
822	6	1.6	138	15	US-10-389-155-46	Sequence 46, Appl	895	6	1.6	161	15	US-10-108-260A-3620	Sequence 3620, Ap
823	6	1.6	138	15	US-10-369-493-9126	Sequence 9126, Ap	896	6	1.6	161	15	US-10-408-765A-2845	Sequence 2845, Ap
824	6	1.6	138	15	US-10-424-599-163385	Sequence 163385,	897	6	1.6	161	16	US-10-408-765A-2845	Sequence 175933,
825	6	1.6	138	15	US-10-389-417-46	Sequence 46, Appl	898	6	1.6	161	16	US-10-437-963-137524	Sequence 137524,
826	6	1.6	138	15	US-10-452-357-33	Sequence 33, Appl	899	6	1.6	162	16	US-10-437-963-137524	Sequence 142605,
827	6	1.6	138	16	US-10-437-963-203261	Sequence 203261,	900	6	1.6	162	16	US-10-437-963-169927	Sequence 169927,
828	6	1.6	138	16	US-10-767-701-38633	Sequence 38633, A	901	6	1.6	163	15	US-10-424-599-151490	Sequence 151490,
829	6	1.6	139	8	US-08-779-784-37	Sequence 37, Appl	902	6	1.6	163	15	US-10-424-599-151490	Sequence 157154,
830	6	1.6	139	9	US-09-881-823-4	Sequence 4, Appl	903	6	1.6	163	15	US-10-424-599-175993	Sequence 175993,
831	6	1.6	139	15	US-10-425-114-41659	Sequence 41659, A	904	6	1.6	163	15	US-10-424-599-187125	Sequence 187125,
832	6	1.6	140	16	US-10-437-963-179933	Sequence 179933,	905	6	1.6	164	15	US-10-389-566-969	Sequence 969, App
833	6	1.6	140	16	US-10-437-963-185178	Sequence 185178,	906	6	1.6	164	15	US-10-424-599-187123	Sequence 187123,
834	6	1.6	140	16	US-10-767-701-39092	Sequence 39092, A	907	6	1.6	164	16	US-10-767-701-40547	Sequence 40547, A
835	6	1.6	140	16	US-10-767-701-56723	Sequence 56723, A	908	6	1.6	165	10	US-09-764-891-3994	Sequence 3994, Ap
836	6	1.6	141	15	US-10-424-599-284856	Sequence 284856,	909	6	1.6	165	10	US-09-769-787-92	Sequence 92, Appl
837	6	1.6	142	9	US-09-772-103-4	Sequence 4, Appl	910	6	1.6	165	15	US-10-424-599-172746	Sequence 172746,
838	6	1.6	142	14	US-10-029-386-32549	Sequence 32549, A	911	6	1.6	165	15	US-10-424-599-235756	Sequence 235756,
839	6	1.6	142	15	US-10-282-122A-67106	Sequence 67106, A	912	6	1.6	165	15	US-10-335-977-6192	Sequence 6192, Ap
840	6	1.6	142	16	US-10-437-963-134512	Sequence 134512,	913	6	1.6	165	16	US-10-437-963-152577	Sequence 152577,
841	6	1.6	142	16	US-10-437-963-141271	Sequence 141271,	914	6	1.6	165	16	US-10-767-701-32177	Sequence 32177, A
842	6	1.6	143	16	US-10-437-963-143435	Sequence 143435,	915	6	1.6	166	17	US-10-472-928-1664	Sequence 1664, Ap
843	6	1.6	144	15	US-10-094-749-2148	Sequence 2148, Ap	916	6	1.6	166	15	US-10-282-122A-64273	Sequence 64273, A
844	6	1.6	144	15	US-10-424-599-143966	Sequence 143966,	917	6	1.6	166	15	US-10-424-599-283375	Sequence 283375,
845	6	1.6	144	15	US-10-425-114-55635	Sequence 55635, A	918	6	1.6	166	15	US-10-425-114-61855	Sequence 61855, A
846	6	1.6	144	15	US-10-425-114-56488	Sequence 56488, A	919	6	1.6	166	15	US-10-425-114-64112	Sequence 64112, A
847	6	1.6	145	9	US-09-821-839-5	Sequence 5, Appl	920	6	1.6	167	16	US-10-437-963-134987	Sequence 134987,
848	6	1.6	145	15	US-10-425-114-36905	Sequence 36905, A	921	6	1.6	168	15	US-10-289-762-72	Sequence 72, Appl
849	6	1.6	145	16	US-10-437-963-129399	Sequence 129399,	922	6	1.6	169	15	US-10-369-493-17361	Sequence 17361, A
850	6	1.6	146	9	US-09-764-869-644	Sequence 644, App	923	6	1.6	169	16	US-10-767-701-36423	Sequence 36423, A
851	6	1.6	146	14	US-10-091-504-644	Sequence 644, App	924	6	1.6	169	16	US-10-767-701-36426	Sequence 36426, A
852	6	1.6	146	15	US-10-369-493-11808	Sequence 11808, A	925	6	1.6	169	16	US-10-767-701-57523	Sequence 57523, A
853	6	1.6	146	15	US-10-227-577-644	Sequence 644, App	926	6	1.6	170	15	US-10-425-114-36746	Sequence 36746, A
854	6	1.6	146	15	US-10-424-599-155439	Sequence 155439,	927	6	1.6	170	15	US-10-425-114-51752	Sequence 51752, A
855	6	1.6	146	15	US-10-424-599-247022	Sequence 247022,	928	6	1.6	170	16	US-10-437-963-110548	Sequence 110548,
856	6	1.6	146	15	US-10-425-114-62197	Sequence 62197, A	929	6	1.6	170	16	US-10-437-963-186646	Sequence 186646,
857	6	1.6	146	15	US-10-425-114-70902	Sequence 70902, A	930	6	1.6	170	16	US-10-767-701-32869	Sequence 32869, A
858	6	1.6	147	15	US-10-424-599-207156	Sequence 207156, A	931	6	1.6	171	10	US-09-892-877-277	Sequence 277, App
859	6	1.6	147	15	US-10-425-114-66983	Sequence 66983, A	932	6	1.6	171	10	US-09-948-783-279	Sequence 279, App
860	6	1.6	147	16	US-10-437-963-109116	Sequence 109116,	933	6	1.6	171	15	US-10-094-749-2193	Sequence 2193, Ap
861	6	1.6	147	16	US-10-767-701-41809	Sequence 41809, A	934	6	1.6	172	9	US-09-864-761-34586	Sequence 34586, A
862	6	1.6	148	15	US-10-425-114-41217	Sequence 41217, A	935	6	1.6	172	9	US-09-864-761-42700	Sequence 42700, A
863	6	1.6	148	16	US-10-437-963-198902	Sequence 198902,	936	6	1.6	172	9	US-09-738-626-6958	Sequence 6958, Ap
864	6	1.6	148	16	US-10-767-701-38117	Sequence 38117, A	937	6	1.6	172	15	US-10-425-114-60659	Sequence 60659, A
865	6	1.6	149	15	US-10-424-599-266128	Sequence 266128,	938	6	1.6	172	15	US-10-425-114-63902	Sequence 63902, A
866	6	1.6	150	15	US-10-424-599-178119	Sequence 178119,	939	6	1.6	172	16	US-10-437-963-176354	Sequence 176354,
867	6	1.6	150	15	US-10-424-599-212497	Sequence 212497,	940	6	1.6	172	16	US-10-437-963-176354	Sequence 59998, A
868	6	1.6	150	15	US-10-424-599-282596	Sequence 282596,	941	6	1.6	172	16	US-10-767-701-59998	Sequence 236, App
869	6	1.6	150	16	US-10-767-701-58488	Sequence 58488, A	942	6	1.6	173	9	US-09-764-868-1052	Sequence 1052, Ap
870	6	1.6	151	16	US-10-767-701-62023	Sequence 62023, A	943	6	1.6	173	13	US-10-052-586-506	Sequence 506, App
871	6	1.6	152	9	US-09-990-205-4	Sequence 4, Appl	944	6	1.6	173	14	US-10-176-758-506	Sequence 506, App
872	6	1.6	152	14	US-10-153-401-4	Sequence 4, Appl	945	6	1.6	173	14	US-10-176-758-506	Sequence 506, App
873	6	1.6	152	15	US-10-424-599-175161	Sequence 175161,	946	6	1.6	173	14	US-10-175-737-506	Sequence 506, App
874	6	1.6	153	15	US-10-424-599-267234	Sequence 267234,	947	6	1.6	173	14	US-10-175-737-506	Sequence 506, App
875	6	1.6	153	15	US-10-767-701-35028	Sequence 35028, A	948	6	1.6	173	14	US-10-174-581-506	Sequence 506, App
876	6	1.6	154	15	US-10-282-122A-46514	Sequence 46514, A	949	6	1.6	173	14	US-10-176-483-506	Sequence 506, App
877	6	1.6	155	16	US-10-437-963-186816	Sequence 186816,	950	6	1.6	173	14	US-10-176-749-506	Sequence 506, App
878	6	1.6	156	14	US-10-029-386-32077	Sequence 32077, A	951	6	1.6	173	14	US-10-176-914-506	Sequence 506, App
879	6	1.6	156	15	US-10-424-599-181140	Sequence 181140,	952	6	1.6	173	14	US-10-173-706-506	Sequence 506, App
880	6	1.6	156	15	US-10-424-599-245615	Sequence 245615,	953	6	1.6	173	14	US-10-175-738-506	Sequence 506, App
881	6	1.6	156	16	US-10-767-701-32834	Sequence 32834, A	954	6	1.6	173	14	US-10-175-752-506	Sequence 506, App
882	6	1.6	157	15	US-10-425-114-51936	Sequence 51936, A	955	6	1.6	173	14	US-10-176-482-506	Sequence 506, App
883	6	1.6	158	14	US-10-152-886-55	Sequence 55, Appl	956	6	1.6	173	14	US-10-176-757-506	Sequence 506, App
884	6	1.6	158	14	US-10-157-031-134	Sequence 134, App	957	6	1.6	173	14	US-10-176-913-506	Sequence 506, App
885	6	1.6	158	15	US-10-424-599-279167	Sequence 279167,	958	6	1.6	173	14	US-10-180-552-506	Sequence 506, App
886	6	1.6	158	16	US-10-437-963-144197	Sequence 144197,	959	6	1.6	173	14	US-10-180-557-506	Sequence 506, App
887	6	1.6	158	16	US-10-767-701-35595	Sequence 35595, A	960	6	1.6	173	14	US-10-173-700-506	Sequence 506, App
888	6	1.6	159	15	US-10-424-599-158470	Sequence 158470,	961	6	1.6	173	14	US-10-174-572-506	Sequence 506, App
889	6	1.6	159	16	US-10-437-963-147590	Sequence 147590,	962	6	1.6	173	14	US-10-174-579-506	Sequence 506, App

963	6	1.6	173	14	US-10-174-582-506	Sequence 506, App
964	6	1.6	173	14	US-10-174-588-506	Sequence 506, App
965	6	1.6	173	14	US-10-175-739-506	Sequence 506, App
966	6	1.6	173	14	US-10-175-740-506	Sequence 506, App
967	6	1.6	173	14	US-10-175-743-506	Sequence 506, App
968	6	1.6	173	14	US-10-176-488-506	Sequence 506, App
969	6	1.6	173	14	US-10-176-492-506	Sequence 506, App
970	6	1.6	173	14	US-10-176-747-506	Sequence 506, App
971	6	1.6	173	14	US-10-176-750-506	Sequence 506, App
972	6	1.6	173	14	US-10-176-985-506	Sequence 506, App
973	6	1.6	173	14	US-10-176-987-506	Sequence 506, App
974	6	1.6	173	14	US-10-176-992-506	Sequence 506, App
975	6	1.6	173	14	US-10-176-993-506	Sequence 506, App
976	6	1.6	173	14	US-10-184-658-506	Sequence 506, App
977	6	1.6	173	14	US-10-176-991-506	Sequence 506, App
978	6	1.6	173	14	US-10-173-695-506	Sequence 506, App
979	6	1.6	173	14	US-10-173-697-506	Sequence 506, App
980	6	1.6	173	14	US-10-173-705-506	Sequence 506, App
981	6	1.6	173	14	US-10-174-576-506	Sequence 506, App
982	6	1.6	173	14	US-10-174-585-506	Sequence 506, App
983	6	1.6	173	14	US-10-174-586-506	Sequence 506, App
984	6	1.6	173	14	US-10-175-747-506	Sequence 506, App
985	6	1.6	173	14	US-10-176-481-506	Sequence 506, App
986	6	1.6	173	14	US-10-176-485-506	Sequence 506, App
987	6	1.6	173	14	US-10-176-487-506	Sequence 506, App
988	6	1.6	173	14	US-10-176-493-506	Sequence 506, App
989	6	1.6	173	14	US-10-176-756-506	Sequence 506, App
990	6	1.6	173	14	US-10-176-911-506	Sequence 506, App
991	6	1.6	173	14	US-10-176-919-506	Sequence 506, App
992	6	1.6	173	14	US-10-176-925-506	Sequence 506, App
993	6	1.6	173	14	US-10-176-978-506	Sequence 506, App
994	6	1.6	173	14	US-10-179-510-506	Sequence 506, App
995	6	1.6	173	14	US-10-180-543-506	Sequence 506, App
996	6	1.6	173	14	US-10-180-544-506	Sequence 506, App
997	6	1.6	173	14	US-10-180-546-506	Sequence 506, App
998	6	1.6	173	14	US-10-180-547-506	Sequence 506, App
999	6	1.6	173	14	US-10-180-549-506	Sequence 506, App
1000	6	1.6	173	14	US-10-180-555-506	Sequence 506, App

ALIGNMENTS

```
RESULT 1
US-09-736-250-1
; Sequence 1, Application US/09736250
; Publication No. US20050014139A1
; GENERAL INFORMATION:
; APPLICANT: SUMITOMO ELECTRIC INDUSTRIES, LTD.
; APPLICANT: NAKAMURA, Takeshi
; TITLE OF INVENTION: HUMAN CYCLIN I AND GENES ENCODING THE SAME
; FILE REFERENCE: 050212-0278
; CURRENT APPLICATION NUMBER: US/09/736,250
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 09/054,492
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: PCT/JP96/02905
; PRIOR FILING DATE: 1996-10-07
; PRIOR APPLICATION NUMBER: 284663/1995
; PRIOR FILING DATE: 1995-10-05
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 1
; LENGTH: 377
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-736-250-1

Query Match      100.0%; Score 377; DB 12; Length 377;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MKFPGPLENQLSFLEKAITREAOQMWKVNVRKMPNSQNVSPSORDEVIQWLAKLYQFN 60
```

; Sequence 5, Application US/09736250
; Publication No. US20050014139A1
; GENERAL INFORMATION:
; APPLICANT: SUMITOMO ELECTRIC INDUSTRIES, LTD.
; APPLICANT: NAKAMURA, Takeshi

; TITLE OF INVENTION: HUMAN CYCLIN I AND GENES ENCODING THE SAME
; FILE REFERENCE: 050212-0278
; CURRENT APPLICATION NUMBER: US/09/736,250
; CURRENT FILING DATE: 2000-12-15

; PRIOR APPLICATION NUMBER: 09/054,492
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: PCT/JP96/02905
; PRIOR FILING DATE: 1996-10-07

; PRIOR APPLICATION NUMBER: 284663/1995
; PRIOR FILING DATE: 1995-10-05
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 5
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Chemically synthesized
US-09-736-250-5

Query Match 3.7%; Score 14; DB 12; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.5e+06; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 0

Qy 343 EDNVSENVGVCQT 356
| | | | | | | | | | | | | | | |
Db 1 EDNVSENVGVCQT 14

RESULT 4

US-09-865-548A-151
; Sequence 151, Application US/09865548A
; Publication No. US20030096298A1

; GENERAL INFORMATION:
; APPLICANT: Barnea, Eilon
; APPLICANT: Beer, Ilan

; APPLICANT: Ziv, Tamir
; APPLICANT: Admon, Arie
; TITLE OF INVENTION: METHOD OF IDENTIFYING PEPTIDES CAPABLE OF BINDING TO MHC MOLECULE

; TITLE OF INVENTION: PEPTIDES IDENTIFIED THEREBY AND THEIR USES
; FILE REFERENCE: 01/22080
; CURRENT APPLICATION NUMBER: US/09/865,548A

; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: US 60/290,958
; PRIOR FILING DATE: 2001-05-16

; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 151
; LENGTH: 9

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: synthetic peptide
US-09-865-548A-151

Query Match 2.4%; Score 9; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0

Qy 72 LLDRLFLATV 80
| | | | | | | | | | | | | | | |
Db 1 LLDRLFLATV 9

RESULT 5

US-10-006-177-8
; Sequence 8, Application US/10006177
; Publication No. US20030165513A1

; GENERAL INFORMATION:

; APPLICANT: Ramakrishna, Venky
; APPLICANT: Ross, Mark

; TITLE OF INVENTION: Cytotoxic T-Lymphocyte-Inducing Immunogens for Prevention, Treatm
; FILE REFERENCE: 26747-35
; CURRENT APPLICATION NUMBER: US/10/006,177

; CURRENT FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: US/60/251,022
; PRIOR FILING DATE: 2000-12-04

; PRIOR APPLICATION NUMBER: US/60/256,824
; PRIOR FILING DATE: 2000-12-20
; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 9

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Epitopic Peptide
US-10-006-177-8

Query Match 2.4%; Score 9; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0

Qy 72 LLDRLFLATV 80
| | | | | | | | | | | | | | | |
Db 1 LLDRLFLATV 9

RESULT 6

US-09-129-112-2

; Sequence 2, Application US/09129112
; Patent No. US20020019995A1

; GENERAL INFORMATION:
; APPLICANT: Etzler, Marilyn E.
; APPLICANT: Murphy, Judith B.

; TITLE OF INVENTION: A No. US20020019995A1 Factor Binding Protein From Legume Roots
; FILE REFERENCE: 023070-079810US
; CURRENT APPLICATION NUMBER: US/09/129,112

; CURRENT FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: US 08/907,226
; PRIOR FILING DATE: 1997-08-06

; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2

; LENGTH: 462
; TYPE: PRT
; ORGANISM: Dolichos biflorus

; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (52)..(73)

; OTHER INFORMATION: motif identified as conserved region among a
; NAME/KEY: PEPTIDE
; LOCATION: (128)..(144)

; OTHER INFORMATION: motif identified as conserved region among a
; NAME/KEY: PEPTIDE
; LOCATION: (173)..(195)

; OTHER INFORMATION: motif identified as conserved region among a
; NAME/KEY: PEPTIDE
; LOCATION: (200)..(220)

; OTHER INFORMATION: motif identified as conserved region among a
; NAME/KEY: PEPTIDE
; LOCATION: (200)..(220)

; OTHER INFORMATION: motif identified as conserved region among a
; NAME/KEY: PEPTIDE
; LOCATION: (200)..(220)

; OTHER INFORMATION: motif identified as conserved region among a
; NAME/KEY: PEPTIDE
; LOCATION: (200)..(220)

; OTHER INFORMATION: motif identified as conserved region among a
; NAME/KEY: PEPTIDE
; LOCATION: (200)..(220)

; OTHER INFORMATION: motif identified as conserved region among a
; NAME/KEY: PEPTIDE
; LOCATION: (200)..(220)

; OTHER INFORMATION: motif identified as conserved region among a
; NAME/KEY: PEPTIDE
; LOCATION: (200)..(220)

; OTHER INFORMATION: motif identified as conserved region among a
; NAME/KEY: PEPTIDE
; LOCATION: (200)..(220)

; OTHER INFORMATION: motif identified as conserved region among a
; NAME/KEY: PEPTIDE
; LOCATION: (200)..(220)

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 165 LLFSLPKLS 173
| | | | | | | | | |
Db 20 LLFSLPKLS 28

RESULT 7

US-10-425-114-42971
; Sequence 42971, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 42971
; LENGTH: 83
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700673310_FLI.1.pep
US-10-425-114-42971

Query Match 2.1%; Score 8; DB 15; Length 83;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 168 SLPKLS 175
| | | | | | | | | |
Db 36 SLPKLS 43

RESULT 8

US-10-424-599-245711
; Sequence 245711, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 245711
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_63909C.1.pep
US-10-424-599-245711

Query Match 2.1%; Score 8; DB 15; Length 99;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 279 LHPSSVPG 286
| | | | | | | | | |
Db 51 LHPSSVPG 58

RESULT 9

US-10-424-599-196677
; Sequence 196677, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 196677
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)...(216)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_19626C.1.pep
US-10-424-599-196677

Query Match 2.1%; Score 8; DB 15; Length 216;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 168 SLPKLS 175
| | | | | | | | | |
Db 185 SLPKLS 192

RESULT 10

US-10-424-599-196680
; Sequence 196680, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 196680
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_19629C.1.pep
US-10-424-599-196680

Query Match 2.1%; Score 8; DB 15; Length 289;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 168 SLPKLS 175
| | | | | | | | | |
Db 242 SLPKLS 249

RESULT 11

US-10-437-963-145582
; Sequence 145582, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 145582
; LENGTH: 379
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_46289C.1.pep
US-10-437-963-145582

Query Match 2.1%; Score 8; DB 16; Length 379;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 262 YRPLKHTL 269
Db 148 YRPLKHTL 155
|||||

RESULT 12
US-09-866-562-62
; Sequence 62, Application US/09866562
; Patent No. US20020009758A1
; GENERAL INFORMATION:
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Klee, Jennifer
; APPLICANT: Switzer, Anne
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER.
; FILE REFERENCE: 210121.502
; CURRENT APPLICATION NUMBER: US/09/866,562
; CURRENT FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 96
; SEQ ID NO 62
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-866-562-62

Query Match 2.1%; Score 8; DB 9; Length 391;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 247 LSTLQSSL 254
Db 84 LSTLQSSL 91
|||||

RESULT 13
US-10-236-392-92
; Sequence 92, Application US/10236392
; Publication No. US20040067490A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David W
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Burgess, Catherine, E
; APPLICANT: Casman, Stacie J
; APPLICANT: Catterton, Elina
; APPLICANT: Chapoval, Andrei

; APPLICANT: Crabtree, Julie
; APPLICANT: Edinger, Shlomit, R
; APPLICANT: Ellerman, Karen
; APPLICANT: Gerlach, Valerie
; APPLICANT: Gorman, Linda
; APPLICANT: Grosse, William M
; APPLICANT: Gusev, Vladamir
; APPLICANT: Kekuda, Ramesh
; APPLICANT: LaRochelle, William J
; APPLICANT: Li, Li
; APPLICANT: MacDougall, John R
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Miller, Charles E
; APPLICANT: Millet, Isabelle
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Pena, Carol A
; APPLICANT: Peyman, John A
; APPLICANT: Rastelli, Luca
; APPLICANT: Reiger, Daniel K
; APPLICANT: Rothenberg, Mark E
; APPLICANT: Shenoy, Suresh
; APPLICANT: Shimkets, Richard A
; APPLICANT: Smithson, Glennda
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-442A
; CURRENT APPLICATION NUMBER: US/10/236,392
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US09/540,763
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: US60/390,155
; PRIOR FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US09/635,949
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: US60/318,765
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US60/357,303
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US60/367,753
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: US60/369,479
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US09/659,634
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: US60/318,120
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US60/318,130
; PRIOR FILING DATE: 2001-09-07
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 794
; SOFTWARE: Custom
; SEQ ID NO 92
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-236-392-92

Query Match 2.1%; Score 8; DB 15; Length 416;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 247 LSTLQSSL 254
Db 84 LSTLQSSL 91
|||||

RESULT 14
US-10-425-114-51949
; Sequence 51949, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua

; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 51949
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700103547_FLI.pep
US-10-425-114-51949

Query Match 2.1%; Score 8; DB 15; Length 418;
Best Local Similarity 100.0%; Pred.No. 75;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LSPSQHLA 179
|||
Db 166 LSPSQHLA 173

RESULT 15
US-10-767-701-44456
; Sequence 44456, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 44456
; LENGTH: 514
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C7731_1.pep
US-10-767-701-44456

Query Match 2.1%; Score 8; DB 16; Length 514;
Best Local Similarity 100.0%; Pred.No. 91;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LSPSQHLA 179
|||
Db 262 LSPSQHLA 269

Search completed: February 11, 2005, 03:25:20
Job time : 107.777 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 11, 2005, 03:06:34 ; Search time 28.9258 Seconds
(without alignments)
1254.025 Million cell updates/sec

Title: US-09-736-250-1

Perfect score: 377

Sequence: 1 MKPQPLENQLSLLEKAI.....LSRQEGHSCPPLQPVSV 377

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : PIR 79:*

1: Pirl:*

2: Pirl:*

3: Pirl:*

4: Pirl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	103	27.3	178	2 J80264	cyclin I - human
2	8	2.1	842	2 A87341	sensory box/SGDEF
3	8	2.1	1715	2 G84429	hypothetical prote
4	7	1.9	61	2 D82732	hypothetical prote
5	7	1.9	85	2 G84490	hypothetical prote
6	7	1.9	95	2 D1534	hypothetical prote
7	7	1.9	95	2 C81692	conserved hypotet
8	7	1.9	108	2 D4221	orf4 protein - Aut
9	7	1.9	108	2 C72852	AcOrf-19 protein -
10	7	1.9	110	2 T41765	ACMPV orf19 - Bom
11	7	1.9	113	2 G83745	hypothetical prote
12	7	1.9	123	2 H87603	transcription regu
13	7	1.9	126	2 B69320	conserved hypotet
14	7	1.9	131	2 AD0633	probable secreted
15	7	1.9	154	2 T35544	probable quinolina
16	7	1.9	155	2 G82534	30S ribosomal prot
17	7	1.9	184	2 S85816	RNA-directed DNA p
18	7	1.9	188	2 B82696	cytochrome B561 XF
19	7	1.9	189	2 AB2169	hypothetical prote
20	7	1.9	214	2 T42530	hypothetical prote
21	7	1.9	230	2 C71548	probable ABC trans
22	7	1.9	237	2 D88095	protein f39E9.1 [i
23	7	1.9	238	2 T40721	hypothetical prote
24	7	1.9	238	2 A83233	conserved hypotet
25	7	1.9	242	2 S49462	cyclin - rice
26	7	1.9	269	2 T04394	NBS-LRR type resis
27	7	1.9	284	1 S74516	(adenine-N6,N6-)-d
28	7	1.9	294	2 T05604	hypothetical prote
29	7	1.9	301	2 T37172	probable lysr-fami

hypothetical prote
probable transcrip
hypothetical prote
transcription fact
hypothetical prote
hypothetical prote
prostatic spermine
alcohol dehydrogen
isocitrate dehydro
peroxin-like prot
RING-H2 finger pro
hypothetical prote
aminoalcoholphosph
alpha-1-antiprotei
protein kinase-lik
corticosteroid-bin
unknown protein [i
coenzyme F420 hydr
contrapsin precurs
hypothetical prote
hypothetical prote
hedgehog homolog v
taxadienol acetyl
probable UDP-n-ace
hypothetical prote
tyrosine kinase (f
53K glycoprotein -
hypothetical prote
homeotic protein B
oligopeptide ABC t
plasma hyaluronan-
probable fumarate
hypothetical prote
hypothetical prote
hypothetical prote
translation regula
probable translati
hypothetical prote
hypothetical prote
hypothetical prote
ent-kaurene syntha
hypothetical prote
beta-glucosidase (
probable tail leng
probable tail comp
probable AAA-type
probable tail leng
probable tail leng
probable tail comp
sucrose-phosphate
exodeoxyribonuclea
probable tail leng
probable regulator
chromosome segrega
apical endosomal p
multimerin, endoth
structural mainten
cell surface prote
cystic fibrosis tr
oxfX protein - Esc
25-hydroxyvitamin
splenin - human
thymopoietin - hum
probable photost
phosphoenolpyruvat
puc3A protein - Rh
puc2A protein - Rh
hypothetical prote
hypothetical prote
pepsin B (EC 3.4.2
transcription regu
hypothetical prote
transcription fact
hypothetical prote

103	6	1.6	88	2	A97936	conserved hypotet	176	1.6	123	2	S27937	hypothetical prote
104	6	1.6	93	2	S75571	hypothetical prote	177	1.6	124	2	AD3151	hypothetical prote
105	6	1.6	95	2	S17605	ig heavy chain v r	178	1.6	125	2	F87685	hypothetical prote
106	6	1.6	97	2	S55372	ig heavy chain v r	179	1.6	126	2	S29103	hypothetical prote
107	6	1.6	97	2	S95132	conserved hypotet	180	1.6	127	2	B31807	ig heavy chain v r
108	6	1.6	97	2	AC2732	hypothetical prote	181	1.6	127	2	T43781	hypothetical prote
109	6	1.6	98	2	S21812	ig heavy chain v r	182	1.6	128	2	PN0647	epsN protein - Vib
110	6	1.6	98	2	AB3072	conserved hypotet	183	1.6	129	2	AI1705	hypothetical prote
111	6	1.6	98	2	G98214	hypothetical prote	184	1.6	130	2	C90052	hypothetical prote
112	6	1.6	100	2	A25913	ig heavy chain pre	185	1.6	131	2	E36819	Cl3 protein - rabb
113	6	1.6	100	2	S14490	ig heavy chain v r	186	1.6	132	2	JQ0737	RnpA protein - Mic
114	6	1.6	100	2	B71102	hypothetical prote	187	1.6	134	2	B71354	probable small pro
115	6	1.6	101	2	S03466	ig heavy chain v r	188	1.6	134	2	JC7301	Down syndrome crit
116	6	1.6	102	2	A60674	insulin-like growt	189	1.6	135	2	S31913	ig gamma-2A chain
117	6	1.6	103	2	T28354	hypothetical prote	190	1.6	135	1	D71107	hypothetical prote
118	6	1.6	104	2	B83115	50S ribosomal prot	191	1.6	139	2	F84024	arsenate reductase
119	6	1.6	104	2	F72753	hypothetical prote	192	1.6	139	2	A32456	ig heavy chain pre
120	6	1.6	105	2	B55208	frdb homolog socA2	193	1.6	139	2	A70881	hypothetical prote
121	6	1.6	105	2	T32799	hypothetical prote	194	1.6	139	2	T28243	hypothetical prote
122	6	1.6	106	2	S14489	ig heavy chain v r	195	1.6	141	2	S52446	ig heavy chain v r
123	6	1.6	106	2	S26322	ig heavy chain v r	196	1.6	141	2	H82220	hypothetical prote
124	6	1.6	106	2	C86086	hypothetical prote	197	1.6	142	2	B48648	acetylhydroxy acid
125	6	1.6	107	2	PQ0322	exo-alpha-sialidas	198	1.6	142	2	T36312	hypothetical prote
126	6	1.6	107	2	S14492	ig heavy chain v r	199	1.6	143	2	H64000	hypothetical prote
127	6	1.6	107	2	S14493	ig heavy chain v r	200	1.6	143	2	A54793	ponticulin precurs
128	6	1.6	107	2	S14491	ig heavy chain v r	201	1.6	144	2	S11244	ig gamma-2a chain
129	6	1.6	108	2	S07331	ig heavy chain v r	202	1.6	144	2	B75054	probable endonucle
130	6	1.6	109	2	PH1026	ig heavy chain v r	203	1.6	145	2	S30247	Kin-1 protein - hu
131	6	1.6	109	2	PH1035	ig heavy chain v r	204	1.6	146	2	T26379	hypothetical prote
132	6	1.6	109	2	G82929	ATP synthase C cha	205	1.6	147	2	S53574	probable membrane
133	6	1.6	110	2	S26323	ig heavy chain v r	206	1.6	147	2	C64958	flagellar protein
134	6	1.6	110	2	PH1034	ig heavy chain v r	207	1.6	147	2	A98964	flagellar filij pro
135	6	1.6	111	2	S26324	ig heavy chain v r	208	1.6	147	2	A85812	flagellar filij pro
136	6	1.6	111	2	C69168	conserved hypotet	209	1.6	150	2	S39910	S-receptor kinase
137	6	1.6	111	2	G70521	hypothetical prote	210	1.6	149	2	S75155	hypothetical prote
138	6	1.6	112	2	S11108	ig heavy chain v r	211	1.6	149	2	T49200	hypothetical prote
139	6	1.6	112	2	S11100	ig heavy chain v r	212	1.6	149	2	C81959	probable palin NMA
140	6	1.6	113	2	S11098	ig heavy chain v r	213	1.6	150	2	S31411	S-receptor kinase-
141	6	1.6	113	2	E81138	succinate dehydrog	214	1.6	150	2	E97158	hypothetical prote
142	6	1.6	113	2	S11101	ig heavy chain v r	215	1.6	151	2	F69212	autotrophic growth
143	6	1.6	113	2	D72454	hypothetical prote	216	1.6	152	2	G69487	LSU ribosomal prot
144	6	1.6	114	2	S11099	ig heavy chain v r	217	1.6	152	2	H69129	ribosomal protein
145	6	1.6	114	2	S11104	ig heavy chain v r	218	1.6	153	2	PQ0255	polyprotein (clone
146	6	1.6	114	2	S11106	ig heavy chain v r	219	1.6	153	2	D70345	conserved hypotet
147	6	1.6	114	2	S11105	ig heavy chain v r	220	1.6	154	1	R5WX30	ribosomal protein
148	6	1.6	114	2	S57692	probable membrane	221	1.6	154	2	D64359	ribosomal protein
149	6	1.6	115	2	D84852	hypothetical prote	222	1.6	155	2	C75145	lsu ribosomal prot
150	6	1.6	115	1	HVMS14	ig heavy chain pre	223	1.6	155	2	G71184	probable ribosomal
151	6	1.6	115	2	S11103	ig heavy chain v r	224	1.6	158	2	JC7302	Down syndrome crit
152	6	1.6	115	2	S26470	ig heavy chain v r	225	1.6	158	2	H71229	hypothetical prote
153	6	1.6	115	2	S11107	ig heavy chain v r	226	1.6	162	2	T36686	probable integral
154	6	1.6	115	2	S69592	hypothetical prote	227	1.6	163	2	T48132	hypothetical prote
155	6	1.6	115	2	A25511	conserved hypotet	228	1.6	165	2	B64121	nonheme ferritin h
156	6	1.6	115	2	H75491	hypothetical prote	229	1.6	165	2	F95099	conserved hypotet
157	6	1.6	116	1	GIWS10	ig heavy chain pre	230	1.6	165	2	H97967	conserved hypotet
158	6	1.6	116	2	PL0198	anti-DNA autoantib	231	1.6	165	2	S62563	adaptin complex sm
159	6	1.6	116	2	A33932	ig mu chain precur	232	1.6	166	1	S07369	interleukin-3 prec
160	6	1.6	116	2	S42494	ig heavy chain v r	233	1.6	166	2	S73928	single-stranded DN
161	6	1.6	116	2	S11102	ig heavy chain v r	234	1.6	166	2	I64221	conserved hypotet
162	6	1.6	117	2	S38563	ig heavy chain v r	235	1.6	167	2	JC2336	hypothetical prote
163	6	1.6	117	2	S10111	ig heavy chain v r	236	1.6	168	2	JC6566	interleukin-3 beta
164	6	1.6	117	2	JC2282	ribosomal protein	237	1.6	168	2	AI2865	transcription regu
165	6	1.6	118	2	PQ0266	ig heavy chain v r	238	1.6	168	2	G97642	hypothetical prote
166	6	1.6	118	2	AE1214	hypothetical prote	239	1.6	169	2	D83998	acetyl-CoA carboxy
167	6	1.6	119	2	E33876	carcinoembryonic a	240	1.6	169	2	C95919	probable periplasm
168	6	1.6	119	2	S49467	phosphoribosyl-AMP	241	1.6	170	2	H71454	hypothetical prote
169	6	1.6	120	2	PL0087	ig heavy chain v r	242	1.6	172	2	B56684	acetylhydroxy acid
170	6	1.6	120	2	A87462	hypothetical prote	243	1.6	173	2	T32335	hypothetical prote
171	6	1.6	121	2	S77497	ribosomal protein	244	1.6	174	2	E69213	aspartate carbamoy
172	6	1.6	121	2	T25485	hypothetical prote	245	1.6	174	2	B75013	phosphoribosylamin
173	6	1.6	122	2	A49049	ig heavy chain v r	246	1.6	174	2	C69539	conserved hypotet
174	6	1.6	122	2	A72025	conserved hypotet	247	1.6	175	2	T08948	hypothetical prote
175	6	1.6	122	2	G86597	C7716 hypothetical	248	1.6	177	2	T36367	transcription init

249	6	1.6	177	2	E71138	probable phosphori	322	228	2	E89923	hypothetical prote
250	6	1.6	179	2	A4684	hypothetical prote	323	229	2	E95862	probable transcrip
251	6	1.6	180	2	C75171	ssu ribosomal prot	324	230	2	S75576	ribulose-phosphate
252	6	1.6	181	2	E70209	conserved hypotet	325	230	2	E83554	probable pseudouri
253	6	1.6	181	2	E86654	transcription regu	326	230	2	C72256	rnfB-related prote
254	6	1.6	183	2	D83712	shikimate kinase a	327	231	1	F1SP3	photosystem I chai
255	6	1.6	183	2	G87250	molybdenum cofacto	328	231	2	T20304	hypothetical prote
256	6	1.6	184	2	AC3427	transposase BME114	329	233	2	PV0001	hypothetical prote
257	6	1.6	185	2	G91138	hypothetical prote	330	233	2	F1367	16S pseudouridylat
258	6	1.6	185	2	B85984	hypothetical prote	331	234	2	F86855	conserved hypotet
259	6	1.6	185	2	B65111	17.3 kD protein in	332	234	2	E64434	hypothetical prote
260	6	1.6	185	2	T49611	hypothetical prote	333	235	2	A56757	14-3-3 regulatory
261	6	1.6	185	2	T24375	hypothetical prote	334	235	2	E83752	hypothetical prote
262	6	1.6	186	2	G59667	hypothetical prote	335	235	2	T26489	hypothetical prote
263	6	1.6	186	2	B90548	50S ribosomal prot	336	235	2	E95876	conserved hypotet
264	6	1.6	186	2	F86379	protein F219.28 [337	236	2	AB0681	probable ABC trans
265	6	1.6	186	2	T31951	hypothetical prote	338	237	1	A39017	modulation control
266	6	1.6	186	2	T09296	apolipoprotein III	339	238	2	A81422	probable RNA polym
267	6	1.6	187	1	F0VM53	gag polypeptide -	340	238	2	D75513	L-serine dehydrata
268	6	1.6	187	2	D2501	hypothetical prote	341	239	2	T51270	hypothetical prote
269	6	1.6	187	2	A72737	hypothetical prote	342	240	2	E72740	hypothetical prote
270	6	1.6	189	2	T46076	hypothetical prote	343	241	2	D72751	hypothetical prote
271	6	1.6	189	2	S49743	hypothetical prote	344	242	2	A75023	hypothetical prote
272	6	1.6	189	2	AD2916	transcription regu	345	242	2	H97151	hypothetical prote
273	6	1.6	189	2	G37690	hypothetical prote	346	242	2	AH3537	nta operon transcr
274	6	1.6	190	2	T08258	conserved hypotet	347	243	2	F83429	conserved hypotet
275	6	1.6	190	2	D88957	protein ZK697.8 [1	348	244	2	S38568	transcription init
276	6	1.6	193	2	E70226	conserved hypotet	349	244	2	H96934	uncharacterized me
277	6	1.6	194	2	A52310	hypothetical prote	350	246	2	B96707	hypothetical prote
278	6	1.6	195	2	H96532	hypothetical prote	351	246	2	AF2684	conserved hypotet
279	6	1.6	195	2	G72697	hypothetical prote	352	246	2	S60883	ATP-binding protei
280	6	1.6	196	2	H95023	hypothetical prote	353	247	2	E95207	conserved hypotet
281	6	1.6	196	2	B36980	uncharacterized co	354	247	2	JG0016	epidermal cell dif
282	6	1.6	196	2	A37895	hypothetical prote	355	248	2	B97794	hypothetical prote
283	6	1.6	197	2	A83845	hypothetical prote	356	249	1	S68688	myb-related protei
284	6	1.6	197	2	T24133	hypothetical prote	357	249	2	C70436	conserved hypotet
285	6	1.6	199	2	B86659	hypothetical prote	358	249	2	S38308	SNAP-25 protein -
286	6	1.6	200	2	A86025	probable regulator	359	249	2	S38309	SNAP-25 protein -
287	6	1.6	200	2	H91178	probable transcrip	360	249	2	S37693	cyclin G - mouse
288	6	1.6	200	2	S47740	hypothetical prote	361	249	2	S51621	cyclin G - rat
289	6	1.6	200	2	E89871	hypothetical prote	362	250	2	T04496	hypothetical prote
290	6	1.6	201	2	T29387	hypothetical prote	363	250	2	T31835	conserved hypotet
291	6	1.6	201	2	I38850	LEKX-4 - human	364	251	2	E98072	conserved hypotet
292	6	1.6	202	2	T15874	hypothetical prote	365	252	2	T13588	NADH2 dehydrogenas
293	6	1.6	202	2	E75053	hypothetical prote	366	252	2	E82040	general secretion
294	6	1.6	203	2	T45907	hypothetical prote	367	254	2	D82963	conserved hypotet
295	6	1.6	204	2	T44357	hypothetical prote	368	255	2	G97173	chemotaxis protein
296	6	1.6	206	2	T40519	BAG-family molecu	369	256	2	H83291	conserved hypotet
297	6	1.6	207	1	LNCHL	hepatic lectin - c	370	256	2	G02523	cyclin G - human
298	6	1.6	209	2	C86736	two-component syst	371	258	2	T09031	hypothetical prote
299	6	1.6	209	2	G70091	ABC transporter (A	372	259	2	D82331	peptidyl-prolyl ci
300	6	1.6	210	2	G75180	hypothetical prote	373	259	2	T36003	hypothetical prote
301	6	1.6	211	2	F83998	mutants block spor	374	260	2	S76509	hypothetical prote
302	6	1.6	212	2	G90056	hypothetical prote	375	260	2	E87431	hypothetical prote
303	6	1.6	212	2	S31707	floral homeotic pr	376	261	2	S20610	calpastatin - mous
304	6	1.6	213	2	A13452	glycerol metabolis	377	261	2	A82106	flagellar L-ring p
305	6	1.6	214	2	F72664	superoxide dismuta	378	261	2	T09075	hypothetical prote
306	6	1.6	216	2	A71445	hypothetical prote	379	262	2	I49361	natural killer cel
307	6	1.6	216	2	T37472	fibroblast growth	380	262	2	A45813	T-cell surface gly
308	6	1.6	217	2	B64092	butyrate-acetoacet	381	262	2	D97466	probable repressor
309	6	1.6	217	2	F83196	probable two-compo	382	264	2	T02174	probable alcohol d
310	6	1.6	217	2	T33926	hypothetical prote	383	264	2	E95410	probable ABC trans
311	6	1.6	219	2	AG0333	heme exporter prot	384	264	2	T32387	hypothetical prote
312	6	1.6	219	2	S22276	ribosomal protein	385	265	2	T27673	hypothetical prote
313	6	1.6	220	1	S22516	S-allele-associate	386	266	2	I49050	Ly-49E-GE antigen
314	6	1.6	222	2	A46658	calcium channel pr	387	267	2	H83426	3'-phosphoadenosin
315	6	1.6	222	2	S30728	calcium channel pr	388	267	2	A75131	hypothetical prote
316	6	1.6	223	2	F83034	urease accessory p	389	267	2	I55686	LGJ-1 - mouse
317	6	1.6	224	2	S61386	icm1 protein - leg	390	267	2	I49053	Ly-49G.2 antigen -
318	6	1.6	224	2	D87236	conserved membrane	391	267	2	A71087	hypothetical prote
319	6	1.6	227	2	T11329	H4-transporting tw	392	268	2	S08229	chlorophyll a/b-bi
320	6	1.6	227	2	F90616	ATP synthase F0 ch	393	268	2	S00553	MSS18 protein - ye
321	6	1.6	227	2	F90618	ATP synthase F0 ch	394	269	1	WZB524	gene 24 protein -

395	6	1.6	269	2	A70719	probable enoyl-coA	468	6	1.6	302	2	B38163	cobV protein - Pse
396	6	1.6	269	2	T37798	probable coiled-co	469	6	1.6	302	2	T27602	hypothetical prote
397	6	1.6	269	2	S58439	transcription fact	470	6	1.6	303	2	F98284	3-hydroxybutyryl-C
398	6	1.6	270	2	T46961	molybdenum cofacto	471	6	1.6	303	2	AC2399	3-hydroxybutyryl-C
399	6	1.6	270	2	T50952	transposase relate	472	6	1.6	303	2	T00969	probable mitochond
400	6	1.6	272	2	E64182	cysZ protein - Hae	473	6	1.6	303	2	T16004	hypothetical prote
401	6	1.6	272	2	T32438	hypothetical prote	474	6	1.6	304	2	S02284	potassium channel
402	6	1.6	272	2	G75520	hypothetical prote	475	6	1.6	304	2	G82288	conserved hypotet
403	6	1.6	277	2	AF2404	hypothetical prote	476	6	1.6	304	2	D86998	probable secreted
404	6	1.6	279	2	A11189	B. subtilis ycgQ p	477	6	1.6	306	2	AE1394	conserved hypotet
405	6	1.6	279	2	AB1548	B. subtilis ycgQ p	478	6	1.6	306	2	AH1769	conserved hypotet
406	6	1.6	279	2	T25587	hypothetical prote	479	6	1.6	307	1	G64717	pyridoxal phosphat
407	6	1.6	279	2	E37097	hypothetical prote	480	6	1.6	307	1	ACBPT7	capsid assembly pr
408	6	1.6	279	2	A89920	methyl-accepting c	481	6	1.6	307	2	F86865	conserved hypotet
409	6	1.6	280	2	H69228	conserved hypotet	482	6	1.6	307	2	C75584	hypothetical prote
410	6	1.6	280	2	I49052	fumarate hydratase	483	6	1.6	307	2	S47244	C-raf protein - ze
411	6	1.6	280	2	S46059	Ly-49G.1 antigen -	484	6	1.6	308	2	AE2829	hypothetical prote
412	6	1.6	281	2	A11858	probable membrane	485	6	1.6	309	2	C81317	hypothetical prote
413	6	1.6	281	2	H95085	chorismate mutase/	486	6	1.6	309	2	T50797	probable glycosylt
414	6	1.6	281	2	D97953	conserved hypotet	487	6	1.6	310	2	F0MVFB	hypothetical prote
415	6	1.6	282	2	S29040	conserved hypotet	488	6	1.6	310	2	A98939	gag polyprotein -
416	6	1.6	282	2	T35000	Na+-transporting A	489	6	1.6	310	2	E85787	probable kinase [i
417	6	1.6	282	2	F96946	probable protein a	490	6	1.6	310	2	H87058	probable kinase Z2
418	6	1.6	282	2	C70390	methyl-accepting c	491	6	1.6	310	2	S07522	l-asparaginase/U-9
419	6	1.6	283	2	S45458	formate dehydrogen	492	6	1.6	311	2	AH0867	capsid assembly pr
420	6	1.6	284	2	A11423	PET8 protein - Yea	493	6	1.6	311	2	H69513	transcription acti
421	6	1.6	284	2	G90671	B. subtilis DNA-bi	494	6	1.6	311	2	G81402	5-methyltetrahydro
422	6	1.6	284	2	C85522	probable ARAC-type	495	6	1.6	312	2	T31834	oxidoreductase Cj0
423	6	1.6	284	2	A64757	probable ARAC-type	496	6	1.6	312	2	D69336	hypothetical prote
424	6	1.6	286	2	B90156	Ykgp protein - Esc	497	6	1.6	313	2	C69803	conserved hypotet
425	6	1.6	287	2	T42968	hypothetical prote	498	6	1.6	313	2	G95883	hypothetical prote
426	6	1.6	288	2	G64102	hypothetical prote	499	6	1.6	314	2	AG0485	probable ABC trans
427	6	1.6	288	2	JC4011	phosphatidate cyti	500	6	1.6	315	2	G88485	2-dehydro-3-deoxyg
428	6	1.6	288	2	I58372	cyclin D2 - rat	501	6	1.6	315	2	H82128	protein F23F12.1 [
429	6	1.6	288	2	S74895	cyclin D2 - rat	502	6	1.6	316	2	B72499	3-oxoacyl-(acyl-ca
430	6	1.6	288	2	S40173	hypothetical prote	503	6	1.6	316	2	AG0121	probable carbamate
431	6	1.6	289	2	A42822	ExoU protein - Rhi	504	6	1.6	316	2	S75096	probable sideropho
432	6	1.6	289	2	A41984	cyclin D2 - human	505	6	1.6	316	2	D97865	hypothetical prote
433	6	1.6	289	2	S39721	cyclin D2 - mouse	506	6	1.6	316	2	D79865	hypothetical prote
434	6	1.6	289	2	E81259	spore coat polysac	507	6	1.6	316	2	AG2977	hypothetical prote
435	6	1.6	291	2	JC4579	hypothetical prote	508	6	1.6	316	2	B96749	hypothetical prote
436	6	1.6	291	2	S57925	cyclin D2 - chicke	509	6	1.6	316	2	C96020	probable sugar upt
437	6	1.6	291	2	H89894	cyclin D2 - Africa	510	6	1.6	317	2	C86479	probable annexin p
438	6	1.6	291	2	A86681	conserved hypotet	511	6	1.6	317	2	G82635	methanol dehydrog
439	6	1.6	291	2	D82491	hypothetical prote	512	6	1.6	317	2	S76961	hypothetical prote
440	6	1.6	292	2	D98096	hypothetical prote	513	6	1.6	317	2	T32101	hypothetical prote
441	6	1.6	292	2	B35232	conserved hypotet	514	6	1.6	319	2	B98305	hypothetical prote
442	6	1.6	292	2	A64634	conserved hypotet	515	6	1.6	319	2	H69882	deacetylase homolo
443	6	1.6	292	2	D86670	hypothetical prote	516	6	1.6	320	2	S73995	probable lipoprote
444	6	1.6	294	2	T49271	pseudouridine synt	517	6	1.6	320	2	H71259	probable membrane
445	6	1.6	294	2	S23095	CELL DIVISION CONT	518	6	1.6	321	2	T11274	NADH2 dehydrogenas
446	6	1.6	294	2	G33962	protein kinase (EC	519	6	1.6	322	1	D64937	probable sugar kin
447	6	1.6	294	2	AB0772	hypothetical prote	520	6	1.6	322	2	A97657	ferrichrome ABC tr
448	6	1.6	294	2	C86802	hypothetical prote	521	6	1.6	322	2	AI2880	ABC transporter, m
449	6	1.6	295	2	T20629	hypothetical prote	522	6	1.6	322	2	S42426	aspartate-semialde
450	6	1.6	295	2	G02401	hypothetical prote	523	6	1.6	323	2	S27596	replication-associ
451	6	1.6	296	2	F71336	cyclin G1 - human	524	6	1.6	324	2	S75735	probable malate de
452	6	1.6	296	2	B75555	probable glutamate	525	6	1.6	324	2	F70609	hypothetical prote
453	6	1.6	296	2	D71891	probable lipase/es	526	6	1.6	326	2	G70760	hypothetical prote
454	6	1.6	296	2	B84527	hypothetical prote	527	6	1.6	326	2	A83273	asparaginase (EC 3
455	6	1.6	297	2	H75449	hypothetical prote	528	6	1.6	326	2	S28706	fatty acid biosynt
456	6	1.6	297	2	AC1706	riboflavin kinase/	529	6	1.6	326	2	H95867	hypothetical prote
457	6	1.6	297	2	AD1335	hypothetical prote	530	6	1.6	327	2	AI0515	thiamin-binding pe
458	6	1.6	298	1	A69879	conserved hypotet	531	6	1.6	327	2	S67168	probable membrane
459	6	1.6	298	2	G89898	hypothetical prote	532	6	1.6	328	2	A99416	alcohol dehydrogen
460	6	1.6	298	2	T25695	hypothetical prote	533	6	1.6	328	2	S29925	cyclin 2 - alfalfa
461	6	1.6	299	2	D81067	hypothetical prote	534	6	1.6	328	2	A70629	probable glnH prot
462	6	1.6	300	1	WMLJBI	bel-1 protein - hu	535	6	1.6	329	2	T31716	hypothetical prote
463	6	1.6	300	1	S75379	MU1232 protein hom	536	6	1.6	330	2	B88990	protein C36C5.11 [
464	6	1.6	300	2	D87609	conserved hypotet	537	6	1.6	331	2	T08257	cytochrome d ubiqu
465	6	1.6	301	2	G64339	formylmethanofuran	538	6	1.6	331	2	F71943	high-affinity nick
466	6	1.6	301	2	F72029	phosphatidylserine	539	6	1.6	331	2	A87652	hypothetical prote
467	6	1.6	301	2	E86595	phosphatidylserine	540	6	1.6	332	2	F97071	phosphoribosylamin

541	6	1.6	332	2	B82607	conserved hypotet	614	1.6	370	2	S68777	vasopressin recept
542	6	1.6	333	2	B72306	hypothetical prote	615	1.6	370	2	AG3073	hypothetical prote
543	6	1.6	334	2	S13734	licheninase (EC 3	616	1.6	370	2	B98213	probable maltose/m
544	6	1.6	335	1	A96810	unknown protein T1	617	1.6	373	2	T34743	hypothetical prote
545	6	1.6	335	1	A49897	anthranilate phosp	618	1.6	373	2	AF2939	oxidoreductase Atu
546	6	1.6	335	2	T31561	hypothetical prote	619	1.6	374	2	T32207	hypothetical prote
547	6	1.6	335	2	T31559	hypothetical prote	620	1.6	375	2	C82842	hypothetical prote
548	6	1.6	335	2	T31560	hypothetical prote	621	1.6	375	2	F88947	protein C39P7.2 [1
549	6	1.6	335	2	T05722	licheninase (EC 3	622	1.6	375	2	T33778	hypothetical prote
550	6	1.6	336	2	AE2922	zinc-binding dehyd	623	1.6	376	2	A55874	DNA-directed DNA p
551	6	1.6	336	2	F97696	hypothetical zinc-	624	1.6	376	2	D71830	hypothetical prote
552	6	1.6	336	2	E75040	hydrogenase expres	625	1.6	376	2	T47519	hypothetical prote
553	6	1.6	336	2	D71121	probable hydrogena	626	1.6	376	2	T49255	protein kinase-lik
554	6	1.6	336	2	S42382	hypothetical prote	627	1.6	377	2	AD3363	conserved hypotet
555	6	1.6	337	2	T32099	hypothetical prote	628	1.6	377	2	A64685	hypothetical prote
556	6	1.6	337	2	C97607	hypothetical prote	629	1.6	377	2	T49604	hypothetical prote
557	6	1.6	337	2	T27615	hypothetical prote	630	1.6	378	2	T18486	hypothetical prote
558	6	1.6	338	1	R5HS3L	ribosomal protein	631	1.6	379	1	S43263	ubiquinol-cytochro
559	6	1.6	338	2	E95251	ornithine carbanoy	632	1.6	379	1	S43264	ubiquinol-cytochro
560	6	1.6	338	2	B98116	ornithine carbanoy	633	1.6	379	2	T20394	hypothetical prote
561	6	1.6	338	2	A83389	probable permease	634	1.6	379	2	T03608	chilling-induced p
562	6	1.6	338	2	T47427	hypothetical prote	635	1.6	379	2	H69478	NADH2 dehydrogenas
563	6	1.6	338	2	H69022	hypothetical prote	636	1.6	379	2	T13758	NADH2 dehydrogenas
564	6	1.6	339	1	F69852	L-iditol 2-dehydro	637	1.6	380	2	S64417	cyclin B5 - yeast
565	6	1.6	339	2	T24725	hypothetical prote	638	1.6	380	2	A98343	hypothetical prote
566	6	1.6	340	2	A72338	transcription regu	639	1.6	381	2	T13701	NADH2 dehydrogenas
567	6	1.6	342	2	A10286	pap operon transcr	640	1.6	381	2	AC1432	DNA polymerase III
568	6	1.6	342	2	B70812	hypothetical prote	641	1.6	381	2	AC1433	DNA polymerase III
569	6	1.6	344	1	D64620	GTP cyclohydrolase	642	1.6	381	2	G97114	uncharacterized me
570	6	1.6	344	2	C71834	GTP cyclohydrolase	643	1.6	383	2	E75589	hypothetical prote
571	6	1.6	345	2	E70794	probable asd prote	644	1.6	383	2	S66729	probable membrane
572	6	1.6	345	2	S51548	killer toxin K28 -	645	1.6	384	1	W2WL41	E2 protein - human
573	6	1.6	345	2	T37139	hypothetical prote	646	1.6	384	2	E83040	hypothetical prote
574	6	1.6	345	2	T25590	hypothetical prote	647	1.6	385	2	E83414	conserved hypotet
575	6	1.6	345	2	AF2596	hypothetical prote	648	1.6	385	2	T20918	hypothetical prote
576	6	1.6	346	2	H97378	malate dehydrogena	649	1.6	387	2	A53586	albumin-binding pr
577	6	1.6	346	2	C88961	probable l-malate	650	1.6	387	2	G82983	probable MFS trans
578	6	1.6	346	2	B75439	protein P59A7.5 [1	651	1.6	389	2	D64333	pyruvate synthase
579	6	1.6	347	2	T50990	hypothetical prote	652	1.6	389	2	S53975	probable membrane
580	6	1.6	349	2	F69205	3-hydroxy-3-methyl	653	1.6	389	2	A25881	lysostaphin precu
581	6	1.6	349	2	T30093	hypothetical prote	654	1.6	389	2	E95422	probable transmemb
582	6	1.6	349	2	S74439	iron(III) dicitrat	655	1.6	390	1	C64996	probable hydro-ly
583	6	1.6	349	2	C59107	hypothetical 39K p	656	1.6	390	2	D85865	probable enzyme Z3
584	6	1.6	349	2	JH0235	hypothetical prote	657	1.6	390	2	E91021	probable enzyme [1
585	6	1.6	350	2	T40466	probable acetyltra	658	1.6	390	2	D69757	multidrug-efflux t
586	6	1.6	350	2	B42230	conserved hypotet	659	1.6	390	2	D83057	probable aminotran
587	6	1.6	351	2	F87199	aspartate semialde	660	1.6	390	2	T09563	hypothetical prote
588	6	1.6	351	2	AB2963	endoglucanase (imp	661	1.6	391	2	A44063	paired box transcr
589	6	1.6	351	2	C98320	hypothetical prote	662	1.6	391	2	S74688	hypothetical prote
590	6	1.6	353	2	E98142	hypothetical prote	663	1.6	392	2	T13722	NADH2 dehydrogenas
591	6	1.6	353	2	AF3145	hypothetical prote	664	1.6	392	2	T30026	hypothetical prote
592	6	1.6	353	2	E95885	probable iron ABC	665	1.6	392	2	G75056	dehydrogenase PAB0
593	6	1.6	355	2	H71812	hypothetical prote	666	1.6	392	2	F81676	heat shock gene re
594	6	1.6	355	2	B64707	hypothetical prote	667	1.6	393	1	XXALAE	acetyl-CoA C-acety
595	6	1.6	355	2	T15471	hypothetical prote	668	1.6	393	2	T12608	NADH2 dehydrogenas
596	6	1.6	355	2	A37348	HD-GYP domain cont	669	1.6	393	2	T13501	NADH2 dehydrogenas
597	6	1.6	356	2	C70025	multidrug-efflux t	670	1.6	393	2	T13565	NADH2 dehydrogenas
598	6	1.6	356	2	G95875	probable spermidin	671	1.6	393	2	T13775	NADH2 dehydrogenas
599	6	1.6	357	2	H81450	chorismate mutase	672	1.6	393	2	T12630	NADH2 dehydrogenas
600	6	1.6	359	2	H65201	p.s system, fructo	673	1.6	393	2	T12609	NADH2 dehydrogenas
601	6	1.6	360	2	A85016	hypothetical prote	674	1.6	393	2	S62335	171-7 protein - ir
602	6	1.6	361	2	B84716	hypothetical prote	675	1.6	394	2	E83213	NADH2 dehydrogenas
603	6	1.6	361	2	T17282	hypothetical prote	676	1.6	394	2	E83213	probable acyl-CoA
604	6	1.6	363	2	AC0244	conserved hypotet	677	1.6	394	2	A70469	aspartate transami
605	6	1.6	364	2	D86253	hypothetical prote	678	1.6	394	2	T19028	hypothetical prote
606	6	1.6	365	2	S21056	recf protein - pse	679	1.6	394	2	T32042	hypothetical prote
607	6	1.6	366	2	F72703	probable heat shoc	680	1.6	395	2	T13756	NADH2 dehydrogenas
608	6	1.6	367	2	T20914	hypothetical prote	681	1.6	395	2	T13779	NADH2 dehydrogenas
609	6	1.6	368	2	E69796	two-component resp	682	1.6	395	2	S52423	protein kinase (EC
610	6	1.6	369	2	G83644	RecF protein PA000	683	1.6	395	2	T29379	hypothetical prote
611	6	1.6	369	2	T36633	probable heavy met	684	1.6	395	2	C88955	protein K04F1.10 [
612	6	1.6	369	2	AD0555	probable ATP-bindi	685	1.6	395	2	AD0678	probable membrane
613	6	1.6	369	2	T46950	probable ATPase co	686	1.6	395	2	E90896	probable transport

687	6	1.6	395	2	B85721	probable transport	760	423	2	T14531	S-locus-specific g
688	6	1.6	395	2	A64908	membrane protein y	761	423	2	JC7677	allatostatin recep
689	6	1.6	395	2	B81358	transmembrane tran	762	424	1	XUHUAB	acetyl-CoA C-acylt
690	6	1.6	396	2	A13554	xylose transport s	763	424	2	S71798	MAD-3 protein homo
691	6	1.6	397	2	T39184	bomaphin - human	764	425	2	B81236	nitrogen assimilat
692	6	1.6	397	2	T19029	hypothetical prote	765	425	2	D82009	probable two-compo
693	6	1.6	397	2	T37955	hypothetical prote	766	426	2	F82139	ATP-dependent Clp
694	6	1.6	398	1	W2WL42	E2 protein - human	767	426	2	B87385	chromate-transport
695	6	1.6	398	2	B86353	protein F2E2.6 [im	768	426	2	B84164	neutral proteinase
696	6	1.6	398	2	J00356	phospholipase C (E	769	426	2	D71552	probable oligopept
697	6	1.6	398	2	B49231	phospholipase C, a	770	428	2	G69988	NDF-sugar denydrog
698	6	1.6	398	2	A30565	phospholipase C (E	771	429	2	B84985	hypothetical prote
699	6	1.6	399	2	T22168	hypothetical prote	772	429	2	F71713	glycerol-3-phospha
700	6	1.6	399	2	I38901	JNK-activating pro	773	429	2	D87375	lpsE protein [impo
701	6	1.6	399	2	B64488	hypothetical prote	774	429	2	T14534	S-locus-specific g
702	6	1.6	400	2	I50219	connexin 45.6 - ch	775	431	2	H82237	histidinol dehydro
703	6	1.6	400	2	C30791	probable integrase	776	431	2	B64454	ribulose-bisphosph
704	6	1.6	400	2	B85600	probable P4-family	777	431	2	B81927	probable oxidoredu
705	6	1.6	400	2	C97623	aspartate aminotra	778	431	2	G81179	oxidoreductase, pr
706	6	1.6	400	2	AC2846	aspartate aminotra	779	431	2	AH1027	probable pilus ass
707	6	1.6	401	1	B35177	chromate resistanc	780	432	2	A69056	hypothetical prote
708	6	1.6	401	2	G82737	argininosuccinate	781	432	1	ITHUC	alpha-1-antichymot
709	6	1.6	401	2	D85030	hypothetical prote	782	433	2	AE2658	glycolate oxidase
710	6	1.6	402	2	A87278	flagellin modifika	783	433	2	B97440	glycolate oxidase
711	6	1.6	402	2	T15490	hypothetical prote	784	434	2	T09706	cyclin cymE2, B-t
712	6	1.6	403	2	B95991	probable transcrip	785	435	1	S65982	transport protein
713	6	1.6	405	2	A39088	alpha-1-antiprotei	786	435	2	H75443	aspartyl-tRNA synt
714	6	1.6	405	2	T31912	hypothetical prote	787	435	2	S67205	probable membrane
715	6	1.6	405	2	A96917	probable permease	788	437	1	TVMSRF	protein kinase A-r
716	6	1.6	405	2	AD2164	hypothetical prote	789	437	2	S46613	2e5 proteasome reg
717	6	1.6	406	1	JC5041	fosmidomycin resis	790	437	2	A49425	Sonic hedgehog pro
718	6	1.6	406	2	A97986	aminotripeptidase	791	437	2	A36372	membrane transport
719	6	1.6	406	2	S24788	cyclin A - bovine	792	438	2	D84331	hypothetical prote
720	6	1.6	406	2	AH0563	fosmidomycin resis	793	438	2	D64065	exodeoxyribonuclea
721	6	1.6	406	2	H85545	fosmidomycin resis	794	440	2	JC2532	secretin receptor
722	6	1.6	406	2	D90635	fosmidomycin resis	795	440	2	AF0615	killing factor Kic
723	6	1.6	406	2	H73215	conserved hypothet	796	440	2	S43911	mukF protein - Esc
724	6	1.6	407	2	C95116	peptidase t [impor	797	440	2	E90754	mukF protein [impo
725	6	1.6	407	1	J80759	membrane dipeptida	798	440	2	C85618	mukF protein (kill
726	6	1.6	409	2	C82072	D-3-phosphoglycera	799	440	2	B75044	hypothetical prote
727	6	1.6	409	2	C82644	transcription regu	800	440	2	S77194	hypothetical prote
728	6	1.6	409	2	S47440	secy protein - red	801	441	2	C95307	probable transport
729	6	1.6	409	2	E91246	probable L-sorbose	802	443	2	AE0458	X-Pro dipeptidase
730	6	1.6	410	1	S18442	membrane dipeptida	803	444	2	T01721	hypothetical prote
731	6	1.6	410	1	S27204	membrane dipeptida	804	445	2	T49924	embryogenic callus
732	6	1.6	410	1	S33757	membrane dipeptida	805	445	2	S44541	hypothetical prote
733	6	1.6	410	2	S75695	hypothetical prote	806	445	2	A56024	GDP dissociation i
734	6	1.6	410	2	S50151	L-sorbose 1-phosph	807	445	2	C56956	GDP dissociation i
735	6	1.6	411	2	A82452	tryptophan-specifi	808	445	2	B54091	rab GDP dissociati
736	6	1.6	411	2	C64052	NADH2 dehydrogenas	809	445	2	E72674	hypothetical prote
737	6	1.6	413	1	S03631	homeotic protein S	810	445	2	S36039	MAP kinase activat
738	6	1.6	413	2	H75628	hypothetical prote	811	447	2	B83015	heat shock protein
739	6	1.6	413	2	B86094	probable L-sorbose	812	447	2	T17299	hypothetical prote
740	6	1.6	414	2	D84111	uracil transport p	813	449	2	T49125	hypothetical prote
741	6	1.6	414	2	A84604	hypothetical prote	814	450	2	T37628	glycerol dehydroge
742	6	1.6	414	2	H84596	hypothetical prote	815	452	2	T43278	cadmium resistanc
743	6	1.6	415	2	D85061	probable adenosine	816	453	2	AG2117	hypothetical prote
744	6	1.6	416	2	S33473	interleukin-1 rece	817	454	2	T47127	glutamate-ammonia
745	6	1.6	418	2	A90556	grp-binding protei	818	454	2	H86231	hypothetical prote
746	6	1.6	418	2	A46226	somatostatin recep	819	455	2	AH0208	probable transport
747	6	1.6	418	2	AE2462	hypothetical prote	820	455	2	H71028	hypothetical prote
748	6	1.6	419	2	G71311	probable phosphogl	821	456	2	T24442	hypothetical prote
749	6	1.6	419	2	F36788	hypothetical prote	822	456	2	T49192	hypothetical prote
750	6	1.6	419	2	C81179	spermidine/putresc	823	457	2	B84725	probable glucosylt
751	6	1.6	420	2	B97843	glycine hydroxymet	824	457	2	S39079	puff C-8 protein -
752	6	1.6	420	2	C72774	probable cleavage	825	457	2	A54694	MAP kinase activat
753	6	1.6	421	2	AF3316	aspartate transami	826	458	2	AC1173	amino acid transpo
754	6	1.6	421	2	AF1314	hypothetical prote	827	458	2	AD1530	amino acid transpo
755	6	1.6	421	2	AF1686	hypothetical prote	828	458	2	D70410	cytosolic axial fi
756	6	1.6	421	2	D69643	imidazole-5-prop	829	459	2	H96715	hypothetical prote
757	6	1.6	421	2	C64320	probable membrane	830	459	2	AF1197	two-component sens
758	6	1.6	422	2	S37280	cyclin A - mouse	831	459	2	AI1172	two-component sens
759	6	1.6	422	2	S38501	cyclin A2 - mouse	832	461	2	T05332	probable cytochrom

833	6	1.6	461	2	JN0097	secreted 45K prote	906	1.6	512	2	S23355	alpha-amylase (EC
834	6	1.6	462	2	A33170	tube protein - fru	907	1.6	512	2	S06115	alpha-amylase (EC
835	6	1.6	462	2	AH1017	probable integral	908	1.6	512	2	H87297	thiamin-pyrophosph
836	6	1.6	463	2	G97300	aspartyl/asparagin	909	1.6	513	2	D97665	modr protein homol
837	6	1.6	463	2	T29442	hypothetical prote	910	1.6	513	2	S58200	probable membrane
838	6	1.6	464	2	T48339	hypothetical prote	911	1.6	519	2	T43756	ATPase subunit 1 [
839	6	1.6	464	2	F89828	conserved hypotbet	912	1.6	519	2	S17783	tachykinin recepto
840	6	1.6	465	1	JC1318	triacylglycerol li	913	1.6	522	2	H72267	conserved hypotbet
841	6	1.6	465	2	A83046	probable amino aci	914	1.6	523	2	T22484	hypothetical prote
842	6	1.6	467	2	S08618	modulation protein	915	1.6	523	2	T51475	RGA-like protein -
843	6	1.6	467	2	S71797	MAD-2 protein homo	916	1.6	523	2	G96777	hypothetical prote
844	6	1.6	468	2	S51583	hypothetical prote	917	1.6	524	1	GVNVCV	spike glycoprotein
845	6	1.6	469	1	NMIV27	exo-alpha-sialidas	918	1.6	524	2	T14870	hypothetical prote
846	6	1.6	469	1	NMIVH3	exo-alpha-sialidas	919	1.6	526	2	T29484	hypothetical prote
847	6	1.6	469	1	NMIVN2	exo-alpha-sialidas	920	1.6	526	2	S22811	hypothetical prote
848	6	1.6	469	1	NMIV2	exo-alpha-sialidas	921	1.6	532	2	T15354	hypothetical prote
849	6	1.6	469	2	JQ1644	probable MRSA prot	922	1.6	532	2	A57173	oculocutaneous alb
850	6	1.6	469	2	D72722	hypothetical prote	923	1.6	533	2	A70464	D-3-phosphoglycera
851	6	1.6	469	2	A99656	hypothetical prote	924	1.6	533	2	S53320	(N-acetylneuraminy
852	6	1.6	471	2	H71957	probable outer mem	925	1.6	535	2	B72268	conserved hypotbet
853	6	1.6	471	2	S41407	hypothetical prote	926	1.6	536	2	H72268	conserved hypotbet
854	6	1.6	471	2	B72314	hypothetical prote	927	1.6	536	2	A84474	hypothetical prote
855	6	1.6	473	2	T39028	citrate synthase p	928	1.6	537	1	FOMVGV	gag polyprotein -
856	6	1.6	473	2	G97033	beta-glucosidase f	929	1.6	537	2	C90389	conserved hypotbet
857	6	1.6	474	2	AC0402	conserved hypotbet	930	1.6	539	2	T03469	probable hydrogena
858	6	1.6	475	2	JN0578	p-Aminobenzoic aci	931	1.6	541	2	H87532	transporter, proba
859	6	1.6	476	2	S59339	proline oxidase -	932	1.6	543	2	C90506	hypothetical prote
860	6	1.6	477	2	C85361	hypothetical prote	933	1.6	543	2	C86212	hypothetical prote
861	6	1.6	478	2	H71345	probable polynucle	934	1.6	545	2	S28117	gas-vesicle operon
862	6	1.6	479	2	A55382	nicotinic acetylch	935	1.6	547	2	AB2639	pH adaptation potass
863	6	1.6	479	2	S67202	probable membrane	936	1.6	547	2	T45635	hypothetical prote
864	6	1.6	479	2	T34348	hypothetical prote	937	1.6	548	2	T30369	DNA ligase-like pr
865	6	1.6	480	2	S01079	lysostaphin precur	938	1.6	548	2	AD0287	peptide transport
866	6	1.6	481	2	T15440	hypothetical prote	939	1.6	548	2	C97421	phad protein (X933
867	6	1.6	482	2	S08384	modulation protein	940	1.6	548	2	S52735	Cw17R protein - mo
868	6	1.6	482	2	S10133	cysteine-trna liga	941	1.6	550	2	G95359	Probable ABC trans
869	6	1.6	483	1	S76165	modulation protein	942	1.6	551	2	AC2376	hypothetical prote
870	6	1.6	484	2	AG2889	hypothetical prote	943	1.6	551	2	H98306	hypothetical prote
871	6	1.6	485	2	G83359	hypothetical prote	944	1.6	553	2	G83786	glycerol-3-phospha
872	6	1.6	485	2	T19853	hypothetical prote	945	1.6	553	2	C84920	hypothetical prote
873	6	1.6	487	2	T38641	probable metal tra	946	1.6	553	2	G81181	electron transfer
874	6	1.6	488	2	D70876	probable polyketid	947	1.6	555	2	E87576	choline dehydrogen
875	6	1.6	488	2	T30914	xylan 1,4-beta-xyl	948	1.6	557	2	S56292	hypothetical prote
876	6	1.6	489	1	NMBEF1	UL41 protein - hum	949	1.6	560	2	S27387	interferon alpha r
877	6	1.6	491	1	A69398	MJ0100 protein hom	950	1.6	563	2	AH1245	DNA repair and gen
878	6	1.6	491	1	S24354	p53-binding protei	951	1.6	563	2	AD1608	DNA repair and gen
879	6	1.6	492	2	A35354	UL 41 protein - hu	952	1.6	564	2	S41974	DNA ligase (ATP) (
880	6	1.6	493	2	T48630	high affinity nitr	953	1.6	565	2	S73707	Na(+) translocatin
881	6	1.6	494	2	F89810	NADH dehydrogenase	954	1.6	567	2	A33974	membrane transport
882	6	1.6	494	2	D64944	probable permease	955	1.6	568	2	E75502	threonine ammonia-
883	6	1.6	494	2	F85794	probable transport	956	1.6	569	2	T11357	NADH2 dehydrogenas
884	6	1.6	494	2	B90946	probable transport	957	1.6	569	2	B84904	probable laccase (
885	6	1.6	494	2	T08751	hypothetical prote	958	1.6	569	2	S47277	gp88 protein - mur
886	6	1.6	495	1	S77406	protein kinase pkn	959	1.6	570	2	T38489	helicase - fission
887	6	1.6	495	2	A75608	aldehyde dehydroge	960	1.6	570	2	G72595	hypothetical prote
888	6	1.6	495	2	C84089	hypothetical prote	961	1.6	571	2	C71528	probable pts pep p
889	6	1.6	495	2	C83598	hypothetical prote	962	1.6	572	2	T29880	hypothetical prote
890	6	1.6	496	2	E83849	spore germination	963	1.6	573	2	C84645	hypothetical prote
891	6	1.6	496	2	T48547	diaminopimelate de	964	1.6	575	2	B64174	hypothetical prote
892	6	1.6	496	2	T09936	hypothetical prote	965	1.6	576	2	AE0409	sulfite reductase
893	6	1.6	498	2	AF3279	malonate-semialden	966	1.6	578	2	S51379	probable phosphoes
894	6	1.6	499	2	C70405	hypothetical prote	967	1.6	579	2	A56740	spem-egg recognit
895	6	1.6	499	2	B85507	hypothetical prote	968	1.6	580	2	S72211	N-acetyl-beta-D-gl
896	6	1.6	500	1	JC5819	cytochrome P450 2D	969	1.6	581	2	G71520	proline-trna ligas
897	6	1.6	504	2	T37164	probable monooxyge	970	1.6	581	2	T31745	hypothetical prote
898	6	1.6	505	2	C86443	unknown protein li	971	1.6	583	2	T07848	pectinesterase (EC
899	6	1.6	506	2	AD3338	cobyrnic acid synth	972	1.6	584	2	E71643	poly-beta-hydroxyb
900	6	1.6	506	2	F88954	protein K04Fl.14 [973	1.6	584	2	E72308	hypothetical prote
901	6	1.6	509	2	S46314	hydroxymethylgluta	974	1.6	585	2	G96731	probable phosphogl
902	6	1.6	510	2	T20276	hypothetical prote	975	1.6	585	2	G81920	probable electron
903	6	1.6	511	1	IKECB8	colicin B - Escher	976	1.6	585	2	AE3240	chromosome partiti
904	6	1.6	511	2	G90321	hypothetical prote	977	1.6	588	2	AC0169	conserved hypotbet
905	6	1.6	511	2	T26124	hypothetical prote	978	1.6	588	2	I37202	B-CAM protein - hu

979 1.6 589 2 D84530 probable Tail-like
 980 1.6 590 2 A25680 nuclear histone-bi
 981 1.6 591 2 F69901 DNA helicase recQ
 982 1.6 592 2 T13742 hypothetical prote
 983 1.6 593 2 G71301 hypothetical prote
 984 1.6 594 1 A44073 Cif1 protein - yea
 985 1.6 594 2 C96638 hypothetical prote
 986 1.6 595 2 F71650 DNA mismatch repai
 987 1.6 596 2 S59944 hydroxymethylgluta
 988 1.6 596 2 E82728 succinate dehydrog
 989 1.6 597 2 S65672 GABA transport pro
 990 1.6 597 2 D89765 hypothetical prote
 991 1.6 598 2 D84242 hypothetical prote
 992 1.6 598 2 B90589 sugar ABC transpor
 993 1.6 601 2 F84979 sulfite reductase
 994 1.6 601 2 E87548 hypothetical prote
 995 1.6 602 2 E97365 DNA helicase XF138
 996 1.6 602 2 AH2585 ATP-dependent DNA
 997 1.6 603 2 S15074 calpastatin - rat
 998 1.6 603 2 T27901 hypothetical prote
 999 1.6 604 1 S00726 protein kinase A-r
 1000 1.6 605 2 AG0123 probable antigenic

ALIGNMENTS

RESULT 1
 JE0264
 Cyclin I - human
 C:Species: Homo sapiens (man)
 C:Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 09-Jul-2004
 C:Accession: JE0264
 R:Zhu, X.; Naz, R.K.
 Biochem. Biophys. Res. Commun. 249, 56-60, 1998
 A:Title: Expression of a novel isoform of cyclin I in human testis.
 A:Reference number: JE0264; MUID:98381026; PMID:9705831
 A:Accession: JE0264
 A:Molecule type: mRNA
 A:Residues: 1-178 <ZHU>
 A:Cross-references: UNIPROT:Q14094
 C:Comment: This protein may have a physiological role in spermatogenesis and/or human sp

Query Match 27.3%; Score 103; DB 2; Length 178;
 Best Local Similarity 100.0%; Pred. No. 7.3e-97;
 Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 76 FLATVKAHPKYLSCIAISCFPLAAKTVEEDRIIPVLKVLARDSPCGCSSSILRMERIIL 135
 |||||
 Db 76 FLATVKAHPKYLSCIAISCFPLAAKTVEEDRIIPVLKVLARDSPCGCSSSILRMERIIL 135
 |||||

Qy 136 DKLAWDLHTATPLDFLHFHFAIAVSTRPQLFLSPKLSPSQHL 178
 |||||
 Db 136 DKLAWDLHTATPLDFLHFHFAIAVSTRPQLFLSPKLSPSQHL 178
 |||||

RESULT 2
 A87341
 sensory box/GGDEF family protein [imported] - Caulobacter crescentus
 C:Species: Caulobacter crescentus
 C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
 C:Accession: A87341
 R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
 B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
 n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
 Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A:Title: Complete Genome Sequence of Caulobacter crescentus.
 A:Reference number: A87249; MUID:21173698; PMID:11259647
 A:Accession: A87341
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-842 <STO>
 A:Cross-references: UNIPROT:Q9AA66; GB:AE005673; NID:g13421971; PIDN:AAK22725.1; GSPDB:G

C:Genetics:
 A:Gene: CC0740

Query Match 2.1%; Score 8; DB 2; Length 842;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 69 ASSLLDRF 76
 |||||
 Db 40 ASSLLDRF 47

RESULT 3
 G84429
 hypothetical protein At2g01840 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
 C:Accession: G84429
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; MUID:20083487; PMID:10617197
 A:Accession: G84429
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1715 <STO>
 A:Cross-references: UNIPROT:Q9SIS9; GB:AE002093; NID:g4522005; PIDN:AAD21778.1; GSPDB:GNI
 C:Genetics:
 A:Gene: At2g01840
 A:Map position: 2

Query Match 2.1%; Score 8; DB 2; Length 1715;
 Best Local Similarity 100.0%; Pred. No. 37;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 303 TAAFYHHL 310
 |||||
 Db 814 TAAFYHHL 821

RESULT 4
 D82732
 hypothetical protein XF1033 [imported] - Xylella fastidiosa (strain 9a5c)
 C:Species: Xylella fastidiosa
 C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
 C:Accession: D82732
 R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
 Nature 406, 151-157, 2000
 A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
 A:Reference number: A82515; MUID:20365717; PMID:10910347
 A:Note: for a complete list of authors see reference number A59328 below
 A:Accession: D82732
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-61 <SIM>
 A:Cross-references: UNIPROT:Q9PEJ5; GB:AE003940; NID:g9105966; PIDN:AAF8384
 A:Experimental source: strain 9a5c
 R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Laig
 Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrier, H.
 as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
 submitted to Genbank, June 2000
 A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franco, S.C.; Franco, M.C.; Frohm
 J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig
 chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.
 , F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.
 Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
 A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
 M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z.
 A:Reference number: A59328
 A:Contents: annotation

C;Genetics:
A;Gene: XF1033

Query Match 1.9%; Score 7; DB 2; Length 61;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Gaps 0;

Qy 154 FHAIYVS 160
| | | | |
Db 15 FHAIYVS 21

RESULT 5

G84490
Hypothetical protein At2g10340 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: G84490
R;Lin. X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: G84490
A;Status: Preliminary
A;Molecule type: DNA
A;Residues: 1-85 <STO>
A;Cross-references: UNIPROT:Q9SHW3; GB:AE002093; NID:G4733979; PIDN:AAD28661.1; GSPDB:GN
C;Genetics:
A;Gene: At2g10340
A;Map position: 2

Query Match 1.9%; Score 7; DB 2; Length 85;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 97 LAATKVE 103
| | | | |
Db 34 LAATKVE 40

RESULT 6

D71534
Hypothetical protein CT271 - Chlamydia trachomatis (serotype D, strain UW3/Cx)
C;Species: Chlamydia trachomatis
C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004
C;Accession: D71534
R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell,
Science 282, 754-759, 1998
A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia tra
A;Reference number: A71570; MUID:99000809; PMID:9784136
A;Accession: D71534
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-95 <ARN>
A;Cross-references: UNIPROT:O84273; GB:AE001300; GB:AE001273; NID:G3328682; PIDN:AAC6786
A;Experimental source: serotype D, strain UW-3/Cx
C;Genetics:
A;Gene: CT271

Query Match 1.9%; Score 7; DB 2; Length 95;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 LSFLLK 18
| | | | |
Db 54 LSFLLK 60

RESULT 7

CB1692
conserved hypothetical protein TC0543 [imported] - Chlamydia muridarum (strain Nigg)

C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: CB1692
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; MUID:20150255; PMID:10684935
A;Accession: CB1692
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-95 <TET>
A;Cross-references: UNIPROT:Q9PKC3; GB:AE002322; GB:AE002160; NID:G7190572; PIDN:AAF3938
A;Experimental source: strain Nigg (MoPn)
C;Genetics:
A;Gene: TC0543

Query Match 1.9%; Score 7; DB 2; Length 95;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 LSFLLK 18
| | | | |
Db 54 LSFLLK 60

RESULT 8

D44221
orf4 protein - Autographa californica nuclear polyhedrosis virus
C;Species: Autographa californica nuclear polyhedrosis virus, ACNPNV
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: D44221
R;Braunagel, S.C.; Daniel, K.D.; Reilly, L.M.; Guarino, L.A.; Hong, T.; Summers, M.D.
Virology 191, 1003-1008, 1992
A;Title: Sequence, genomic organization of the EcoRI-A fragment of Autographa californi
VP8 of rotavirus.
A;Reference number: A44221; MUID:93079853; PMID:1333113
A;Accession: D44221
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-108 <BRA>
A;Cross-references: UNIPROT:P41424; GB:S52569
C;Superfamily: ACNPNV hypothetical protein 19

Query Match 1.9%; Score 7; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 LSFLLK 18
| | | | |
Db 100 LSFLLK 106

RESULT 9

C72852
AcOrf-19 protein - Autographa californica nuclear polyhedrosis virus
C;Species: Autographa californica nuclear polyhedrosis virus, ACNPNV
A;Note: dsDNA virus
C;Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 09-Jul-2004
C;Accession: C72852
R;Ayres, M.D.; Howard, S.C.; Kuzio, J.; Lopez-Ferber, M.; Possee, R.D.
Virology 202, 586-605, 1994
A;Title: The complete DNA sequence of Autographa californica nuclear polyhedrosis virus.
A;Reference number: A72850; MUID:94303173; PMID:8030224
A;Accession: C72852
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-108 <AYR>
A;Cross-references: UNIPROT:P41424; GB:L22858; NID:G510708; PIDN:AAA66649.1; PID:G559088
C;Genetics:
A;Gene: AcOrf-19
C;Superfamily: ACNPNV hypothetical protein 19

Mon Feb 14 12:27:13 2005

```
Query Match      1.9%; Score 7; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12 LSFLLK 18
      |||||
Db      100 LSFLLK 106

RESULT 10
T41765
AcMNPV orf19 - Bombyx mori nuclear polyhedrosis virus (isolate T3)
C:Species: Bombyx mori nuclear polyhedrosis virus, BmSNPV
A:Variety: isolate T3
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T41765
R:Goni, S.; Majima, K.; Maeda, S.
J.Gen. Virol. 80, 1323-1337, 1999
A>Title: Sequence analysis of the genome of Bombyx mori nucleopolyhedrovirus.
A:Reference number: Z22020; MUID:99281911; PMID:10355780
A:Accession: T41765
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-110 <KAM>
A:Cross-references: UNIPROT:O92387; EMBL:L33180; NID:g3745835; PIDN:AAC63694.1; PID:g374
A:Experimental source: isolate T3
C:Genetics:
A:Note: Orf 11
C:Superfamily: AcMNPV hypothetical protein 19

Query Match      1.9%; Score 7; DB 2; Length 110;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12 LSFLLK 18
      |||||
Db      102 LSFLLK 108

RESULT 11
G83746
hypothetical protein BH0775 [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C:Accession: G83746
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A>Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: G83746
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-113 <STO>
A:Cross-references: UNIPROT:O9KES4; GB:AP001509; GB:BA000004; NID:g10173176; PIDN:BA04
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH0775

Query Match      1.9%; Score 7; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      164 QLLFSLP 170
      |||||
Db      77 QLLFSLP 83

RESULT 12
H87603
transcription regulator, ArsrR family [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C:Accession: H87603
```

```
R.Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A>Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: H87603
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-123 <STO>
A:Cross-references: UNIPROT:Q9A4H0; GB:AE005673; NID:gl3424478; PIDN:AAK24828.1; GSPDB:G
C:Genetics:
A:Gene: CC2864

Query Match      1.9%; Score 7; DB 2; Length 123;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      175 SQHLAVL 181
      |||||
Db      63 SQHLAVL 69

RESULT 13
B69320
conserved hypothetical protein AF0562 - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C:Accession: B69320
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A:Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.N
Smith, H.O.; Woese, C.R.; Venter, J.C.
A>Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeon
A:Reference number: A69250; MUID:98049343; PMID:9389475
A:Accession: B69320
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-126 <KLE>
A:Cross-references: UNIPROT:O29691; GB:AE001066; GB:AE000782; NID:g2689389; PIDN:AAB90679

Query Match      1.9%; Score 7; DB 2; Length 126;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      367 PCPPLQP 373
      |||||
Db      93 PCPPLQP 99

RESULT 14
AD0633
probable secreted protein STY1158 [imported] - Salmonella enterica subsp. enterica serov
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: this species has also been called Salmonella typhi
C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: AD0633
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Comerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A>Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AD0633
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-131 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD08247.1; PID:g16502294; GSPDB:GN00176
C:Genetics:
A:Gene: STY1158
```

Query Match 1.9%; Score 7; DB 2; Length 131;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 224 ELLOKQAQ 230
|||||
Db 63 ELLOKQAQ 69

RESULT 15
T35544
Probable quinolinate synthetase - Streptomyces coelicolor (fragment)
C/Species: Streptomyces coelicolor
C/Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 26-May-2000
C/Accession: T35544
R/Seeger, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, March 1999
A/Reference number: Z21581
A/Accession: T35544
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: DNA
A/Residues: 1-154 <SEE>
A/Cross-references: EMBL:AL049497; PIDN:CAB39889.1; GSPDB:GN00070; SCOPEDB:SC6G10.35
A/Experimental source: strain A3(2)
C/Genetics:
A/Gene: SCOPEDB:SC6G10.35
C/Superfamily: Helicobacter pylori quinolinate synthetase A

Query Match 1.9%; Score 7; DB 2; Length 154;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 44 QRDEVIQ 50
|||||
Db 70 QRDEVIQ 76

Search completed: February 11, 2005, 03:16:11
Job time : 56.9258 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 11, 2005, 03:11:19 ; Search time 100.276 Seconds
(without alignments)
1925.221 Million cell updates/sec

Title: US-09-736-250-1
Perfect score: 377
Sequence: 1 MKPFGPLENORLSFLEKAI.....LSRQEGHASPCLPQPVSM 377

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0
Searched: 1612378 seqs, 512079187 residues

Word size : 0
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : UniProt_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	377	100.0	377	1	CYCI_HUMAN	Q14094 homo sapien
2	240	63.7	377	2	Q6FHH0	Q6fhh0 homo sapien
3	90	23.9	377	2	Q99LF2	Q99lf2 mus musculus
4	53	14.1	377	2	Q8C7E2	Q8c7e2 mus musculus
5	51	13.5	377	1	CYCI_MOUSE	Q322v9 mus musculus
6	29	7.7	382	2	Q6DJQ8	Q6djq8 xenopus tro
7	29	7.7	382	2	Q6P7H3	Q6p7h3 xenopus lae
8	13	3.4	355	2	Q6NUZ7	Q6nuz7 brachydanio
9	13	3.4	355	2	Q803P0	Q803p0 brachydanio
10	9	2.4	462	2	Q9XFC9	Q9xfc9 dolichos bi
11	8	2.1	227	2	Q83YJ9	Q83yj9 bifidobacte
12	8	2.1	231	2	Q86FL6	Q86fl6 schistosoma
13	8	2.1	332	2	Q6NWA8	Q6nwa8 brachydanio
14	8	2.1	359	2	Q66IZ0	Q66iz0 xenopus lae
15	8	2.1	364	2	Q947Z5	Q947z5 oryza sativ
16	8	2.1	374	2	Q899B7	Q899b7 clostridium
17	8	2.1	379	2	Q8H088	Q8h088 oryza sativ
18	8	2.1	379	2	Q87MS1	Q87ms1 vibrio para
19	8	2.1	397	2	Q82S78	Q82s78 nitrosomona
20	8	2.1	422	2	Q8BGF8	Q8bgf8 m mus muscu
21	8	2.1	600	2	Q6BXL7	Q6bxl7 debaryomyce
22	8	2.1	667	2	Q35267	Q35267 rattus norv
23	8	2.1	764	2	Q9LRH7	Q9lrh7 pisum sativ
24	8	2.1	842	2	Q9AA66	Q9aa66 caulobacter
25	8	2.1	959	2	Q6BQ15	Q6bq15 debaryomyce
26	8	2.1	1325	1	RIP2_CHICK	Q8gxf1 gallus gall
27	8	2.1	1715	2	Q9S1E9	Q9sis9 arabidopsis
28	7	1.9	59	2	Q81R19	Q81r19 bacillus an
29	7	1.9	61	2	Q9PEJ5	Q9pej5 xylella fas
30	7	1.9	62	2	Q69X51	Q69x51 oryza sativ
31	7	1.9	62	2	Q82BE3	Q82be3 streptomyce

32	7	1.9	70	2	Q6HZR5	Q6hzr5 bacillus an
33	7	1.9	70	2	Q63CB1	Q63cb1 bacillus ce
34	7	1.9	70	2	Q6HJS3	Q6hjs3 bacillus th
35	7	1.9	72	2	Q81EB1	Q81ee1 bacillus ce
36	7	1.9	85	2	Q9SHW3	Q9shw3 arabidopsis
37	7	1.9	87	2	Q6MCG8	Q6mcg8 parachlamyd
38	7	1.9	91	2	Q8MSZ0	Q8msz0 drosophila
39	7	1.9	91	2	Q6T3A6	Q6t3a6 gallus gall
40	7	1.9	95	2	Q84273	Q84273 chlamydia t
41	7	1.9	95	2	Q9PKC3	Q9pkc3 chlamydia m
42	7	1.9	101	2	Q72J99	Q72j99 thermus the
43	7	1.9	102	2	Q8EXR4	Q8ekr4 shewanella
44	7	1.9	104	2	Q98M40	Q98m40 rhizobium l
45	7	1.9	104	2	Q89WR9	Q89wr9 bradyrhizob
46	7	1.9	105	2	Q739L5	Q739l5 bacillus ce
47	7	1.9	105	2	Q9D9I8	Q9d9i8 mus musculus
48	7	1.9	106	2	Q7Q3J4	Q7q3j4 anopheles g
49	7	1.9	108	1	Y019 NPVAC	P41424 autographa
50	7	1.9	108	2	Q8B9M9	Q8b9m9 rachiplusia
51	7	1.9	110	2	Q92387	Q92387 bombyx mori
52	7	1.9	111	2	Q83XW4	Q83xw4 flavobacter
53	7	1.9	113	2	Q9KES4	Q9kes4 bacillus ha
54	7	1.9	114	2	Q6XFG9	Q6xfg9 nectarinia
55	7	1.9	115	2	Q6XFH2	Q6xfh2 nectarinia
56	7	1.9	116	2	Q6XFP4	Q6xff4 nectarinia
57	7	1.9	116	2	Q6XFP5	Q6xff5 nectarinia
58	7	1.9	116	2	Q6XFP6	Q6xff6 nectarinia
59	7	1.9	116	2	Q6XFP8	Q6xff8 nectarinia
60	7	1.9	116	2	Q6XFG1	Q6xfg1 nectarinia
61	7	1.9	116	2	Q6XFG4	Q6xfg4 nectarinia
62	7	1.9	116	2	Q6XFG7	Q6xfg7 nectarinia
63	7	1.9	116	2	Q6XFG8	Q6xfg8 nectarinia
64	7	1.9	116	2	Q6XPH0	Q6xfh0 nectarinia
65	7	1.9	116	2	Q6XPH3	Q6xfh3 nectarinia
66	7	1.9	116	2	Q6XPH5	Q6xfh5 nectarinia
67	7	1.9	122	2	Q6ZV25	Q6zv25 homo sapien
68	7	1.9	123	2	Q7UG57	Q7ug57 rhodospirell
69	7	1.9	123	2	Q9A4H0	Q9a4h0 caulobacter
70	7	1.9	126	1	Y562 ARCFU	Q29691 archaeoglob
71	7	1.9	127	2	Q706Q4	Q706q4 pseudomonas
72	7	1.9	127	2	Q727X0	Q727x0 desulfovibr
73	7	1.9	128	2	Q9BQK6	Q9bqk6 homo sapien
74	7	1.9	129	2	Q67MF9	Q67mf9 symbiobacte
75	7	1.9	131	2	Q6K4C4	Q6k4c4 oryza sativ
76	7	1.9	131	2	Q8Z7N6	Q8z7n6 salmomella
77	7	1.9	131	2	Q8ZQ37	Q8zq37 salmonella
78	7	1.9	133	2	Q8FR22	Q8fr22 corynebacte
79	7	1.9	133	2	Q9W219	Q9w219 drosophila
80	7	1.9	136	2	Q7VJM3	Q7vjm3 helicobacte
81	7	1.9	155	1	RS7_XYLFA	Q9pa89 xylella fas
82	7	1.9	155	1	RS7_XYLFT	Q87a34 xylella fas
83	7	1.9	158	2	Q6K2D2	Q6k2d2 oryza sativ
84	7	1.9	159	2	Q67JP3	Q67jp3 symbiobacte
85	7	1.9	187	2	Q8PI65	Q8pi65 xanthomonas
86	7	1.9	188	2	Q9PDQ1	Q9pdq1 xylella fas
87	7	1.9	189	2	Q8YT22	Q8yt22 anabaena sp
88	7	1.9	194	2	Q67T42	Q67t42 symbiobacte
89	7	1.9	195	2	Q9N2Z8	Q9n2z8 caenorhabdi
90	7	1.9	196	2	Q6DIU8	Q6diu8 medicago sa
91	7	1.9	197	2	Q86S66	Q86s66 caenorhabdi
92	7	1.9	197	2	Q945D3	Q945d3 castanea sa
93	7	1.9	198	2	Q7PLD2	Q7pld2 drosophila
94	7	1.9	198	2	Q9MM84	Q9mm84 darevskia l
95	7	1.9	198	2	Q9MM85	Q9mm85 darevskia b
96	7	1.9	198	2	Q9MM89	Q9mm89 darevskia s
97	7	1.9	198	2	Q8PIG7	Q8pig7 xanthomonas
98	7	1.9	199	2	Q923X5	Q923x5 ralstonia s
99	7	1.9	199	2	Q7NIF3	Q7nif3 glaucobacter
100	7	1.9	207	2	Q72U42	Q72u42 leptospira
101	7	1.9	207	2	Q8F103	Q8f103 leptospira
102	7	1.9	208	2	Q92QA2	Q92qa2 rhizobium m
103	7	1.9	209	2	Q7QY62	Q7qy62 gardia lam
104	7	1.9	216	2	Q9FY89	Q9fy89 arabidopsis

105 Q6er63 oryza sativ 1.9 217 2 Q6ER63
106 Q9zhb6 homo sapien 7 1.9 218 1 11F7 HUMAN
107 Q7ru00 7 1.9 219 2 Q7RU00
108 Q9nv10 7 1.9 220 2 Q9NV10
109 Q9ih84 7 1.9 225 2 Q9IH84
110 Q84183 7 1.9 230 2 Q84183
111 Q9PK13 7 1.9 230 2 Q9PK13
112 Q6KiH0 7 1.9 231 2 Q6KIH0
113 Q73DX8 7 1.9 234 2 Q73DX8
114 Q835F8 7 1.9 235 2 Q835F8
115 Q17116 7 1.9 237 2 Q17116
116 Q9P723 7 1.9 238 1 YHRE_SCHPO
117 Q9R6N1 7 1.9 238 2 Q9R6N1
118 Q65M11 7 1.9 238 2 Q65M11
119 Q8u685 7 1.9 238 2 Q8U685
120 Q82N00 7 1.9 239 2 Q82N00
121 Q40670 7 1.9 242 2 Q40670
122 Q8XP16 7 1.9 242 2 Q8XP16
123 Q7V465 7 1.9 247 2 Q7V465
124 PCNA_PYRFU 7 1.9 249 1 PCNA_PYRFU
125 Q8K5K7 7 1.9 254 2 Q8K5K7
126 Q829U0 7 1.9 256 2 Q829U0
127 Q75FF8 7 1.9 257 2 Q75FF8
128 Q8EXB2 7 1.9 257 2 Q8EXB2
129 Q7WX06 7 1.9 261 2 Q7WX06
130 Q72UY5 7 1.9 263 2 Q72UY5
131 Q8EZV8 7 1.9 263 2 Q8EZV8
132 Q84LD1 7 1.9 265 2 Q84LD1
133 Q48980 7 1.9 269 2 Q48980
134 Q8G3K6 7 1.9 269 2 Q8G3K6
135 Q81L10 7 1.9 273 2 Q81L10
136 Q8AYG9 7 1.9 273 2 Q8AYG9
137 Q75LH4 7 1.9 278 2 Q75LH4
138 KSGA_SVNY3 7 1.9 284 1 KSGA_SVNY3
139 Q9XQ2 7 1.9 285 2 Q9XQ2
140 Q69780 7 1.9 287 2 Q69780
141 Q8KLH5 7 1.9 287 2 Q8KLH5
142 Q9KX2 7 1.9 291 2 Q9KX2
143 Q7BAA7 7 1.9 292 2 Q7BAA7
144 Q8U05 7 1.9 294 2 Q8U05
145 Q85J80 7 1.9 294 2 Q85J80
146 Q87PG9 7 1.9 297 2 Q87PG9
147 Q6NY19 7 1.9 299 2 Q6NY19
148 Q6TEN3 7 1.9 299 2 Q6TEN3
149 Q7ZTX1 7 1.9 299 2 Q7ZTX1
150 Q538G9 7 1.9 301 2 Q538G9
151 Q8F8Q3 7 1.9 301 2 Q8F8Q3
152 Q9H7A0 7 1.9 303 2 Q9H7A0
153 Q20844 7 1.9 307 2 Q20844
154 Q8SYJ3 7 1.9 310 2 Q8SYJ3
155 Q8EN25 7 1.9 313 2 Q8EN25
156 Q65MX4 7 1.9 315 2 Q65MX4
157 Q9ILR1 7 1.9 315 2 Q9ILR1
158 Q62YB6 7 1.9 319 2 Q62YB6
159 Q7VAR7 7 1.9 322 2 Q7VAR7
160 Q9XTY9 7 1.9 324 2 Q9XTY9
161 Q57599 7 1.9 327 2 Q57599
162 Q9UG89 7 1.9 330 2 Q9UG89
163 Q8S6X8 7 1.9 330 2 Q8S6X8
164 Q7XG76 7 1.9 330 2 Q7XG76
165 Q7XPU3 7 1.9 330 2 Q7XPU3
166 Q7VGA5 7 1.9 330 2 Q7VGA5
167 Q6N231 7 1.9 330 2 Q6N231
168 Q8ZSP5 7 1.9 333 2 Q8ZSP5
169 Q8BTR1 7 1.9 335 2 Q8BTR1
170 Q8BTR2 7 1.9 336 2 Q8BTR2
171 Q6Y8J4 7 1.9 337 1 ADH1_ZYMMO
172 Q6Y8J4 7 1.9 337 2 Q6Y8J4
173 Q6T7F5 7 1.9 338 2 Q6T7F5
174 Q9D4G2 7 1.9 338 2 Q9D4G2
175 Q82FE3 7 1.9 344 2 Q82FE3
176 Q63XJ6 7 1.9 344 2 Q63XJ6
177 Q75H97 7 1.9 345 2 Q75H97

178 Q6er63 oryza sativ 1.9 350 2 Q6ER63
179 Q9zhb6 homo sapien 7 1.9 350 2 Q9ZHB6
180 Q7ru00 7 1.9 350 2 Q7RU00
181 Q9nv10 7 1.9 350 2 Q9NV10
182 Q9ih84 7 1.9 350 2 Q9IH84
183 Q84183 7 1.9 353 2 Q84183
184 Q9PK13 7 1.9 355 2 Q9PK13
185 Q6KiH0 7 1.9 357 2 Q6KIH0
186 Q73DX8 7 1.9 357 2 Q73DX8
187 Q835F8 7 1.9 358 2 Q835F8
188 Q17116 7 1.9 362 2 Q17116
189 Q9P723 7 1.9 363 1 P1T1 CHICK
190 Q9R6N1 7 1.9 364 2 Q9R6N1
191 Q65M11 7 1.9 364 2 Q65M11
192 Q8u685 7 1.9 364 2 Q8U685
193 Q82N00 7 1.9 365 2 Q82N00
194 Q40670 7 1.9 367 2 Q40670
195 Q8XP16 7 1.9 369 1 IDH2 YEAST
196 Q7V465 7 1.9 369 2 Q7V465
197 Q73947 7 1.9 370 2 Q73947
198 Q8K5K7 7 1.9 372 2 Q8K5K7
199 Q829U0 7 1.9 375 2 Q829U0
200 Q75FF8 7 1.9 379 2 Q75FF8
201 Q8EXB2 7 1.9 379 2 Q8EXB2
202 Q7WX06 7 1.9 379 2 Q7WX06
203 Q72UY5 7 1.9 380 2 Q72UY5
204 Q8EZV8 7 1.9 380 2 Q8EZV8
205 Q84LD1 7 1.9 383 2 Q84LD1
206 Q48980 7 1.9 384 2 Q48980
207 Q8G3K6 7 1.9 385 1 Y421 METH
208 Q81L10 7 1.9 386 2 Q81L10
209 Q8AYG9 7 1.9 390 2 Q8AYG9
210 Q75LH4 7 1.9 390 2 Q75LH4
211 P2666 7 1.9 390 2 P2666
212 Q9XQ2 7 1.9 391 2 Q9XQ2
213 Q69780 7 1.9 393 2 Q69780
214 Q8KLH5 7 1.9 394 1 NADA CORGL
215 Q9KX2 7 1.9 394 2 Q9KX2
216 Q7BAA7 7 1.9 396 1 CBG RAT
217 Q8U05 7 1.9 403 1 A1AF_CAVPO
218 Q85J80 7 1.9 404 1 Q85J80
219 Q87PG9 7 1.9 404 2 Q87PG9
220 Q6NY19 7 1.9 409 2 Q6NY19
221 Q6TEN3 7 1.9 409 2 Q6TEN3
222 Q7ZTX1 7 1.9 410 1 COTR_CAVPO
223 Q538G9 7 1.9 414 2 Q538G9
224 Q8F8Q3 7 1.9 415 2 Q8F8Q3
225 Q9H7A0 7 1.9 417 2 Q9H7A0
226 Q20844 7 1.9 420 2 Q20844
227 Q8SYJ3 7 1.9 420 2 Q8SYJ3
228 Q8EN25 7 1.9 421 2 Q8EN25
229 Q65MX4 7 1.9 421 2 Q65MX4
230 Q9ILR1 7 1.9 423 2 Q9ILR1
231 Q62YB6 7 1.9 423 2 Q62YB6
232 Q7VAR7 7 1.9 423 2 Q7VAR7
233 Q9XTY9 7 1.9 427 2 Q9XTY9
234 Q57599 7 1.9 436 1 ACDD METAC
235 Q9UG89 7 1.9 436 1 Q9UG89
236 Q8S6X8 7 1.9 436 1 Q8S6X8
237 Q7XG76 7 1.9 436 1 Q7XG76
238 Q7XPU3 7 1.9 436 1 Q7XPU3
239 Q7VGA5 7 1.9 437 1 Q7VGA5
240 Q6N231 7 1.9 437 1 Q6N231
241 Q8ZSP5 7 1.9 439 1 Q8ZSP5
242 Q8BTR1 7 1.9 439 1 Q8BTR1
243 Q8BTR2 7 1.9 443 2 Q8BTR2
244 P20368 7 1.9 444 1 MURA CHLTR
245 Q6Y8J4 7 1.9 446 1 Q6Y8J4
246 Q6T7F5 7 1.9 446 2 Q6T7F5
247 Q9D4G2 7 1.9 449 2 Q9D4G2
248 Q82FE3 7 1.9 453 2 Q82FE3
249 Q63XJ6 7 1.9 453 2 Q63XJ6
250 Q75H97 7 1.9 462 2 Q75H97

Q8nbp3 homo sapien
Q8ngl5 homo sapien
Q96lB5 homo sapien
Q9h2P8 homo sapien
Q9f198 arabidopsis
Q8gxas arabidopsis
Q8h143 arabidopsis
Q75fz4 leptospira
Q8ey06 leptospira
Q85fz3 bacillus li
Q7qwb6 giardia lam
Q9ygl7 gallus gall
Q6mzm8 homo sapien
Q6n000 homo sapien
Q66i82 brachydanio
Q8d5ul erwinia car
Q8rc12 mycobacteri
P28211 saccharomyc
Q6cbz6 yarrowia li
Q91xb8 arabidopsis
Q91ua0 arabidopsis
Q8zt42 arabidopsis
Q8le24 arabidopsis
Q9ma11 arabidopsis
Q93hp3 streptomyce
Q8hm13 carapus ber
Q64hw4 oncorhynchu
Q8et70 oceanobacil
Q8tgu1 brachydanio
Q26521 methanobact
Q13901 schizosacch
Q75aw7 ashbya goss
Q8ix24 homo sapien
Q8mmf3 bdellovibri
Q8c0f1 homo sapien
Q91x79 arabidopsis
Q8nr10 corynebacte
Q9f364 streptomyce
P31211 rattus norv
CBG RAT
P22324 cavia porce
P19496 methanobact
Q9fvq8 arabidopsis
Q82156 streptomyce
Q9ew33 streptomyce
P22323 cavia porce
Q82a16 streptomyce
Q7r2j2 giardia lam
Q6rc07 mycobacteri
Q7x5j6 oryza sativ
Q9ssz5 oryza sativ
Q64bh3 uncultured
Q6cne2 kluyveromyc
Q9sw36 arabidopsis
Q8gp73 streptococc
Q9ah92 streptococc
Q9x0v7 thermotoga
Q9x0v7 thermotoga
Q64bh3 uncultured
Q8prg5 methanosarc
Q8tr28 methanosarc
Q50538 methanosarc
Q8tjcz methanosarc
Q8c639 mus musculu
Q9c411 methanosarc
Q9c1673 rattus norv
Q89g6 taxus chine
Q8m6f0 taxus cuspi
Q8em10 oceanobacil
Q84461 chlamydia t
P19541 saccharomyc
Q88pr9 pseudomonas
Q6v0k4 mycobacteri
Q6av91 oryza sativ
Q61561 mus musculu
Q6fjy2 candida gla

251	7	1.9	471	2	Q90577	Q90577 gallus gall	324	7	1.9	845	2	Q80Z08	Q80Z08 mus musculu
252	7	1.9	475	2	Q8KU28	Q8KU28 rhodococcus	325	7	1.9	852	2	Q35192	Q35192 mus musculu
253	7	1.9	477	2	Q7SBD7	Q7SBD7 neurospora	326	7	1.9	858	2	O18466	O18466 hiruodi medi
254	7	1.9	482	2	Q72GB4	Q72GB4 thermus the	327	7	1.9	867	2	Q8IKI7	Q8IKI7 plasmodium
255	7	1.9	488	2	Q6CBY3	Q6CBY3 yarrowia li	328	7	1.9	869	2	Q9C744	Q9C744 arabidopsis
256	7	1.9	491	2	Q6CWP9	Q6CWP9 kluyveromyc	329	7	1.9	873	2	Q9I8E6	Q9I8E6 fugu rubrip
257	7	1.9	495	2	Q683K1	Q683K1 arabidopsis	330	7	1.9	876	1	EGLI_SACFI	P22506 saccharomyc
258	7	1.9	495	2	Q8CW96	Q8CW96 arabidopsis	331	7	1.9	885	1	FLSB_XANAC	Q8P80 xanthomonas
259	7	1.9	513	1	T160_HUMAN	Q92993 homo sapien	332	7	1.9	886	1	FLSB_XANCP	Q8P363 xanthomonas
260	7	1.9	513	1	T160_MOUSE	Q8CHK4 mus musculu	333	7	1.9	895	2	Q8CON3	Q8CON3 mus musculu
261	7	1.9	516	2	Q8C415	Q8C415 mus musculu	334	7	1.9	895	2	Q65CL1	Q65CL1 mus musculu
262	7	1.9	517	1	STG1_HUMAN	Q9N88 homo sapien	335	7	1.9	934	2	Q7UET9	Q7UET9 rhodopirell
263	7	1.9	517	1	STG1_MOUSE	Q92581 mus musculu	336	7	1.9	951	2	Q9FVX8	Q9FVX8 oryza sativ
264	7	1.9	517	2	Q8BNW6	Q8BNW6 mus musculu	337	7	1.9	952	2	Q8X5G8	Q8X5G8 escherichia
265	7	1.9	519	2	Q7QSC6	Q7QSC6 giardia lam	338	7	1.9	960	2	Q7N7N1	Q7N7N1 photorhabdu
266	7	1.9	520	2	Q6H4F1	Q6H4F1 oryza sativ	339	7	1.9	969	2	Q8X3L3	Q8X3L3 escherichia
267	7	1.9	533	2	Q6Y3A2	Q6Y3A2 hordeum vul	340	7	1.9	982	2	Q7PGV3	Q7PGV3 anopheles g
268	7	1.9	544	1	BRH1_DROME	Q24255 drosophila	341	7	1.9	982	2	Q84VD8	Q84VD8 oryza sativ
269	7	1.9	544	2	Q7RXQ4	Q7RXQ4 neurospora	342	7	1.9	989	2	Q8NUJ8	Q8NUJ8 pichia past
270	7	1.9	550	2	Q97D46	Q97D46 clostridium	343	7	1.9	990	1	K6PI_PICPA	Q92448 pichia past
271	7	1.9	550	2	Q35270	Q35270 rattus norv	344	7	1.9	996	2	Q9S112	Q9S112 arabidopsis
272	7	1.9	556	2	Q9VF62	Q9VF62 drosophila	345	7	1.9	1006	2	Q9U360	Q9U360 caenorhabdi
273	7	1.9	560	2	Q14520	Q14520 homo sapien	346	7	1.9	1008	2	Q8H8Y7	Q8H8Y7 oryza sativ
274	7	1.9	570	2	Q8EJA7	Q8EJA7 shewanella	347	7	1.9	1011	2	Q7PIC1	Q7PIC1 anopheles g
275	7	1.9	573	2	Q9YDG3	Q9YDG3 aeropyrum p	348	7	1.9	1015	2	Q6ZQH7	Q6ZQH7 mus musculu
276	7	1.9	574	2	Q9VT95	Q9VT95 drosophila	349	7	1.9	1026	2	Q7AEP0	Q7AEP0 escherichia
277	7	1.9	592	2	Q90W89	Q90W89 brachydanio	350	7	1.9	1026	2	Q8X299	Q8X299 escherichia
278	7	1.9	593	2	Q98SM8	Q98SM8 brachydanio	351	7	1.9	1026	2	Q8XEJ2	Q8XEJ2 escherichia
279	7	1.9	592	2	Q8T6B7	Q8T6B7 dictyosteli	352	7	1.9	1035	2	Q6QI79	Q6QI79 rattus norv
280	7	1.9	594	1	NU5M_HIPAM	Q9ZZV1 hippopotamu	353	7	1.9	1045	1	SPS_BETVU	Q49031 beta vulgar
281	7	1.9	599	1	CAP4_ARATH	Q9EA65 arabidopsis	354	7	1.9	1061	2	Q7R334	Q7R334 plasmodium
282	7	1.9	602	2	Q9UW13	Q9UW13 candida alb	355	7	1.9	1069	2	Q9J746	Q9J746 neisseria m
283	7	1.9	605	1	YS73_GEOSL	P61404 geobacter s	356	7	1.9	1080	2	Q8XAH7	Q8XAH7 escherichia
284	7	1.9	606	2	Q68GDO	Q68GDO bubalus bub	357	7	1.9	1080	2	Q6H9T7	Q6H9T7 phage phi 4
285	7	1.9	608	2	Q8SS67	Q8SS67 encephalito	358	7	1.9	1085	2	Q53720	Q53720 mycobacteri
286	7	1.9	611	1	CAP3_ARATH	Q8GX47 arabidopsis	359	7	1.9	1085	2	Q7U243	Q7U243 mycobacteri
287	7	1.9	633	1	RPOC_CYACA	Q18897 cyanidium c	360	7	1.9	1092	2	Q7D9W9	Q7D9W9 mycobacteri
288	7	1.9	634	2	Q6FRC2	Q6FRC2 candida gla	361	7	1.9	1102	2	Q889D8	Q889D8 rhodobacter
289	7	1.9	635	2	Q8MKM9	Q8MKM9 drosophila	362	7	1.9	1117	2	Q6C316	Q6C316 yarrowia li
290	7	1.9	639	2	Q9SGH6	Q9SGH6 arabidopsis	363	7	1.9	1125	2	Q9VLE6	Q9VLE6 drosophila
291	7	1.9	663	2	Q9NV65	Q9NV65 homo sapien	364	7	1.9	1133	2	Q6MKG4	Q6MKG4 bdellovibri
292	7	1.9	668	2	Q8CON1	Q8CON1 mus musculu	365	7	1.9	1165	2	Q72TU4	Q72TU4 leptospira
293	7	1.9	670	2	Q81762	Q81762 arabidopsis	366	7	1.9	1165	2	Q8FIC9	Q8FIC9 leptospira
294	7	1.9	685	1	STM1_MOUSE	P70302 mus musculu	367	7	1.9	1187	2	Q8KOC0	Q8KOC0 mus musculu
295	7	1.9	685	2	Q8K1E1	Q8K1E1 mus musculu	368	7	1.9	1190	2	Q9HS95	Q9HS95 halobacteri
296	7	1.9	689	2	Q9FWE0	Q9FWE0 arabidopsis	369	7	1.9	1216	1	AEGP_RAT	Q63191 rattus norv
297	7	1.9	691	2	Q80YB4	Q80YB4 mus musculu	370	7	1.9	1221	2	Q9BIW9	Q9BIW9 caenorhabdi
298	7	1.9	695	2	Q35272	Q35272 rattus norv	371	7	1.9	1221	2	Q9N5Z3	Q9N5Z3 caenorhabdi
299	7	1.9	695	2	Q80X11	Q80X11 mus musculu	372	7	1.9	1228	1	MRN1_HUMAN	Q13201 homo sapien
300	7	1.9	696	2	Q7PV95	Q7PV95 anopheles g	373	7	1.9	1228	2	Q6P3T8	Q6P3T8 homo sapien
301	7	1.9	696	2	Q8JKI5	Q8JKI5 heliothis z	374	7	1.9	1265	2	Q9MIT3	Q9MIT3 arabidopsis
302	7	1.9	697	2	Q8I3Q9	Q8I3Q9 plasmodium	375	7	1.9	1389	2	Q6WG27	Q6WG27 mycobacteri
303	7	1.9	699	2	Q8BMX6	Q8BMX6 mus musculu	376	7	1.9	1402	2	Q96668	Q96668 dictyosteli
304	7	1.9	709	2	Q49733	Q49733 arabidopsis	377	7	1.9	1411	2	Q8JKS5	Q8JKS5 heliothis z
305	7	1.9	713	2	Q8EVR3	Q8EVR3 mycoplasma	378	7	1.9	1443	2	Q80TN2	Q80TN2 mus musculu
306	7	1.9	723	2	Q35193	Q35193 mus musculu	379	7	1.9	1452	2	Q6WG26	Q6WG26 mycobacteri
307	7	1.9	730	2	Q64760	Q64760 arabidopsis	380	7	1.9	1534	2	Q7PIC2	Q7PIC2 anopheles g
308	7	1.9	733	2	Q6T1W9	Q6T1W9 aneurinibac	381	7	1.9	1554	2	Q8KZL5	Q8KZL5 streptococ
309	7	1.9	737	2	Q7F9L4	Q7F9L4 oryza sativ	382	7	1.9	1557	2	Q7PX40	Q7PX40 anopheles g
310	7	1.9	743	1	COG8_CAEEL	Q44502 caenorhabdi	383	7	1.9	1605	2	Q89ZN3	Q89ZN3 bacteroides
311	7	1.9	745	2	Q9D230	Q9D230 mus musculu	384	7	1.9	1748	2	Q6CYG5	Q6CYG5 kluyveromyc
312	7	1.9	758	2	Q9I2M9	Q9I2M9 pseudomonas	385	7	1.9	1818	2	Q8EVF1	Q8EVF1 mycoplasma
313	7	1.9	770	2	Q8YMK4	Q8YMK4 anabaena sp	386	7	1.9	1840	2	Q9HED6	Q9HED6 neurospora
314	7	1.9	789	2	Q39548	Q39548 cucurbita m	387	7	1.9	1920	2	Q94ZJ8	Q94ZJ8 oryza sativ
315	7	1.9	797	2	Q9QWK0	Q9QWK0 rattus norv	388	7	1.9	1928	2	Q6VZT3	Q6VZT3 canarypox v
316	7	1.9	802	2	Q35271	Q35271 mus musculu	389	7	1.9	1964	2	Q8SMQ7	Q8SMQ7 loligo peal
317	7	1.9	804	2	Q35202	Q35202 mus musculu	390	7	1.9	2153	2	Q6LFD0	Q6LFD0 plasmodium
318	7	1.9	807	2	Q8Z1J2	Q8Z1J2 salmonella	391	7	1.9	2410	2	Q6MZA5	Q6MZA5 mycobacteri
319	7	1.9	822	2	Q7KUX2	Q7KUX2 drosophila	392	7	1.9	2474	2	Q6RT24	Q6RT24 mus musculu
320	7	1.9	823	2	Q6SJRO	Q6SJRO arabidopsis	393	7	1.9	3298	2	Q9VB11	Q9VB11 drosophila
321	7	1.9	825	2	Q6PD00	Q6PD00 mus musculu	394	7	1.9	4315	2	Q6RKJ3	Q6RKJ3 botrytis ci
322	7	1.9	826	2	Q80XK5	Q80XK5 mus musculu	395	7	1.9	5020	2	Q8E9W3	Q8E9W3 shewanella
323	7	1.9	841	2	Q92RX8	Q92RX8 rhizobium m	396	7	1.9	7756	2	Q70LM5	Q70LM5 bacillus br

397 1.9 14130 2 Q6MZ72 Q6mz72 mycobacteri 470 6 1.6 84 2 Q8V9P8 Q8v9p8 sulfolobus
398 1.9 16990 2 Q6MZA4 Q6mza4 mycobacteri 471 6 1.6 85 1 YME3 THIFE 1.6 85 2 Q8V9P8 Q8v9p8 sulfolobus
399 1.6 13 Q47607 Q47607 escherichia 472 6 1.6 85 2 Q8V9P8 Q8v9p8 sulfolobus
400 1.6 31 Q81G64 Q81g64 bacillus ce 473 6 1.6 85 2 Q8V9P8 Q8v9p8 sulfolobus
401 1.6 36 Q8DMG4 Q8dmg4 streptococc 474 6 1.6 85 2 Q8V9P8 Q8v9p8 sulfolobus
402 1.6 39 Q6BR23 Q6br23 debrayomyce 475 6 1.6 85 2 Q8V9P8 Q8v9p8 sulfolobus
403 1.6 41 Q81N8 Q81n8 bacillus an 476 6 1.6 86 2 Q8V9P8 Q8v9p8 sulfolobus
404 1.6 42 Q9LE12 Q9le12 equisetum s 477 6 1.6 86 2 Q8V9P8 Q8v9p8 sulfolobus
405 1.6 42 Q9EW7 Q9ew7 streptomyc 478 6 1.6 87 1 BC10_BOVIN BC10_BOVIN felis silve
406 1.6 45 Q81F15 Q81f15 trypanosoma 479 6 1.6 87 1 BC10_BOVIN BC10_BOVIN felis silve
407 1.6 53 1 LHA2 RHOAC Q35090 rhodopsu 480 6 1.6 87 1 BC10_HUMAN BC10_HUMAN
408 1.6 53 2 Q8DUB8 Q8dub8 streptococc 481 6 1.6 87 1 BC10_MOUSE BC10_MOUSE
409 1.6 56 2 Q76N70 Q76n70 glycine max 482 6 1.6 87 1 BC10_MOUSE BC10_MOUSE
410 1.6 58 2 Q8S5W8 Q8s5w8 oryza sativ 483 6 1.6 87 2 Q91B61 Q91b61 brachydanio
411 1.6 59 2 Q72ZA6 Q72za6 bacillus ce 484 6 1.6 88 2 Q79XU2 Q79xu2 streptococc
412 1.6 59 2 Q8IKW0 Q8ikw0 bacillus an 485 6 1.6 88 2 Q79XU2 Q79xu2 streptococc
413 1.6 60 2 Q52650 Q52650 rhodopsu 486 6 1.6 88 2 Q8K780 Q8k780 streptococc
414 1.6 60 2 Q52652 Q52652 rhodopsu 487 6 1.6 88 2 Q8K780 Q8k780 streptococc
415 1.6 60 2 Q8X4F9 Q8x4f9 escherichia 488 6 1.6 88 2 Q9A0P0 Q9a0p0 streptococc
416 1.6 61 2 Q98A74 Q98a74 rhizobium 1 489 6 1.6 88 2 Q734G6 Q734g6 bacillus ce
417 1.6 61 2 Q8G115 Q8g115 brucella su 490 6 1.6 88 2 Q7CMW8 Q7cmw8 streptococc
418 1.6 62 2 Q931L5 Q931l5 thermus the 491 6 1.6 88 2 Q7CN26 Q7cn26 streptococc
419 1.6 62 2 Q6AXY5 Q6axy5 rattus norv 492 6 1.6 88 2 Q82VJ2 Q82vj2 nitrosomona
420 1.6 63 2 Q94CJ7 Q94cj7 arabidopsis 493 6 1.6 88 2 Q8DQT3 Q8dqt3 streptococc
421 1.6 63 2 Q65QW3 Q65qw3 manheimia 494 6 1.6 88 2 Q8DQT3 Q8dqt3 streptococc
422 1.6 64 2 Q7PA35 Q7pa35 rickettsia 495 6 1.6 90 2 P89505 P89505 saccharomyc
423 1.6 64 2 Q92G32 Q92g32 rickettsia 496 6 1.6 90 2 Q8WZ11 Q8wz11 homo sapien
424 1.6 65 1 RPR_DROME Q24475 drosophila 497 6 1.6 90 2 Q7MQJ9 Q7mqj9 myrio vuln
425 1.6 65 2 Q82AP8 Q82ap8 streptomyc 498 6 1.6 90 2 Q7TXY0 Q7txy0 mycobacteri
426 1.6 66 2 Q81S33 Q81s33 bacillus an 499 6 1.6 91 2 Q638E6 Q638e6 bacillus ce
427 1.6 66 2 Q8DVA6 Q8dva6 streptococc 500 6 1.6 91 2 Q81AX4 Q81ax4 bacillus an
428 1.6 66 2 Q8QIA5 Q8qia5 hepatitis c 501 6 1.6 91 2 Q81YQ9 Q81yq9 bacillus an
429 1.6 66 2 Q91JF9 Q91jf9 hepatitis c 502 6 1.6 91 2 Q83BK5 Q83bk5 coxiella th
430 1.6 67 2 Q10735 Q10735 sus scrofa 503 6 1.6 91 2 Q6HG02 Q6hg02 bacillus th
431 1.6 67 2 Q6HSB6 Q6hsb6 bacillus an 504 6 1.6 92 1 PHAF RHIME 1.6 92 1 PHAF RHIME
432 1.6 67 2 Q633G7 Q633g7 bacillus ce 505 6 1.6 92 2 Q658X0 Q658x0 rhizobium m
433 1.6 67 2 Q817C9 Q817c9 bacillus ce 506 6 1.6 92 2 Q6J2A9 Q6j2a9 pseudomonas
434 1.6 67 2 Q6HC00 Q6hc00 bacillus th 507 6 1.6 92 2 Q7U6Q0 Q7u6q0 synchococc
435 1.6 67 2 Q6V5X9 Q6v5x9 human immun 508 6 1.6 92 2 Q9RJB2 Q9rjb2 streptomyc
436 1.6 68 2 Q8VAR4 Q8var4 white spot 509 6 1.6 92 2 Q7TW51 Q7tw51 uncultured
437 1.6 68 2 Q913B6 Q913b6 white spot 510 6 1.6 93 2 Q9W5C8 Q9w5c8 drosophila
438 1.6 69 2 Q913B6 Q913b6 white spot 511 6 1.6 93 2 P74056 P74056 synchocyst
439 1.6 69 2 Q71109 Q71109 bovine aden 512 6 1.6 93 2 Q6N625 Q6n625 rhodopsu
440 1.6 70 1 MEL_POLHE P59261 polistes he 513 6 1.6 94 2 Q8TFH9 Q8tfh9 schizosacch
441 1.6 70 2 Q97S32 Q97s32 streptococc 514 6 1.6 94 2 Q6N7U0 Q6n7u0 rhodopsu
442 1.6 70 2 Q6A1W6 Q6a1w6 desulfotale 515 6 1.6 94 2 Q7U8T3 Q7u8t3 synchococc
443 1.6 71 2 Q82950 Q82950 bacillus su 516 6 1.6 94 2 Q7TL25 Q7tl25 uncultured
444 1.6 71 2 Q80XY2 Q80xy2 mus musculu 517 6 1.6 95 2 Q9NZW7 Q9nzw7 homo sapien
445 1.6 72 2 Q81F00 Q81f00 trypanosoma 518 6 1.6 95 2 Q9ZE55 Q9ze55 carnobacter
446 1.6 72 2 Q7MQA0 Q7mqao vibrio vuln 519 6 1.6 95 2 Q89IL0 Q89il0 bradyrhizob
447 1.6 73 1 YA13 CANEF Q7vqv2 candidatus 520 6 1.6 95 2 Q84029 Q84029 influenza a
448 1.6 74 2 Q8UZE1 Q8uze1 pyrococcus 521 6 1.6 96 2 Q61692 Q61692 drosophila
449 1.6 74 2 Q8W261 Q8w261 arabidopsis 522 6 1.6 96 2 Q6AY00 Q6ay00 rattus norv
450 1.6 75 2 Q8Y180 Q8y180 raietonia s 523 6 1.6 97 2 Q7RDA7 Q7rda7 plasmodium
451 1.6 76 2 Q93T61 Q93t61 corynebacte 524 6 1.6 97 2 Q9LJP9 Q9ljp9 arabidopsis
452 1.6 78 2 Q7VAB7 Q7vab7 prochloroco 525 6 1.6 97 2 Q7X2K5 Q7x2k5 helicobacte
453 1.6 78 2 Q878T6 Q878t6 streptococc 526 6 1.6 97 2 Q8UFY0 Q8ufy0 agrobacteri
454 1.6 79 2 Q8QMD6 Q8qmd6 cucurbit ye 527 6 1.6 97 2 Q97Q06 Q97q06 streptococc
455 1.6 79 2 Q808I4 Q808i4 cucurbit ye 528 6 1.6 98 2 Q9H4C2 Q9h4c2 homo sapien
456 1.6 80 2 Q44820 Q44820 homo sapien 529 6 1.6 98 2 Q644Y9 Q644y9 eurycea bis
457 1.6 80 2 Q6JHS2 Q6jhs2 vibrio fisc 530 6 1.6 98 2 Q6K2J0 Q6k2j0 oryza sativ
458 1.6 81 2 Q18915 Q18915 bos taurus 531 6 1.6 98 2 Q7X2K3 Q7x2k3 helicobacte
459 1.6 81 2 Q8HYZ3 Q8hyz3 bos taurus 532 6 1.6 98 2 Q98J78 Q98j78 rhizobium 1
460 1.6 81 2 Q93R21 Q93r21 streptomyc 533 6 1.6 99 1 RL36 CANAL 1.6 99 1 RL36 CANAL
461 1.6 81 2 Q8Q141 Q8q141 sulfolobus 534 6 1.6 99 2 Q6ERT5 Q6ert5 oryza sativ
462 1.6 82 2 Q7Q348 Q7q348 anopheles 9 535 6 1.6 99 2 Q7X2K7 Q7x2k7 helicobacte
463 1.6 82 2 Q7Q348 Q7q348 anopheles 9 536 6 1.6 99 2 Q7X2K7 Q7x2k7 helicobacte
464 1.6 83 2 Q82FW9 Q82fw9 streptomyc 537 6 1.6 99 2 Q7N4G6 Q7n4g6 photorhabdu
465 1.6 83 2 Q7TM54 Q7tm54 uncultured 538 6 1.6 100 2 Q58804 Q58804 pyrococcus
466 1.6 83 2 Q8BCV7 Q8bcv7 mirafiori 1 539 6 1.6 100 2 Q6TBQ7 Q6tbq7 steller sea
467 1.6 84 2 Q7OFY7 Q7ofy7 anopheles 9 540 6 1.6 101 2 Q67UW1 Q67uw1 oryza sativ
468 1.6 84 2 Q88S15 Q88s15 lactobacilli 541 6 1.6 101 2 Q67UW1 Q67uw1 oryza sativ
469 1.6 84 2 Q9RKJ8 Q9rkj8 streptomyc 542 6 1.6 101 2 Q67T43 Q67t43 symbiobacte

470 6 1.6 84 2 Q8V9P8 Q8v9p8 sulfolobus
471 6 1.6 85 1 YME3 THIFE 1.6 85 2 Q8V9P8 Q8v9p8 sulfolobus
472 6 1.6 85 2 Q8V9P8 Q8v9p8 sulfolobus
473 6 1.6 85 2 Q8V9P8 Q8v9p8 sulfolobus
474 6 1.6 85 2 Q8V9P8 Q8v9p8 sulfolobus
475 6 1.6 85 2 Q8V9P8 Q8v9p8 sulfolobus
476 6 1.6 86 2 Q8V9P8 Q8v9p8 sulfolobus
477 6 1.6 86 2 Q8V9P8 Q8v9p8 sulfolobus
478 6 1.6 87 1 BC10_BOVIN BC10_BOVIN felis silve
479 6 1.6 87 1 BC10_BOVIN BC10_BOVIN felis silve
480 6 1.6 87 1 BC10_HUMAN BC10_HUMAN
481 6 1.6 87 1 BC10_MOUSE BC10_MOUSE
482 6 1.6 87 1 BC10_MOUSE BC10_MOUSE
483 6 1.6 87 2 Q91B61 Q91b61 brachydanio
484 6 1.6 88 2 Q79XU2 Q79xu2 streptococc
485 6 1.6 88 2 Q79XU2 Q79xu2 streptococc
486 6 1.6 88 2 Q8K780 Q8k780 streptococc
487 6 1.6 88 2 Q8K780 Q8k780 streptococc
488 6 1.6 88 2 Q9A0P0 Q9a0p0 streptococc
489 6 1.6 88 2 Q734G6 Q734g6 bacillus ce
490 6 1.6 88 2 Q7CMW8 Q7cmw8 streptococc
491 6 1.6 88 2 Q7CN26 Q7cn26 streptococc
492 6 1.6 88 2 Q82VJ2 Q82vj2 nitrosomona
493 6 1.6 88 2 Q8DQT3 Q8dqt3 streptococc
494 6 1.6 88 2 Q8DQT3 Q8dqt3 streptococc
495 6 1.6 90 2 P89505 P89505 saccharomyc
496 6 1.6 90 2 Q8WZ11 Q8wz11 homo sapien
497 6 1.6 90 2 Q7MQJ9 Q7mqj9 myrio vuln
498 6 1.6 90 2 Q7TXY0 Q7txy0 mycobacteri
499 6 1.6 91 2 Q638E6 Q638e6 bacillus ce
500 6 1.6 91 2 Q81AX4 Q81ax4 bacillus an
501 6 1.6 91 2 Q81YQ9 Q81yq9 bacillus an
502 6 1.6 91 2 Q83BK5 Q83bk5 coxiella th
503 6 1.6 91 2 Q6HG02 Q6hg02 bacillus th
504 6 1.6 92 1 PHAF RHIME 1.6 92 1 PHAF RHIME
505 6 1.6 92 2 Q658X0 Q658x0 rhizobium m
506 6 1.6 92 2 Q6J2A9 Q6j2a9 pseudomonas
507 6 1.6 92 2 Q7U6Q0 Q7u6q0 synchococc
508 6 1.6 92 2 Q9RJB2 Q9rjb2 streptomyc
509 6 1.6 92 2 Q7TW51 Q7tw51 uncultured
510 6 1.6 93 2 Q9W5C8 Q9w5c8 drosophila
511 6 1.6 93 2 P74056 P74056 synchocyst
512 6 1.6 93 2 Q6N625 Q6n625 rhodopsu
513 6 1.6 94 2 Q8TFH9 Q8tfh9 schizosacch
514 6 1.6 94 2 Q6N7U0 Q6n7u0 rhodopsu
515 6 1.6 94 2 Q7U8T3 Q7u8t3 synchococc
516 6 1.6 94 2 Q7TL25 Q7tl25 uncultured
517 6 1.6 95 2 Q9NZW7 Q9nzw7 homo sapien
518 6 1.6 95 2 Q9ZE55 Q9ze55 carnobacter
519 6 1.6 95 2 Q89IL0 Q89il0 bradyrhizob
520 6 1.6 95 2 Q84029 Q84029 influenza a
521 6 1.6 96 2 Q61692 Q61692 drosophila
522 6 1.6 96 2 Q6AY00 Q6ay00 rattus norv
523 6 1.6 97 2 Q7RDA7 Q7rda7 plasmodium
524 6 1.6 97 2 Q9LJP9 Q9ljp9 arabidopsis
525 6 1.6 97 2 Q7X2K5 Q7x2k5 helicobacte
526 6 1.6 97 2 Q8UFY0 Q8ufy0 agrobacteri
527 6 1.6 97 2 Q97Q06 Q97q06 streptococc
528 6 1.6 98 2 Q9H4C2 Q9h4c2 homo sapien
529 6 1.6 98 2 Q644Y9 Q644y9 eurycea bis
530 6 1.6 98 2 Q6K2J0 Q6k2j0 oryza sativ
531 6 1.6 98 2 Q7X2K3 Q7x2k3 helicobacte
532 6 1.6 98 2 Q98J78 Q98j78 rhizobium 1
533 6 1.6 99 1 RL36 CANAL 1.6 99 1 RL36 CANAL
534 6 1.6 99 2 Q6ERT5 Q6ert5 oryza sativ
535 6 1.6 99 2 Q7X2K7 Q7x2k7 helicobacte
536 6 1.6 99 2 Q7N4G6 Q7n4g6 photorhabdu
537 6 1.6 99 2 Q7N4G6 Q7n4g6 photorhabdu
538 6 1.6 100 2 Q58804 Q58804 pyrococcus
539 6 1.6 100 2 Q6TBQ7 Q6tbq7 steller sea
540 6 1.6 101 2 Q67UW1 Q67uw1 oryza sativ
541 6 1.6 101 2 Q67UW1 Q67uw1 oryza sativ
542 6 1.6 101 2 Q67T43 Q67t43 symbiobacte

543	6	1.6	101	2	Q72D05	Q72d05 desulfovibr	616	2	Q84060	Q84060 influenza a
544	6	1.6	102	2	Q9CT23	Q9ct23 mus musculu	617	1	YG4U YEAST	Y3308 nanocarhae
545	6	1.6	102	2	Q6I114	Q6i114 drosophila	618	2	Q74MW7	Q74mw7 neurospora
546	6	1.6	102	2	Q746T6	Q746t6 geobacter s	619	2	Q7RY92	Q7ry92 arabidopsis
547	6	1.6	102	2	Q8C2B7	Q8c2b7 mus musculu	620	2	Q8L3S7	Q8l3s7 arabidopsis
548	6	1.6	102	2	Q9D8U9	Q9d8u9 m mus muscu	621	2	Q9SLC8	Q9slc8 arabidopsis
549	6	1.6	102	2	Q6Y8M2	Q6y8m2 human immun	622	2	Q72C35	Q72c35 desulfovibr
550	6	1.6	103	2	Q8Z7S8	Q8z7s8 oryza sativ	623	2	Q83R32	Q83r32 shigella fl
551	6	1.6	103	2	Q8KK27	Q8kk27 proteus vul	624	2	Q9ANL7	Q9anl7 bradyrhizob
552	6	1.6	103	2	Q6D912	Q6d912 erwinia car	625	1	RV44 MOUSE	RV44 mus musculu
553	6	1.6	103	2	Q07664	Q07664 influenza a	626	2	Q8ZV94	Q8zv94 pyrobaculum
554	6	1.6	103	2	Q07665	Q07665 influenza a	627	2	P87272	P87272 saccharomyc
555	6	1.6	103	2	Q5LED5	Q5led5 influenza a	628	2	Q6XFP0	Q6xfp0 nectarinia
556	6	1.6	103	2	Q9YVP9	Q9yvp9 melanoplus	629	2	Q6ES28	Q6es28 oryza sativ
557	6	1.6	104	1	RL24_PSEAB	Q9hwe6 pseudomonas	630	2	Q8VTC5	Q8vtc5 helicobacte
558	6	1.6	104	1	RL24_PSEPK	Q88qm4 pseudomonas	631	2	Q8YK1	Q8ykb1 anabaena sp
559	6	1.6	104	1	RL24_PSESM	Q889w0 pseudomonas	632	2	Q9RWK4	Q9rww4 deinococcus
560	6	1.6	104	2	Q9YGE2	Q9yge2 aeropyrum p	633	2	RV45 MOUSE	RV45 mus musculu
561	6	1.6	104	2	Q8NV76	Q8nv76 staphylococ	634	2	Q9XZE8	Q9xze8 oxytricha t
562	6	1.6	104	2	Q72XS2	Q72xs2 bacillus ce	635	2	Q6XFE4	Q6xfe4 nectarinia
563	6	1.6	104	2	Q815G2	Q815g2 bacillus ce	636	2	Q6XFE5	Q6xfe5 nectarinia
564	6	1.6	104	2	Q81X21	Q81x21 bacillus an	637	2	Q6XFE7	Q6xfe7 nectarinia
565	6	1.6	105	2	Q96YV4	Q96yv4 sulfolobus	638	2	Q6XFE9	Q6xfe9 nectarinia
566	6	1.6	105	2	Q44813	Q44813 caenorhabdi	639	2	Q6XFX0	Q6xfx0 nectarinia
567	6	1.6	105	2	Q7M0S1	Q7m0s1 myxococcus	640	2	Q6XFX2	Q6xfx2 nectarinia
568	6	1.6	106	2	Q8X3P5	Q8x3p5 escherichia	641	2	Q6XFX5	Q6xfx5 nectarinia
569	6	1.6	107	2	Q6YV07	Q6yv07 oryza sativ	642	2	Q6XFX9	Q6xfx9 nectarinia
570	6	1.6	107	2	Q6HQV5	Q6hqv5 bacillus ce	643	2	Q6XFY0	Q6xfy0 nectarinia
571	6	1.6	107	2	Q631F8	Q631f8 bacillus ce	644	2	Q6XFY1	Q6xfy1 nectarinia
572	6	1.6	107	2	Q6HB93	Q6hb93 bacillus th	645	2	Q8SB17	Q8sb17 oryza sativ
573	6	1.6	107	2	Q7LZ26	Q7lzz6 influenza a	646	2	Q9LGI1	Q9lgi1 oryza sativ
574	6	1.6	108	2	Q9H2R1	Q9h2r1 homo sapien	647	2	Q67R66	Q67r66 symbiobacte
575	6	1.6	109	1	ATPL_UREPA	Q9p08 ureaplasma	648	1	RL18_BUCAK	RL18 buchnera ap
576	6	1.6	109	1	Y4J7_METAC	Q8tip5 methanosaar	649	2	Q8LEM9	Q8lem9 arabidopsis
577	6	1.6	109	2	Q8PR10	Q8pr10 xanthomonas	650	2	Q9ZTH7	Q9zth7 physalis ci
578	6	1.6	109	2	Q6F792	Q6f792 acinetobact	651	2	Q65SD3	Q65sd3 oryza sativ
579	6	1.6	109	2	Q81246	Q81246 hepatitis c	652	2	Q6H088	Q6h088 fremyella d
580	6	1.6	109	2	Q81300	Q81300 hepatitis c	653	2	Q8XY03	Q8xy03 raietonia s
581	6	1.6	109	2	Q81482	Q81482 hepatitis c	654	2	Q8Y802	Q8y802 listeria mo
582	6	1.6	110	2	Q95SE7	Q95se7 drosophila	655	2	Q720W6	Q720w6 listeria mo
583	6	1.6	110	2	Q7D4T5	Q7d4t5 mycobacteri	656	1	HIS3_RHOSH	Q3158 rhodobacter
584	6	1.6	110	2	Q7NVA5	Q7nva5 chronobacte	657	2	Q9ME92	Q9me92 oenothera h
585	6	1.6	110	2	Q831I9	Q831i9 shigella fl	658	2	Q9L3V9	Q9l3v9 bacillus ci
586	6	1.6	110	2	Q808E5	Q808e5 hepatitis c	659	2	Q63105	Q63105 rattus norv
587	6	1.6	110	2	Q808E6	Q808e6 hepatitis c	660	2	Q7YV68	Q7yv68 trypanosoma
588	6	1.6	110	2	Q808E7	Q808e7 hepatitis c	661	2	Q9A7K6	Q9a7k6 caulobacter
589	6	1.6	111	1	Y518_METTH	Q66618 methanobact	662	1	RL22_SYNY3	P73315 synechocyst
590	6	1.6	111	2	Q6DY61	Q6dy61 nectarinia	663	2	Q01445	Q01445 caenorhabdi
591	6	1.6	111	2	Q6DY62	Q6dy62 nectarinia	664	2	Q815P1	Q815p1 bacillus ce
592	6	1.6	111	2	Q6DY64	Q6dy64 nectarinia	665	2	Q99NG4	Q99ng4 mus musculu
593	6	1.6	111	2	Q6DY65	Q6dy65 nectarinia	666	2	Q8K3C1	Q8k3c1 mus musculu
594	6	1.6	111	2	Q6DY66	Q6dy66 nectarinia	667	2	Q66897	Q66897 four corner
595	6	1.6	111	2	Q6DY98	Q6dy98 nectarinia	668	2	Q87WR7	Q87wr7 pseudomonas
596	6	1.6	111	2	Q6DYA1	Q6dyal nectarinia	669	2	Q9Z749	Q9z749 chlamydia p
597	6	1.6	111	2	Q6DYA2	Q6dy2 nectarinia	670	2	Q6ARF8	Q6arf8 desulfotale
598	6	1.6	111	2	Q6DYA5	Q6dya5 nectarinia	671	2	Q8B5J5	Q8b5j5 dengue viru
599	6	1.6	111	2	Q8LKE8	Q8lke8 malus domes	672	2	Q8B5J6	Q8b5j6 dengue viru
600	6	1.6	111	2	Q9SNR9	Q9snr9 oryza sativ	673	2	Q8B5J7	Q8b5j7 dengue viru
601	6	1.6	111	2	Q07804	Q07804 mycobacteri	674	2	Q8B5J8	Q8b5j8 dengue viru
602	6	1.6	111	2	Q8MI86	Q8mie6 bdellovibri	675	2	Q8B5J9	Q8b5j9 dengue viru
603	6	1.6	111	2	Q735D6	Q735d6 bacillus ce	676	2	Q8B5K0	Q8b5k0 dengue viru
604	6	1.6	111	2	Q7TV14	Q7tv14 mycobacteri	677	2	Q8B5K1	Q8b5k1 dengue viru
605	6	1.6	111	2	Q82QM5	Q82qm5 streptomyce	678	2	Q8B5K2	Q8b5k2 dengue viru
606	6	1.6	112	2	Q75JB5	Q75jbs dictyosteli	679	2	Q8B5K3	Q8b5k3 dengue viru
607	6	1.6	112	2	Q81672	Q81672 hepatitis c	680	2	Q8B5K4	Q8b5k4 dengue viru
608	6	1.6	113	1	APG1_MOUSE	Q82407 mus musculu	681	2	Q8B5K5	Q8b5k5 dengue viru
609	6	1.6	113	2	Q9Y9K8	Q9y9k8 aeropyrum p	682	2	Q8B5K6	Q8b5k6 dengue viru
610	6	1.6	113	2	Q9JZP9	Q9jzp9 neisseria m	683	2	Q8B5K7	Q8b5k7 dengue viru
611	6	1.6	113	2	Q71179	Q71179 hepatitis c	684	2	Q8B5K8	Q8b5k8 dengue viru
612	6	1.6	113	2	Q80N59	Q80n59 hepatitis c	685	2	Q8B5K9	Q8b5k9 dengue viru
613	6	1.6	113	2	Q80NA2	Q80na2 hepatitis c	686	2	Q8B5L0	Q8b5l0 dengue viru
614	6	1.6	113	2	Q80NA3	Q80na3 hepatitis c	687	2	Q8B5L1	Q8b5l1 dengue viru
615	6	1.6	113	2	Q84030	Q84030 influenza a	688	2	Q8B5L2	Q8b5l2 dengue viru

689	6	1.6	123	2	Q6IAD3	Q6iad3 homo sapien	762	6	1.6	139	2	Q9AK85	Q9ak85 streptomyc
690	6	1.6	123	2	Q9NXX1	Q9nxx1 homo sapien	763	6	1.6	139	2	Q9YWL0	Q9ywl0 melanoplus
691	6	1.6	123	2	Q8VPC3	Q8vpc3 micrococ	764	6	1.6	140	2	Q756H3	Q756h3 ashbya goss
692	6	1.6	123	2	Q3L242	Q3l242 streptomyc	765	6	1.6	140	2	Q716E1	Q716e1 bacterioph
693	6	1.6	123	2	Q7T9V0	Q7t9v0 oxaphyses	766	6	1.6	140	2	Q9ARP0	Q9arp0 oryza sativ
694	6	1.6	123	2	Q86997	Q86997 sugarcane b	767	6	1.6	140	2	Q68252	Q68252 hepatitis c
695	6	1.6	124	1	ZWIA HUMAN	Zwia human	768	6	1.6	141	1	USPA PASMU	Q9c1e9 pasteurella
696	6	1.6	124	1	Q8U6H5	Q8u6h5 agro bacteri	769	6	1.6	141	2	Q7PI81	Q7pi81 anopheles g
697	6	1.6	125	2	Q8LJR5	Q8ljr5 photobacter	770	6	1.6	141	2	Q8Y2R3	Q8y2r3 ralstonia s
698	6	1.6	125	2	Q9A2N6	Q9a2n6 caulobacter	771	6	1.6	141	2	Q98IG1	Q98ig1 rhizobium l
699	6	1.6	126	2	Q6ZU12	Q6zu12 homo sapien	772	6	1.6	141	2	Q9KSI4	Q9ksi4 vibrio chol
700	6	1.6	126	2	Q9H354	Q9h354 homo sapien	773	6	1.6	142	2	Q7Y481	Q7y481 cyanophage
701	6	1.6	126	2	Q9BE92	Q9be92 macaca fasc	774	6	1.6	142	2	Q7Y481	Q7y481 cyanophage
702	6	1.6	126	2	Q51511	Q51511 pneumomonas	775	6	1.6	142	2	Q6Y9F4	Q6y9f4 xerophyta h
703	6	1.6	126	2	Q65VH6	Q65vh6 manheimia	776	6	1.6	142	2	Q6J9F4	Q6j9f4 clostridium
704	6	1.6	127	2	Q74N98	Q74n98 nanoarchaeu	777	6	1.6	142	2	Q8XJG1	Q8xjg1 vibrio para
705	6	1.6	127	2	Q21039	Q21039 dictyostell	778	6	1.6	142	2	Q87I31	Q87i31 vibrio para
706	6	1.6	127	2	Q6H4P1	Q6h4p1 oryza sativ	779	6	1.6	142	2	Q9CMK2	Q9cmk2 pasteurella
707	6	1.6	128	2	Q6LTT5	Q6lts5 photobacter	780	6	1.6	142	2	Q9Z4W4	Q9z4w4 streptomyc
708	6	1.6	128	1	CRB2 LISIN	Q929t6 listeria in	781	6	1.6	142	2	Q91HJ4	Q91hj4 avian param
709	6	1.6	129	2	Q96ZR1	Q96zr1 sulfolobus	782	6	1.6	143	1	PONA DICDI	P54660 dictyostell
710	6	1.6	129	2	Q7UEB1	Q7ueb1 rhodopirell	783	6	1.6	143	1	YIFN HAEIN	P43936 haemophilus
711	6	1.6	129	2	Q8ZSN3	Q8zsn3 nitrosonoma	784	6	1.6	143	2	Q7QYR8	Q7qyr8 giardia lam
712	6	1.6	129	2	Q91C23	Q91cz3 tt virus. o	785	6	1.6	143	2	Q9BE32	Q9be32 macaca fasc
713	6	1.6	130	2	Q9H4C3	Q9h4c3 homo sapien	786	6	1.6	143	2	Q7Y496	Q7y496 cyanophage
714	6	1.6	130	2	Q7YV79	Q7yvf9 trypanosoma	787	6	1.6	143	2	Q6K222	Q6k222 oryza sativ
715	6	1.6	130	2	Q8SD59	Q8sd59 pneumomonas	788	6	1.6	143	2	Q6Y2G3	Q6y2g3 oryza sativ
716	6	1.6	130	2	Q8K4C6	Q8k4c6 oryza sativ	789	6	1.6	143	2	Q6Y2G3	Q6y2g3 coxiella bu
717	6	1.6	130	2	Q99RE3	Q99re3 staphylococ	790	6	1.6	143	2	Q8RIH6	Q8rih6 mus musculu
718	6	1.6	130	2	Q7A007	Q7a007 staphylococ	791	6	1.6	143	2	Q6U390	Q6u390 human herpe
719	6	1.6	130	2	Q7A3K8	Q7a3k8 staphylococ	792	6	1.6	143	2	Q6U391	Q6u391 human herpe
720	6	1.6	130	2	Q6G614	Q6g614 staphylococ	793	6	1.6	143	2	Q9UYT5	Q9uyt5 pyrococcus
721	6	1.6	130	2	Q6GDV0	Q6gdv0 staphylococ	794	6	1.6	144	2	Q96NC1	Q96nc1 homo sapien
722	6	1.6	131	2	Q970U1	Q970u1 sulfolobus	795	6	1.6	144	2	Q96NC1	Q96nc1 homo sapien
723	6	1.6	131	2	Q8TFH6	Q8tfh6 schizosacch	796	6	1.6	145	1	HIN1 HUMAN	Q01804 homo sapien
724	6	1.6	131	2	Q18903	Q18903 caenorhabdi	797	6	1.6	145	2	Q8IEB8	Q8ieb8 plasmodium
725	6	1.6	131	2	Q6B7D4	Q6b7d4 legionella	798	6	1.6	145	2	Q8LID3	Q8lid3 streptomyc
726	6	1.6	131	2	Q7UT01	Q7ut01 rhodopirell	799	6	1.6	145	2	Q6H063	Q6h063 tremella d
727	6	1.6	131	2	Q997Q5	Q997q5 clostridium	800	6	1.6	145	2	Q7AXX9	Q7axx9 salmonella
728	6	1.6	131	2	Q8CZ68	Q8cz68 erwinia car	801	6	1.6	145	2	Q93IQ8	Q93iq8 salmonella
729	6	1.6	132	1	RNPA MICLU	P21172 micrococ	802	6	1.6	146	2	Q9UKT0	Q9uk0 homo sapien
730	6	1.6	132	2	Q70KCO	Q70kco gordonia we	803	6	1.6	146	2	Q9UMQ0	Q9umq0 homo sapien
731	6	1.6	132	2	Q835A7	Q835a7 enterococcu	804	6	1.6	146	2	Q6L7I9	Q6l7i9 canis famil
732	6	1.6	132	2	Q83GC1	Q83gc1 tropheryma	805	6	1.6	146	2	Q8GT54	Q8gt54 hordeum vul
733	6	1.6	132	2	Q83HV8	Q83hv8 tropheryma	806	6	1.6	146	2	Q98NF2	Q98nf2 rhizobium l
734	6	1.6	134	2	Q6H4E5	Q6h4e5 oryza sativ	807	6	1.6	146	2	Q6MNI1	Q6mni1 dellolovibri
735	6	1.6	134	2	Q6H4G1	Q6h4g1 oryza sativ	808	6	1.6	146	2	Q7VFX3	Q7vfx3 helicobacte
736	6	1.6	134	2	Q44672	Q44672 borrelia af	809	6	1.6	147	2	Q6IPW1	Q6ipw1 escherichia
737	6	1.6	134	2	Q64UX9	Q64ux9 bacteroides	810	6	1.6	147	2	Q842F2	Q842f2 streptococc
738	6	1.6	134	2	Q6D168	Q6d168 erwinia un	811	6	1.6	147	2	Q8PRM2	Q8prm2 xanthomonas
739	6	1.6	134	2	Q99MD4	Q99md4 meriones un	812	6	1.6	147	2	Q7MP01	Q7mp01 vibrio vuln
740	6	1.6	135	1	Y886 METKA	Q8tva6 methanopyru	813	6	1.6	147	2	Q87SL6	Q87sl6 vibrio para
741	6	1.6	135	2	Q8PTW9	Q8ptw9 methanosarc	814	6	1.6	147	2	Q8CPK3	Q8cpk3 staphylococ
742	6	1.6	135	2	Q8ZXQ8	Q8zxq8 pyrobaculum	815	6	1.6	147	2	Q8DEG3	Q8deg3 vibrio vuln
743	6	1.6	135	2	Q67LB2	Q67lb2 symbiobacte	816	6	1.6	147	2	Q8DKZ9	Q8dkz9 synecococc
744	6	1.6	136	2	Q96N35	Q96n35 homo sapien	817	6	1.6	147	2	Q8FGK6	Q8fgk6 escherichia
745	6	1.6	136	2	Q9H7X8	Q9h7x8 homo sapien	818	6	1.6	147	2	Q8XBA8	Q8xba8 escherichia
746	6	1.6	136	2	Q6LJB8	Q6ljb8 photobacter	819	6	1.6	147	2	Q6K2J8	Q6k2j8 oryza sativ
747	6	1.6	136	2	Q6NAI8	Q6nai8 rhodopseudo	820	6	1.6	148	2	Q6B7C0	Q6b7c0 legionella
748	6	1.6	136	2	Q7NQ89	Q7nq89 vibrio vuln	821	6	1.6	148	2	Q6B7C1	Q6b7c1 legionella
749	6	1.6	136	2	Q7VX17	Q7vx17 bordetella	822	6	1.6	148	2	Q6B7C2	Q6b7c2 legionella
750	6	1.6	136	2	Q7W7X0	Q7w7x0 bordetella	823	6	1.6	148	2	Q6B7C3	Q6b7c3 legionella
751	6	1.6	136	2	Q7WLB0	Q7wlb0 bordetella	824	6	1.6	148	2	Q6B7C4	Q6b7c4 legionella
752	6	1.6	136	2	Q8DD51	Q8dd51 vibrio vuln	825	6	1.6	148	2	Q6B7C5	Q6b7c5 legionella
753	6	1.6	136	2	Q8JDY2	Q8jdy2 human immun	826	6	1.6	148	2	Q6B7C6	Q6b7c6 legionella
754	6	1.6	138	2	Q9NE26	Q9ne26 leishmania	827	6	1.6	148	2	Q6B7C7	Q6b7c7 legionella
755	6	1.6	138	2	Q8ERQ6	Q8erq6 oceanobacil	828	6	1.6	148	2	Q6B7C8	Q6b7c8 legionella
756	6	1.6	139	1	ARSC BACHD	Q9k8k8 bacillus ha	829	6	1.6	148	2	Q6B7C9	Q6b7c9 legionella
757	6	1.6	139	2	Q58363	Q58363 pyrococcus	830	6	1.6	148	2	Q6B7D0	Q6b7d0 legionella
758	6	1.6	139	2	Q33304	Q33304 mycobacteri	831	6	1.6	148	2	Q6B7D1	Q6b7d1 legionella
759	6	1.6	139	2	Q87LT8	Q87lt8 vibrio para	832	6	1.6	148	2	Q6B7D2	Q6b7d2 legionella
760	6	1.6	139	2	Q89KM2	Q89km2 bradyrhizob	833	6	1.6	148	2	Q6B7D3	Q6b7d3 legionella
761	6	1.6	139	2	Q8F6L3	Q8f6l3 leptospira	834	6	1.6	148	2	Q6B7D3	Q6b7d3 legionella

835	6	1.6	148	2	Q6B7D5	Q6b7d5 legionella	908	1.6	159	2	Q7PNH2	Q7pnh2 anopheles g
836	6	1.6	148	2	Q6B7D6	Q6b7d6 legionella	909	1.6	159	2	Q72PP4	Q72pp4 leptospira
837	6	1.6	148	2	Q92RW8	Q92rw8 rhizobium m	910	1.6	159	2	Q749V4	Q749v4 geobacter s
838	6	1.6	148	2	Q93246	Q93246 crypinus ca	911	1.6	159	2	Q7POT7	Q7pot7 chromobacte
839	6	1.6	149	2	Q9LY57	Q9ly57 arabidopsis	912	1.6	159	2	Q8BXD9	Q8bx9 mus musculus
840	6	1.6	149	2	Q73048	P73048 synechocyst	913	1.6	160	2	Q62357	Q62357 caenorhabdi
841	6	1.6	149	2	Q9JWE1	Q9jwe1 neisseria m	914	1.6	160	2	Q7QAI0	Q7qai0 anopheles g
842	6	1.6	149	2	Q9JXJ2	Q9jxj2 neisseria m	915	1.6	160	2	Q8KZ46	Q8kz46 uncultured
843	6	1.6	150	1	RP21 MOUSE	Q8r040 mus musculu	916	1.6	160	2	Q92KK5	Q92kk5 thizobium m
844	6	1.6	150	2	Q9USE0	Q9use0 schizosacch	917	1.6	160	2	Q6ADH9	Q6adh9 leifsonia x
845	6	1.6	150	2	Q8NP75	Q8nf75 homo sapien	918	1.6	160	2	Q8AXA8	Q8axa8 gallus immu
846	6	1.6	150	2	Q48865	Q48865 agrostis st	919	1.6	160	2	Q8ARD9	Q8aed9 human immu
847	6	1.6	150	2	Q05989	Q05989 brassica ol	920	1.6	161	2	Q64A54	Q64a54 uncultured
848	6	1.6	150	2	Q8RVJ5	Q8rvj5 pinus pinas	921	1.6	161	2	Q64ED7	Q64ed7 uncultured
849	6	1.6	150	2	Q70AJ3	Q70aj3 triticum ae	922	1.6	161	2	Q92229	Q92229 emericella
850	6	1.6	150	2	Q83299	Q83299 escherichia	923	1.6	161	2	Q96D98	Q96d98 homo sapien
851	6	1.6	150	2	Q832A6	Q832a6 escherichia	924	1.6	161	2	Q6ZQV2	Q6zqv2 homo sapien
852	6	1.6	150	2	Q97HB5	Q97hb5 clostridium	925	1.6	161	2	Q7PSZ2	Q7psz2 anopheles g
853	6	1.6	150	2	Q89LZ4	Q89lz4 bradyrhizob	926	1.6	161	2	Q69K10	Q69k10 oryza sativ
854	6	1.6	150	2	Q8F1X8	Q8f1x8 escherichia	927	1.6	161	2	Q9D7K2	Q9d7k2 mus musculu
855	6	1.6	151	1	CT78 HUMAN	Q9br46 homo sapien	928	1.6	162	2	Q8SWG5	Q8swg5 encephalito
856	6	1.6	151	2	Q26932	Q26932 methanobact	929	1.6	162	2	Q94X57	Q94x57 dendropoma
857	6	1.6	151	2	Q9H4C4	Q9h4c4 homo sapien	930	1.6	162	2	Q853J5	Q853j5 mycobacteri
858	6	1.6	151	2	Q84W91	Q84w91 arabidopsis	931	1.6	162	2	Q93F91	Q93f91 streptomyce
859	6	1.6	151	2	Q93GC1	Q93gc1 xanthomonas	932	1.6	162	2	Q7P340	Q7p340 fusobacteri
860	6	1.6	152	1	RL30 ARCPU	Q28375 archaeoglob	933	1.6	162	2	Q8RDM2	Q8rdm2 fusobacteri
861	6	1.6	152	1	RL30 METHH	Q26132 methanobact	934	1.6	162	2	Q98L95	Q98l95 rhizobium l
862	6	1.6	152	2	Q648R1	Q648r1 uncultured	935	1.6	162	2	Q7VXL2	Q7vxl2 bordetella
863	6	1.6	152	2	Q7VK74	Q7vk74 helicobacte	936	1.6	162	2	Q7W5V5	Q7w5v5 bordetella
864	6	1.6	153	2	Q8PV29	Q8pv29 methanosarc	937	1.6	162	2	Q8FGH4	Q8fgh4 escherichia
865	6	1.6	153	2	Q8TR36	Q8tr36 methanosarc	938	1.6	162	2	Q9X930	Q9x930 streptomyce
866	6	1.6	153	2	Q7SG14	Q7sg14 neurospora	939	1.6	162	2	Q6MDE5	Q6mde5 parachlamyd
867	6	1.6	153	2	Q84J58	Q84j58 oryza sativ	940	1.6	163	2	Q6T9Q5	Q6t9q5 vitis ripar
868	6	1.6	153	2	Q66792	Q66792 aquifex aeo	941	1.6	163	2	Q9STI9	Q9st19 arabidopsis
869	6	1.6	153	2	Q89H71	Q89h71 bradyrhizob	942	1.6	163	2	Q93GK3	Q93gk3 klebsiella
870	6	1.6	153	2	P79919	P79919 xenopus lae	943	1.6	163	2	Q639X1	Q639x1 bacillus ce
871	6	1.6	154	1	RL30 METJA	P54046 methanococc	944	1.6	164	2	Q6J7Y5	Q6j7y5 actinoplane
872	6	1.6	154	1	RL30 METVA	P14035 methanococc	945	1.6	164	2	Q8E221	Q8e221 streptococc
873	6	1.6	154	1	SSRP TREPA	Q83214 treponema p	946	1.6	164	2	Q8EA02	Q8ea02 shewanella
874	6	1.6	154	2	Q61XD2	Q61xd2 methanococc	947	1.6	164	2	Q9CVR8	Q9cvr8 mus musculu
875	6	1.6	154	2	Q6M0J3	Q6m0j3 methanococc	948	1.6	164	2	Q9EP94	Q9ep94 mus musculu
876	6	1.6	154	2	Q8RQ15	Q8rq15 bacillus ce	949	1.6	165	1	FTN2 HARIN	P43708 haemophilus
877	6	1.6	154	2	Q85G82	Q85g82 bacillus li	950	1.6	165	1	YAJ5_SCHPO	P99905 schizosacch
878	6	1.6	154	2	Q73MP4	Q73mp4 treponema d	951	1.6	165	2	Q8HQV4	Q8hqv4 tropidola ef
879	6	1.6	154	2	Q7MIX6	Q7mix6 vibrio vuln	952	1.6	165	2	Q61WI6	Q61wi6 escherichia
880	6	1.6	154	2	Q8DAY0	Q8day0 vibrio vuln	953	1.6	165	2	Q97RF8	Q97rf8 streptococc
881	6	1.6	155	1	RL30 PYRAB	Q9vlv6 pyrococcus	954	1.6	165	2	Q87Y87	Q87y87 pseudomonas
882	6	1.6	155	1	RL30 PYRHO	Q9440 pyrococcus	955	1.6	165	2	Q8DQ46	Q8dq46 streptococc
883	6	1.6	155	2	Q849M4	Q849m4 uncultured	956	1.6	165	2	Q9CMY3	Q9cm3 pasteurella
884	6	1.6	155	2	Q97CN4	Q97cn4 thermoplasm	957	1.6	166	1	Q9YI27	Q9y127 carassius a
885	6	1.6	155	2	Q9H7H8	Q9h7h8 pyrococcus	958	1.6	166	1	IL3 RAT	P04823 rattus norv
886	6	1.6	155	2	Q7QLU3	Q7qlu3 anopheles g	959	1.6	166	1	SSB MYCPN	P75542 mycoplasma
887	6	1.6	155	2	Q6WH24	Q6wh24 bacterioph	960	1.6	166	2	Q8RAG3	Q8rag3 thermoanaer
888	6	1.6	155	2	Q7Y3W5	Q7y3w5 bacterioph	961	1.6	166	2	Q6D1N1	Q6d1n1 erwinia car
889	6	1.6	155	2	Q82UC3	Q82uc3 leptospira	962	1.6	166	2	Q8V3I5	Q8v3i5 swinepox vi
890	6	1.6	155	2	Q82VX9	Q82vx9 nitrosomona	963	1.6	167	1	PLMP GRIFR	P81054 grifolia fro
891	6	1.6	155	2	Q8F0Q5	Q8f0q5 leptospira	964	1.6	167	1	Y199 MYCGE	P47441 mycoplasma
892	6	1.6	155	2	Q9DH98	Q9dh98 gallid herp	965	1.6	167	1	Y005_BPHP1	P51706 bacterioph
893	6	1.6	156	1	PVRI METTH	Q26938 methanobact	966	1.6	167	2	Q467I3	Q467i3 bos taurus
894	6	1.6	156	1	SSB1_STRO	Q9ky19 streptomyce	967	1.6	167	2	Q46753	Q46753 bos taurus
895	6	1.6	156	2	Q7WGR7	Q7wgr7 bordetella	968	1.6	167	2	Q46763	Q46763 bos taurus
896	6	1.6	156	2	Q88E81	Q88e81 pseudomonas	969	1.6	167	2	Q46782	Q46782 bos taurus
897	6	1.6	156	2	Q9D8L9	Q9d8l9 mus musculu	970	1.6	167	2	Q6LBC7	Q6lbc7 oligotroph
898	6	1.6	157	2	Q8TXR0	Q8txr0 methanopyru	971	1.6	168	1	RL10 MYCPU	Q98qel mycoplasma
899	6	1.6	157	2	Q6CHV5	Q6chv5 varrowia li	972	1.6	168	2	Q7EZX8	Q7ezx8 oryza sativ
900	6	1.6	157	2	Q7KRA1	Q7kral drosophila	973	1.6	168	2	Q8VQZ1	Q8vqz1 myxococcus
901	6	1.6	157	2	Q6LS75	Q6ls75 photobacter	974	1.6	168	2	Q98K83	Q98k83 rhizobium l
902	6	1.6	158	1	P1GP HUMAN	P57054 h phosphati	975	1.6	168	2	Q8UCX8	Q8ucx8 agrobacteri
903	6	1.6	158	2	Q57824	Q57824 pyrococcus	976	1.6	168	2	Q8QS78	Q8qsr78 pongine her
904	6	1.6	158	2	Q84HN3	Q84hn3 kitaatospo	977	1.6	169	2	Q84Y41	Q84y41 ranunculus
905	6	1.6	158	2	Q98CT6	Q98ct6 rhizobium l	978	1.6	169	2	Q92VT0	Q92vt0 rhizobium m
906	6	1.6	159	2	Q6UY33	Q6uy33 homo sapien	979	1.6	169	2	Q9K962	Q9k962 bacillus ha
907	6	1.6	159	2	Q6ZNY8	Q6zny8 homo sapien	980	1.6	169	2	P97688	P97688 rattus norv

981 Q919p8 brachydanio
982 Q80333 pyrococcus
983 Q86u37 homo sapien
984 Q8h912 homo sapien
985 Q8uq13 smithiantha
986 Q72uc4 leptospira
987 Q8f0q4 leptospira
988 Q96na0 homo sapien
989 Q95rf6 drosophila
990 Q8lr45 oryza sativ
991 Q8xuv7 raietonia s
992 Q8ner8 corynebacte
993 Q7nfm7 gloebacter
994 Q7vbg6 prochloroco
995 Q6mcs2 parachlamyd
996 Q6lca0 mus musculu
997 Q79f75 brevibacter
998 Q79vg4 corynebacte
999 Q7uqy7 rhodopirell
1000 Q8fpx2 corynebacte

ALIGNMENTS

RESULT 1
CYCIN HUMAN
ID CYCIN HUMAN STANDARD; PRT; 377 AA.
AC Q14094;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cyclin I.
GN Name=CCNI;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Forebrain cortex;
RX MEDLINE=96086776; PubMed=7493655; DOI=10.1006/excr.1995.1406;
RT Nakamura T., Sanokawa R., Sasaki Y.F., Ayusawa D., Oishi M., Mori N.;
RT "Cyclin I: a new cyclin encoded by a gene isolated from human brain.";
RL Exp. Cell Res. 221:534-542(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Chen J.H., Luo W.Q., Zhou Y., Zhou H.J., Huang X.W., Yuan J.G.,
RA Qiang B.Q.;
RT "Isolating a new cDNA coding for human cyclin protein.";
RT Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A., AND VARIANT ILE-207.
RA Rieder M.J., Livingston R.J., Daniels M.R., Montoya M.A., Chung M.-W.,
RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
RA Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;
RT "NIHES-SNPs, environmental genome project, NIHES RS15478, Department
RT of Genome Sciences, Seattle, WA (URL: <http://egp.gs.washington.edu>).";
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney, and Muscle;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore I., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.C., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.U.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP SEQUENCE OF 1-178 FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=98381026; PubMed=9705831; DOI=10.1006/bbrc.1998.9052;
RA Zhu X., Naz R.K.;
RT "Expression of a novel isoform of cyclin I in human testis.";
RL Biochem. Biophys. Res. Commun. 249:56-60(1998).
CC -I- TISSUE SPECIFICITY: Highest levels in adult heart, brain and
CC skeletal muscle. Lower levels in fetal placenta, lung, kidney and
CC pancreas. Also high levels in fetal brain and lower levels in
CC fetal lung, liver and kidney. Also abundant in testis and thyroid.
CC -I- DEVELOPMENTAL STAGE: Expression is independent of the cell cycle
CC in lung fibroblasts.
CC -I- SIMILARITY: Belongs to the cyclin family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; D50310; BAA08849.1; -;
CC EMBL; AY207372; AAO13492.1; -;
CC EMBL; BC000420; AAH00420.1; -;
CC EMBL; BC004975; AAH04975.1; -;
CC EMBL; AF135162; AAF43786.1; -;
CC PIR; JEO264; JEO264.
CC Genew; HGNC:1595; CCNI.
CC H-InvDB; HIX0004313; -;
CC GO; GO:0007283; P: spermatogenesis; NAS.
CC InterPro; IPR006670; Cyclin.
CC InterPro; IPR011028; Cyclin.
CC InterPro; IPR006671; Cyclin.
CC Pfam; PF00134; Cyclin N; 1.
CC SMART; SM00385; CYCLIN; 1.
CC PROSITE; PS00292; CYCLINS; FALSE_NEG.
CC Cyclin; Polymorphism.
KW VARIANT 207 207 V->I (in dbSNP:4252903).
FT CONFLICT 9 9 N->D (in Ref. 5).
FT CONFLICT 58 58 Q->R (in Ref. 5).
FT CONFLICT 75 75 R->G (in Ref. 5).
SQ SEQUENCE 377 AA; 42557 MW; 2DE84EFA74698F6C CRC64;
Query Match 100.0%; Score 377; DB 1; Length 377;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 377; Conservative 0; Mismatches 0; Gaps 0;
Qy 1 MKFPGPLENQLSFLLEKAITREAOQKVNVRKMPNSQNSVSPQRDEVIOWLAKLYQFN 60
Db 1 MKFPGPLENQLSFLLEKAITREAOQKVNVRKMPNSQNSVSPQRDEVIOWLAKLYQFN 60
Qy 61 LYPFTFALASLLDRFLATVKAHPKYLSCIAISCFLLAAKTVEDEIPVLKVLARDSFC 120
Db 61 LYPFTFALASLLDRFLATVKAHPKYLSCIAISCFLLAAKTVEDEIPVLKVLARDSFC 120
Qy 121 GCSSEILMERIILDKINLNDLHTATPDLFIHFAITAVSTRPOLLPSLKPSOHLAV 180
Db 121 GCSSEILMERIILDKINLNDLHTATPDLFIHFAITAVSTRPOLLPSLKPSOHLAV 180
Qy 181 LTKQLLHCMAQNQLQFQSGMLANVLSLEMKLIPDWLSITIELLQKQAMDSQLIHC 240

```
Db 181 LTKQLLHMACNQLLQFRGSLAMLVSEMEKLIIPDWLSLTIELLOQAQDSSQLIHR 240
Qy 241 ELVAHLSTLQSSPLNSVYVYRPLKHTLVCTDKGVFLRLHPSSVPGDFSKDNSKPEVPV 300
Db 241 ELVAHLSTLQSSPLNSVYVYRPLKHTLVCTDKGVFLRLHPSSVPGDFSKDNSKPEVPV 300
Qy 301 RGTAAFYHLLPAASGCKQTSTKRKVEEMEVDDFDGIGKRLYNEDNVSENVSGVCGTDLR 360
Db 301 RGTAAFYHLLPAASGCKQTSTKRKVEEMEVDDFDGIGKRLYNEDNVSENVSGVCGTDLR 360
Qy 361 QEGHASPCCPPLQPVSV 377
Db 361 QEGHASPCCPPLQPVSV 377

RESULT 2
ID Q6FH0 PRELIMINARY; PRT; 377 AA.
AC Q6FH0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE CCNI protein (Fragment).
GN Name=CCNI;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Halleck A., Ebert L., Moundinya M., Schick M., Eisenstein S.,
RA Neubert P., Kstrang K., Schattner R., Shen B., Henze S., Mar W.,
RA Korn B., Zuo D., Hu Y., LaBaer J.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the cyclin family.
DR EMBL; CR541783; CAG46582.1; -.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR011028; Cyclin like.
DR Pfam; PF00134; Cyclin_N.
DR SMART; SM00385; CYCLIN; 1.
DR Cyclin.
FT NON_TER 377 377
SQ SEQUENCE 377 AA; 42486 MW; D950A5CCF0D0F514 CRC64;

Query Match 63.7%; Score 240; DB 2; Length 377;
Best Local Similarity 100.0%; Pred. No. 2.2e-241;
Matches 240; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 138 LNWDLHTATPLDLFIHFAIAVSTRPQLLFLSLPKLSPSHLAVLTQLLHMACNQLLQF 197
Db 138 LNWDLHTATPLDLFIHFAIAVSTRPQLLFLSLPKLSPSHLAVLTQLLHMACNQLLQF 197
Qy 198 RGSMLAMVSEMEKLIIPDWLSLTIELLOQAQDSSQLIHRCLVAHLSTLQSSPLN 257
Db 198 RGSMLAMVSEMEKLIIPDWLSLTIELLOQAQDSSQLIHRCLVAHLSTLQSSPLN 257
Qy 258 SVYVYRPLKHTLVCTDKGVFLRLHPSSVPGDFSKDNSKPEVPVGTAAFYHLLPAASGCK 317
Db 258 SVYVYRPLKHTLVCTDKGVFLRLHPSSVPGDFSKDNSKPEVPVGTAAFYHLLPAASGCK 317
Qy 318 QTSTKRKVEEMEVDDFDGIGKRLYNEDNVSENVSGVCGTDLRSRQEGHASPCCPPLQPVSV 377
Db 318 QTSTKRKVEEMEVDDFDGIGKRLYNEDNVSENVSGVCGTDLRSRQEGHASPCCPPLQPVSV 377

RESULT 3
ID Q99LF2 PRELIMINARY; PRT; 377 AA.
AC Q99LF2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
```

```
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cyclin I.
GN Name=Ccni;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=FVB/N; TISSUE=Mammary tumor;
RA MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haie F.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwain P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=FVB/N; TISSUE=Mammary tumor;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the cyclin family.
DR EMBL; BC003290; AA03290.1; -.
DR MGI; MGI:1341077; Ccni.
DR GO; GO:0000074; P:regulation of cell cycle; TAS.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR011028; Cyclin like.
DR InterPro; IPR006671; Cyclin_N.
DR Pfam; PF00134; Cyclin_N; 1.
DR SMART; SM00385; CYCLIN; 1.
DR Cyclin.
SQ SEQUENCE 377 AA; 42227 MW; FDA2D896A5366A9F CRC64;

Query Match 23.9%; Score 90; DB 2; Length 377;
Best Local Similarity 100.0%; Pred. No. 1e-84;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 108 IPVLKVLARDFGCSSEILRMERIILDKLNWDLHTATPLDLFIHFAIAVSTRPQLL 167
Db 108 IPVLKVLARDFGCSSEILRMERIILDKLNWDLHTATPLDLFIHFAIAVSTRPQLL 167
Qy 168 SLPKLSPSHLAVLTQLLHMACNQLLQF 197
Db 168 SLPKLSPSHLAVLTQLLHMACNQLLQF 197

RESULT 4
ID Q8C7E2 PRELIMINARY; PRT; 377 AA.
AC Q8C7E2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE Mus musculus adult pancreas islet cells cDNA, RIKEN full-length
DE enriched library, clone: C820001G04 product: cyclin I, full insert
DE sequence.
GN Name=Ccni;
OS Mus musculus (Mouse).
```


ID AC Q6DJQ8 PRELIMINARY; PRT; 382 AA.
AC Q6DJQ8;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Cn1-prov-prov;
DE Name=ccni-prov;
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8364;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heih F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Tohiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX Klein S., Gerhard D.S.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the cyclin family.
DR EMBL; BC075116; AAH75116.1; -.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR011028; Cyclin like.
DR Pfam; PF00134; Cyclin_N; 1.
DR SMART; SM00385; CYCLIN; 1.
DR Cyclin.
KW Cyclin.
SQ SEQUENCE 382 AA; 42919 MW; E1F28D13AFB42CEA CRC64;
Query Match 7.7%; Score 29; DB 2; Length 382;
Best Local Similarity 100.0%; Pred. No. 5.2e-21;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 128 LRMERIILDKLNDLHTATPLDPLHIFHA 156
Db 130 LRMERIILDKLNDLHTATPLDPLHIFHA 158
RESULT 7
ID Q6P7H3 PRELIMINARY; PRT; 382 AA.
AC Q6P7H3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE MGC68660 protein.
GN Name=MGC68660;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.

OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heih F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Tohiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX Klein S., Gerhard D.S.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the cyclin family.
DR EMBL; BC061670; AAH61670.1; -.
DR GO; GO:0007049; P:cell cycle; IEA.
DR GO; GO:0000910; P:cytokinesis; IEA.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR011028; Cyclin like.
DR InterPro; IPR006671; Cyclin_N.
DR Pfam; PF00134; Cyclin_N; 1.
DR SMART; SM00385; CYCLIN; 1.
DR PROSITE; PS00292; CYCLIN; 1.
KW Cell cycle; Cell division; Cyclin.
SQ SEQUENCE 382 AA; 42913 MW; E19D7C5D8FEC26A CRC64;
Query Match 7.7%; Score 29; DB 2; Length 382;
Best Local Similarity 100.0%; Pred. No. 5.2e-21;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 128 LRMERIILDKLNDLHTATPLDPLHIFHA 156
Db 130 LRMERIILDKLNDLHTATPLDPLHIFHA 158
RESULT 8
ID Q6NUZ7 PRELIMINARY; PRT; 355 AA.
AC Q6NUZ7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cyclin I.
GN Name=ccni;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;

Cyprinidae; Danio.
 NCBI_TaxID=7955;
 [1]
 SEQUENCE FROM N.A.
 TISSUE=Embryo;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [2]
 RP SEQUENCE FROM N.A.
 RC Director MGC Project;
 RA Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: Belongs to the cyclin family.
 DR EMBL; BC068369; AAH68369.1; -.
 DR InterPro; IPR006670; Cyclin.
 DR InterPro; IPR011028; Cyclin-like.
 DR InterPro; IPR006671; Cyclin_N.
 DR Pfam; PF00134; Cyclin_N; 1.
 DR SMART; SM00385; CYCLIN; 1.
 DR PROSITE; PS00292; CYCLINS; UNKNOWN_1.
 KW Cyclin.
 SQ SEQUENCE 355 AA; 39614 MW; ESD4236191F663BF CRC64;
 Query Match 3.4%; Score 13; DB 2; Length 355;
 Best Local Similarity 100.0%; Pred. No. 0.00025;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 89 CIAISCFLLAAKT 101
 DB 91 CIAISCFLLAAKT 103
 RESULT 9
 ID Q803P0 PRELIMINARY; PRT; 355 AA.
 AC Q803P0;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Cyclin I.
 GN Name=ccni;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OC NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AB; TISSUE=Whole body;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AB; TISSUE=Whole body;
 RA Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: Belongs to the cyclin family.
 DR EMBL; BC044400; AAH44400.1; -.
 DR HSP; P30274; IVIN.
 DR ZFIN; ZDB-GENE-040426-2898; ccni.
 DR InterPro; IPR006670; Cyclin.
 DR InterPro; IPR011028; Cyclin-like.
 DR InterPro; IPR006671; Cyclin_N.
 DR Pfam; PF00134; Cyclin_N; 1.
 DR SMART; SM00385; CYCLIN; 1.
 DR PROSITE; PS00292; CYCLINS; UNKNOWN_1.
 KW Cyclin.
 SQ SEQUENCE 355 AA; 39517 MW; D2999F2E9812C880 CRC64;
 Query Match 3.4%; Score 13; DB 2; Length 355;
 Best Local Similarity 100.0%; Pred. No. 0.00025;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 89 CIAISCFLLAAKT 101
 DB 91 CIAISCFLLAAKT 103
 RESULT 10
 ID Q9XFC9 PRELIMINARY; PRT; 462 AA.
 AC Q9XFC9;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Nod factor binding lectin-nucleotide phosphohydrolase.
 GN Name=LNP;
 OS Dolichos biflorus (Horse gram).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC Eurosidia I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Dolichos.
 OC NCBI_TaxID=3840;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Root;
 RX MEDLINE=99254131; PubMed=10318974; DOI=10.1073/pnas.96.10.5856;
 RA Etzler M.E., Kalsi G., Ewing N.N., Roberts N.J., Day R.B.,
 RA Murphy J.B.;
 RT "A nod factor binding lectin with apyrase activity from legume
 RT roots.";
 RL Proc. Natl. Acad. Sci. U.S.A. 96:5856-5861(1999).
 DR EMBL; AF139807; AAD31285.1; -.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR GO; GO:0005529; F:sugar binding; IEA.
 DR InterPro; IPR000407; GDAL CD39_NTPase.
 DR Pfam; PF01150; GDAL CD39; 1.
 DR PROSITE; PS01238; GDAL_CD39_NTPASE; 1.
 KW Hydrolase; Lectin.

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AB; TISSUE=Whole body;
 RA Strausberg R.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: Belongs to the cyclin family.
 DR EMBL; BC044400; AAH44400.1; -.
 DR HSP; P30274; IVIN.
 DR ZFIN; ZDB-GENE-040426-2898; ccni.
 DR InterPro; IPR006670; Cyclin.
 DR InterPro; IPR011028; Cyclin-like.
 DR InterPro; IPR006671; Cyclin_N.
 DR Pfam; PF00134; Cyclin_N; 1.
 DR SMART; SM00385; CYCLIN; 1.
 DR PROSITE; PS00292; CYCLINS; UNKNOWN_1.
 KW Cyclin.
 SQ SEQUENCE 355 AA; 39517 MW; D2999F2E9812C880 CRC64;
 Query Match 3.4%; Score 13; DB 2; Length 355;
 Best Local Similarity 100.0%; Pred. No. 0.00025;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 89 CIAISCFLLAAKT 101
 DB 91 CIAISCFLLAAKT 103
 RESULT 10
 ID Q9XFC9 PRELIMINARY; PRT; 462 AA.
 AC Q9XFC9;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Nod factor binding lectin-nucleotide phosphohydrolase.
 GN Name=LNP;
 OS Dolichos biflorus (Horse gram).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC Eurosidia I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Dolichos.
 OC NCBI_TaxID=3840;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Root;
 RX MEDLINE=99254131; PubMed=10318974; DOI=10.1073/pnas.96.10.5856;
 RA Etzler M.E., Kalsi G., Ewing N.N., Roberts N.J., Day R.B.,
 RA Murphy J.B.;
 RT "A nod factor binding lectin with apyrase activity from legume
 RT roots.";
 RL Proc. Natl. Acad. Sci. U.S.A. 96:5856-5861(1999).
 DR EMBL; AF139807; AAD31285.1; -.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR GO; GO:0005529; F:sugar binding; IEA.
 DR InterPro; IPR000407; GDAL CD39_NTPase.
 DR Pfam; PF01150; GDAL CD39; 1.
 DR PROSITE; PS01238; GDAL_CD39_NTPASE; 1.
 KW Hydrolase; Lectin.

SQ SEQUENCE 462 AA; 51183 MW; 59F865A9D4CC44B CRC64;
 Query Match 2.4%; Score 9; DB 2; Length 462;
 Best Local Similarity 100.0%; Pred. No. 4.8;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 165 LLFSLPKLS 173
 DB 20 LLFSLPKLS 28
 |||||

RESULT 11
 Q83YJ9 PRELIMINARY; PRT; 227 AA.
 ID Q83YJ9
 AC Q83YJ9
 DT 01-JUN-2003 (TREMREL. 24, Created)
 DT 01-JUN-2003 (TREMREL. 24, Last sequence update)
 DT 01-MAR-2004 (TREMREL. 26, Last annotation update)
 DE Hypothetical protein.
 OS Bifidobacterium longum.
 OG Plasmid pNAC3.
 OC Bacteria; Actinobacteria; Actinobacteridae; Bifidobacteriales;
 OC Bifidobacteriaceae; Bifidobacterium.
 OX NCBI_TaxID=216816;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RW041;
 RX PubMed=15003705; DOI=10.1016/j.plasmid.2003.12.003;
 RA Corneau N., Emond E., LaPointe G.;
 RT "Molecular characterization of three plasmids from Bifidobacterium longum";
 RL Plasmid 51:87-100(2004).
 DR EMBL; AY112722; AAM66779.1; -;
 DR InterPro; IPR006025; Pept M Zn BS.
 DR PROSITE; PS00142; ZINC PROTEASE; UNKNOWN_1.
 KW Hypothetical protein; Plasmid.
 SQ SEQUENCE 227 AA; 24946 MW; 4DFF32A39C79A41 CRC64;

Query Match 2.1%; Score 8; DB 2; Length 227;
 Best Local Similarity 100.0%; Pred. No. 28;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 297 EVPVRGTA 304
 DB 7 EVPVRGTA 14
 |||||

RESULT 12
 Q86F16 PRELIMINARY; PRT; 231 AA.
 ID Q86F16
 AC Q86F16
 DT 01-JUN-2003 (TREMREL. 24, Created)
 DT 01-JUN-2003 (TREMREL. 24, Last sequence update)
 DT 01-MAR-2004 (TREMREL. 26, Last annotation update)
 DE Clone ZD120 mRNA sequence.
 OS Schistosoma japonicum (Blood fluke).
 OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigoida;
 OC Schistosomatidae; Schistosomatidae; Schistosoma.
 OX NCBI_TaxID=6182;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22879925; PubMed=12973349; DOI=10.1038/ng1236;
 RA Hu W., Yan Q., Shen D.K., Liu P., Zhu Z.D., Song H.D., Xu X.R.,
 RA Wang Z.J., Rong Y.P., Zeng L.C., Wu J., Zhang X., Wang J.J., Xu X.N.,
 RA Wang S.Y., Fu G., Zhang X.L., Wang Z.Q., Brindley P.J., McManus D.P.,
 RA Xue C.L., Feng Z., Chen Z., Han Z.G.;
 RT "Evolutionary and biomedical implications of a Schistosoma japonicum complementary DNA resource";
 RL Nat. Genet. 35:139-147(2003).
 DR EMBL; AY221048; AAP06071.1; -;
 DR InterPro; IPR002893; ZnF MYND.
 DR Pfam; PF01753; ZF_MYND; 1.
 DR PROSITE; PS01360; ZF_MYND_1; UNKNOWN_1.

DR PROSITE; PS0865; ZF_MYND_2; 1.
 SQ SEQUENCE 231 AA; 27255 MW; D629D635C439D0FD CRC64;
 Query Match 2.1%; Score 8; DB 2; Length 231;
 Best Local Similarity 100.0%; Pred. No. 28;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 SEILRMER 132
 DB 4 SEILRMER 11
 |||||

RESULT 13
 Q6NWAB PRELIMINARY; PRT; 332 AA.
 ID Q6NWAB
 AC Q6NWAB
 DT 05-JUL-2004 (TREMREL. 27, Created)
 DT 05-JUL-2004 (TREMREL. 27, Last sequence update)
 DT 25-OCT-2004 (TREMREL. 28, Last annotation update)
 DE SPT3-associated factor 42.
 GN Name=STAF42; ORFNames=zgc:85851;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Berge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci F., Prange C.,
 RA Raha S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RA Strausberg R.;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney marrow;
 RA Song H.D., Wu X.Y., Sun X.J., Zhou Y., Liu T.X., Deng M., Zhang G.W.,
 RA Sheng Y., Chen Y., Ruan Z., Jiang C.L., Fan H.Y., Zou L.I.,
 RA Kanki J.P., Look A.T., Chen Z.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC067660; AAH67660.1; -;
 DR EMBL; AY423005; AAQ97981.1; -;
 DR ZFIN; ZDB-GENE-040426-58; zgc:85851.
 SQ SEQUENCE 332 AA; 36961 MW; 72E41538D8FDC638 CRC64;

Query Match 2.1%; Score 8; DB 2; Length 332;
 Best Local Similarity 100.0%; Pred. No. 39;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 369 PPIQPSV 376
 |||||

Db 268 PPLQPSV 275

RESULT 14

Q661Z0 PRELIMINARY; PRT; 359 AA.
AC Q661Z0;
DT 25-OCT-2004 (TREMREL. 28, Created)
DT 25-OCT-2004 (TREMREL. 28, Last sequence update)
DT 25-OCT-2004 (TREMREL. 28, Last annotation update)
DE MGC83953 protein.
GN Name=MGC83953;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Oocytes;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S.J., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Oocytes;
RA Klein S., Gerhard D.S.;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the cyclin family.
DR EMBL: BC081135; AAH81135.1; -
DR InterPro: IPR006670; Cyclin.
DR InterPro: IPR011028; Cyclin like.
DR InterPro: IPR006671; Cyclin N.
DR Pfam: PF00134; Cyclin N; 1.
DR SMART: SM00385; CYCLIN; 1.
KW Cyclin.
SQ SEQUENCE 359 AA; 40577 MW; 230B61BE382A6BC7 CRC64;

Query Match 2.1%; Score 8; DB 2; Length 359;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 126 EILRMERI 133

Db 128 EILRMERI 135

RESULT 15

Q947Z5 PRELIMINARY; PRT; 364 AA.
AC Q947Z5;
DT 01-DEC-2001 (TREMREL. 19, Created)
DT 01-DEC-2001 (TREMREL. 19, Last sequence update)
DT 01-OCT-2003 (TREMREL. 25, Last annotation update)
DE Hypothetical protein OSUNBa0067N01.1.
GN Name=OSUNBa0067N01.1;
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Nipponbare;
RA de la Bastide M., Spiegel L., Preston R., Kirchoff K., King L.,
RA Nascimben L., Baker J., Vil M.D., Zutavern T., Santos L., Miller B.,
RA Kuit K., Cunniff D.M., Rodriguez S., Balija V., Shah R., Bahret A.,
RA Yang C., Bell M., Palmer L., O'Shaughnessy A., Dedhia N.,
RA McCombie W.R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC090485; AAK98722.1; -
DR Gramene; Q947Z5; -
DR InterPro: IPR007749; DUF677.
DR Pfam: PF05055; DUF677; 1.
KW Hypothetical protein.
SQ SEQUENCE 364 AA; 39894 MW; 5E0497ACCA3A3F36 CRC64;

Query Match 2.1%; Score 8; DB 2; Length 364;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 262 YRPLKHTL 269

Db 133 YRPLKHTL 140

Search completed: February 11, 2005, 03:18:19
Job time : 145.276 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 11, 2005, 03:00:19 ; Search time 31.8184 Seconds
(without alignments)
884.478 Million cell updates/sec

Title: US-09-736-250-1

Perfect score: 1962

Sequence: 1 MKFPQLENQRLSFLEKAI.....LSRQEGHASPFPPIQPVSM 377

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pap.*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pap.*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pap.*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pap.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pap.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1962	100.0	377	2	US-08-969-106-6
2	1962	100.0	377	3	US-09-054-492B-1
3	1962	100.0	377	4	US-09-338-125-6
4	1309	66.7	254	4	US-09-796-149B-4
5	667	34.0	131	4	US-09-513-999C-5984
6	326.5	16.6	389	4	US-09-949-016-7723
7	271.5	13.8	249	4	US-09-796-149B-3
8	271.5	13.8	295	4	US-09-949-016-6449
9	271.5	13.8	302	4	US-09-949-016-10213
10	265.5	13.5	249	4	US-09-796-149B-7
11	265.5	13.5	253	4	US-09-796-149B-8
12	204	10.4	404	2	US-09-092-770-3
13	204	10.4	404	3	US-09-222-851-3
14	204	10.4	407	4	US-09-949-016-11184
15	202	10.3	403	2	US-09-092-770-4
16	202	10.3	403	3	US-09-222-851-4
17	192	9.8	357	4	US-09-404-296B-10
18	188.5	9.6	367	3	US-09-404-296B-4
19	187.5	9.6	373	4	US-08-895-707-6
20	187.5	9.6	386	3	US-08-895-707-7
21	187.5	9.6	392	1	US-08-706-539-9
22	187.5	9.6	392	3	US-09-027-007-9
23	187.5	9.6	395	1	US-08-485-859-2
24	187.5	9.6	395	1	US-08-706-539-11
25	187.5	9.6	395	1	US-08-522-166-2
26	187.5	9.6	395	1	US-08-488-382A-2
27	187.5	9.6	395	2	US-08-480-912-2

28 187.5 9.6 395 3 US-09-027-007-11 Sequence 11, Appli
29 187.5 9.6 616 3 US-08-895-707-2 Sequence 2, Appli
30 176 9.0 471 4 US-09-538-092-344 Sequence 344, Appl
31 171.5 8.7 436 1 US-08-706-539-10 Sequence 10, Appli
32 171.5 8.7 436 3 US-09-027-007-10 Sequence 10, Appli
33 169 8.6 289 2 US-08-246-361A-4 Sequence 4, Appli
34 169 8.6 289 4 US-09-919-497-54 Sequence 54, Appli
35 169 8.6 289 4 US-09-949-016-6127 Sequence 6127, Ap
36 169 8.6 289 5 PCT-US93-05000-4 Sequence 4, Appli
37 169 8.6 378 4 US-09-949-016-8020 Sequence 8020, Ap
38 168.5 8.6 428 4 US-09-684-169-2 Sequence 2, Appli
39 167 8.5 174 1 US-08-193-977-8 Sequence 8, Appli
40 167 8.5 491 4 US-09-538-092-813 Sequence 813, App
41 166 8.5 236 2 US-08-464-517-22 Sequence 22, Appli
42 166 8.5 236 2 US-08-246-361A-22 Sequence 22, Appli
43 166 8.5 236 3 US-08-463-772-22 Sequence 22, Appli
44 166 8.5 236 5 PCT-US93-05000-22 Sequence 22, Appli
45 166 8.5 309 2 US-08-464-517-4 Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-08-969-106-6
; Sequence 6, Application US/08969106
; Patent No. 5986055
; GENERAL INFORMATION:
; APPLICANT: Yang, M.
; APPLICANT: Nandabalan, K.
; APPLICANT: SCHULZ, V.
; TITLE OF INVENTION: CDK2 INTERACTIONS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/969,106
; FILING DATE: 13-NOV-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7934-057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 377 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-969-106-6

Query Match 100.0%; Score 1962; DB 2; Length 377;

Best Local Similarity 100.0%; Pred. No. 1.9e-213;

Matches 377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKFPQLENQRLSFLEKAITREAAQMKVNRKMPNSQNVSPORDEVIOMLAKLYQFN 60

Db 1 MKFPQLENQRLSFLEKAITREAAQMKVNRKMPNSQNVSPORDEVIOMLAKLYQFN 60

QY 61 LYPETFALASSLLDRFLATVKAHPKYLSCIAISCFFLAAKTVEEDERIPVLKVLARDSPFC 120
DB 61 LYPETFALASSLLDRFLATVKAHPKYLSCIAISCFFLAAKTVEEDERIPVLKVLARDSPFC 120
QY 121 GCSSEILRMERIIIDKLNWDLHTATPLDFLHIFHAIIVSTRPQLLPSLSPSOHLAV 180
DB 121 GCSSEILRMERIIIDKLNWDLHTATPLDFLHIFHAIIVSTRPQLLPSLSPSOHLAV 180
QY 181 LTKQLLHCWACNQLLOFRGSMALAMVSLMEKLIIPDWLSLTIELLOKAQMDSSQLIHCR 240
DB 181 LTKQLLHCWACNQLLOFRGSMALAMVSLMEKLIIPDWLSLTIELLOKAQMDSSQLIHCR 240
QY 241 ELVAHHLSTLOSSPLNSVYVYRPLKHTLVTCDKGVFRLHPSSVPGPDFSKDNSKPEVPV 300
DB 241 ELVAHHLSTLOSSPLNSVYVYRPLKHTLVTCDKGVFRLHPSSVPGPDFSKDNSKPEVPV 300
QY 301 RGTAAFYHHLPAASGCKQTSTKRKVEEMEVDYDGIKRLYNEDNVSNVSGVCGTDLR 360
DB 301 RGTAAFYHHLPAASGCKQTSTKRKVEEMEVDYDGIKRLYNEDNVSNVSGVCGTDLR 360
QY 361 QEGHASPCCPPLQPVSV 377
DB 361 QEGHASPCCPPLQPVSV 377

RESULT 2

US-09-054-492B-1
; Sequence 1, Application US/09054492B
; Patent No. 6218115
; GENERAL INFORMATION:
; APPLICANT: TAKESHI NAKAMURA
; TITLE OF INVENTION: HUMAN CYCLIN I AND GENES ENCODING SAME
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY, MADISON & SUTRO
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/054,492B
; FILING DATE: APRIL 3, 1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: PAUL E. WHITE, JR.
; REGISTRATION NUMBER: 32,011
; REFERENCE/DOCKET NUMBER: 7898/252159
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; TELEX: 6714627CUSH
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 377
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-054-492B-1

Query Match 100.0%; Score 1962; DB 3; Length 377;
Best Local Similarity 100.0%; Pred. No. 1.9e-213;
Matches 377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKFPGPLENQRSLFLEKAITREAOQWKVNRKMPNSQNVSPSORDEVIQWLAKLYQFN 60
DB 1 MKFPGPLENQRSLFLEKAITREAOQWKVNRKMPNSQNVSPSORDEVIQWLAKLYQFN 60

QY 61 LYPETFALASSLLDRFLATVKAHPKYLSCIAISCFFLAAKTVEEDERIPVLKVLARDSPFC 120
DB 61 LYPETFALASSLLDRFLATVKAHPKYLSCIAISCFFLAAKTVEEDERIPVLKVLARDSPFC 120
QY 121 GCSSEILRMERIIIDKLNWDLHTATPLDFLHIFHAIIVSTRPQLLPSLSPSOHLAV 180
DB 121 GCSSEILRMERIIIDKLNWDLHTATPLDFLHIFHAIIVSTRPQLLPSLSPSOHLAV 180
QY 181 LTKQLLHCWACNQLLOFRGSMALAMVSLMEKLIIPDWLSLTIELLOKAQMDSSQLIHCR 240
DB 181 LTKQLLHCWACNQLLOFRGSMALAMVSLMEKLIIPDWLSLTIELLOKAQMDSSQLIHCR 240
QY 241 ELVAHHLSTLOSSPLNSVYVYRPLKHTLVTCDKGVFRLHPSSVPGPDFSKDNSKPEVPV 300
DB 241 ELVAHHLSTLOSSPLNSVYVYRPLKHTLVTCDKGVFRLHPSSVPGPDFSKDNSKPEVPV 300
QY 301 RGTAAFYHHLPAASGCKQTSTKRKVEEMEVDYDGIKRLYNEDNVSNVSGVCGTDLR 360
DB 301 RGTAAFYHHLPAASGCKQTSTKRKVEEMEVDYDGIKRLYNEDNVSNVSGVCGTDLR 360
QY 361 QEGHASPCCPPLQPVSV 377
DB 361 QEGHASPCCPPLQPVSV 377

RESULT 3

US-09-338-125-6
; Sequence 6, Application US/09338125
; Patent No. 6521412
; GENERAL INFORMATION:
; APPLICANT: Yang, M.
; APPLICANT: Nandabalan, K.
; APPLICANT: Schulz, V.
; TITLE OF INVENTION: CDK2 INTERACTIONS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/338,125
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/969,106
; FILING DATE: 13-NOV-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7934-057
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 377 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-09-338-125-6

Query Match 100.0%; Score 1962; DB 4; Length 377;

Best Local Similarity 100.0%; Pred. No. 1.9e-213; Matches 377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKFPGLENORLSFLEKAITREAAQMWKVNVRKMPNSQNVSPSQRDEVIQWLAKLYQFN 60
Db 1 MKFPGLENORLSFLEKAITREAAQMWKVNVRKMPNSQNVSPSQRDEVIQWLAKLYQFN 60

Qy 61 LYPETPALASSLLDRFLATVKAHPKYLSCIAISCFFLAAKTVEEDERIPVLKVLARDSFC 120
Db 61 LYPETPALASSLLDRFLATVKAHPKYLSCIAISCFFLAAKTVEEDERIPVLKVLARDSFC 120

Qy 121 GCSSEIILMERIILDKLNDLHTATPLDFLHIFHAIIVSTRPQLLSPLKSPSOHLAV 180
Db 121 GCSSEIILMERIILDKLNDLHTATPLDFLHIFHAIIVSTRPQLLSPLKSPSOHLAV 180

Qy 181 LTKQLLHMACNQLQFRGSMALAMVLEMEKLPDWLSLTIELLQKQMDSSQLIHCR 240
Db 181 LTKQLLHMACNQLQFRGSMALAMVLEMEKLPDWLSLTIELLQKQMDSSQLIHCR 240

Qy 241 ELVAHHLSTLQSSLPNSVYVYRPLKHTLVTCDKGVFRLHPSSVPGPDFSKDNKPEVPV 300
Db 241 ELVAHHLSTLQSSLPNSVYVYRPLKHTLVTCDKGVFRLHPSSVPGPDFSKDNKPEVPV 300

Qy 301 RGTAAFYHHLPAASCKOTSTKRKVEEVDYDGIKRLYNEDNVNENSGVCGTDLNR 360
Db 301 RGTAAFYHHLPAASCKOTSTKRKVEEVDYDGIKRLYNEDNVNENSGVCGTDLNR 360

Qy 361 QEGHASPCCPPLQPVSV 377
Db 361 QEGHASPCCPPLQPVSV 377

RESULT 4
US-09-796-149B-4
; Sequence 4, Application US/09796149B
; Patent No. 6825033
; GENERAL INFORMATION:
; APPLICANT: Univ. of Southern California
; TITLE OF INVENTION: Mutated cyclin G1 protein
; FILE REFERENCE: 4-31342A/USC
; CURRENT APPLICATION NUMBER: US/09/796,149B
; CURRENT FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-796-149B-4

Query Match 66.7%; Score 1309; DB 4; Length 254;
Best Local Similarity 100.0%; Pred. No. 1.1e-139;
Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 40 VSPSQRDEVIQWLAKLYQFNLYPTFALASSLLDRFLATVKAHPKYLSCIAISCFFLAA 99
Db 1 VSPSQRDEVIQWLAKLYQFNLYPTFALASSLLDRFLATVKAHPKYLSCIAISCFFLAA 60

Qy 100 KTVEDERIPVLKVLARDSFCGSCSSEILMERIILDKLNDLHTATPLDFLHIFHAIIV 159
Db 61 KTVEDERIPVLKVLARDSFCGSCSSEILMERIILDKLNDLHTATPLDFLHIFHAIIV 120

Qy 160 STRPQLLSPLKSPSOHLAVITKQLLHMACNQLQFRGSMALAMVLEMEKLPDWL 219
Db 121 STRPQLLSPLKSPSOHLAVITKQLLHMACNQLQFRGSMALAMVLEMEKLPDWL 180

Qy 220 SLTIELLQKQMDSSQLIHCRVLAHLSLTQSSLPNSVYVYRPLKHTLVTCDKGVRL 279
Db 181 SLTIELLQKQMDSSQLIHCRVLAHLSLTQSSLPNSVYVYRPLKHTLVTCDKGVRL 240

Qy 280 HPSSVPGPDFSKDN 293
Db 241 HPSSVPGPDFSKDN 254

RESULT 5
US-09-513-999C-5984
; Sequence 5984, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 5984
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-513-999C-5984

Query Match 34.0%; Score 667; DB 4; Length 131;
Best Local Similarity 100.0%; Pred. No. 2.3e-67;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 130 MERIILDKLNDLHTATPLDFLHIFHAIIVSTRPQLLSPLKSPSOHLAVITKQLLHCM 189
Db 1 MERIILDKLNDLHTATPLDFLHIFHAIIVSTRPQLLSPLKSPSOHLAVITKQLLHCM 60

Qy 190 ACNQLQFRGSMALAMVLEMEKLPDWLSLTIELLQKQMDSSQLIHCRVLAHLS 249
Db 61 ACNQLQFRGSMALAMVLEMEKLPDWLSLTIELLQKQMDSSQLIHCRVLAHLS 120

Qy 250 LQSSLPNSVY 260
Db 121 LQSSLPNSVY 131

RESULT 6
US-09-949-016-7723
; Sequence 7723, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7723
; LENGTH: 389
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7723

Query Match 16.6%; Score 326.5; DB 4; Length 389;
Best Local Similarity 36.4%; Pred. No. 5.6e-28;
Matches 86; Conservative 44; Mismatches 73; Indels 33; Gaps 7;

Qy 31 VRKMPNSQNVSPSQRDEVIQWLAKLYQFNLYPTFALASSLLDRFLATVKAHPKYLSC 89

Db 86 IEATPNDNTLCPLGNKAKVEDLRSLANFGSGCTETVLAVNILDRLFLAMKVKPKHLS 145
QY 90 IATSCFFLAKTVEEDERIPVLKVLARDSCGSSSEILRMERIIIDKLNWDLHTATPLD 149
Db 146 IGVCSELLAARIVEEDCNIPSTHDVIRISQCKTASDIKMEKIISEKLUHYELEATTALN 205
QY 150 FLHIFHAIIV---STPQLLFSLPKLPSPSHLAVLTQKLLHCWACNQLQF---RGSMLA 203
Db 206 FLHLYHTIILCHTSEKIL-SLDKLE-----AQKACNCRILFSAKPSVLA 252
QY 204 LAMVLEMEKLPDWLSLTIELQ-----KAQDSSQLIHCRELVAHHLSTLQ 252
Db 253 LCLINLEVTL-----KSVLELLEILLVKHSHKINDTEFFYRWRELVSKLAEYSS 302

RESULT 7

US-09-796-149B-3
; Sequence 3, Application US/09796149B
; Patent No. 6825033
; GENERAL INFORMATION:
; APPLICANT: Univ. of Southern California
; TITLE OF INVENTION: Mutated cyclin G1 protein
; FILE REFERENCE: 4-31342A/USC
; CURRENT APPLICATION NUMBER: US/09/796,149B
; CURRENT FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 3
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-796-149B-3

Query Match 13.8%; Score 271.5; DB 4; Length 249;
Best Local Similarity 32.6%; Pred. No. 4.7e-22;
Matches 77; Conservative 51; Mismatches 89; Indels 19; Gaps 5;
QY 45 RDEVQWLAKLYQFNLYPETFALASSLLDRFLATVKAHPKYLSCIAISCFFLAAKTVEE 104
Db 6 RDEVKDLSSLTQFFGFDTEFSLAVNLLDRFLSKMKVQPKHLGCVGLSCFYLAVKSTEE 65
QY 105 DERIPVLKVLARDSCGSSSEILRMERIIIDKLNWDLHTATPLDPLHIFHAIIVSTRPQ 164
Db 66 ERNVPLATDLIRISQYRFTVSDLMRMEKIVLEKVCWKVATTAFOFLQLYYSL----- 118
QY 165 LFLSLP-KLSPSOHLAVLTQKLLHCWACNQLQFSGSMLALAMVLSLEMEKLPDWLSLT 223
Db 119 LQENLPLERRNSINFERLEAQLKACHCRIIFSAKPSVLALSIIALEIQAKCVLFTGI 178
QY 224 ELQK-AQMDSSQLIHCRELVAHHLSTLQ---SLP-----LNSVYVYRPLKHT 268
Db 179 ECLQKHSKINGRDLTFWQELVSKCLTEYSSNCKSPNVQKLKWIIVSGRTARQLKHS 234

RESULT 8

US-09-949-016-6449
; Sequence 6449, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 6449
; LENGTH: 295
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6449

Query Match 13.8%; Score 271.5; DB 4; Length 295;
Best Local Similarity 32.6%; Pred. No. 6.1e-22;
Matches 77; Conservative 51; Mismatches 89; Indels 19; Gaps 5;

QY 45 RDEVQWLAKLYQFNLYPETFALASSLLDRFLATVKAHPKYLSCIAISCFFLAAKTVEE 104
Db 52 RDEVKDLSSLTQFFGFDTEFSLAVNLLDRFLSKMKVQPKHLGCVGLSCFYLAVKSTEE 111
QY 105 DERIPVLKVLARDSCGSSSEILRMERIIIDKLNWDLHTATPLDPLHIFHAIIVSTRPQ 164
Db 112 ERNVPLATDLIRISQYRFTVSDLMRMEKIVLEKVCWKVATTAFOFLQLYYSL----- 164
QY 165 LFLSLP-KLSPSOHLAVLTQKLLHCWACNQLQFSGSMLALAMVLSLEMEKLPDWLSLT 223
Db 165 LQENLPLERRNSINFERLEAQLKACHCRIIFSAKPSVLALSIIALEIQAKCVLFTGI 224
QY 224 ELQK-AQMDSSQLIHCRELVAHHLSTLQ---SLP-----LNSVYVYRPLKHT 268
Db 225 ECLQKHSKINGRDLTFWQELVSKCLTEYSSNCKSPNVQKLKWIIVSGRTARQLKHS 280

RESULT 9

US-09-949-016-10213
; Sequence 10213, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10213
; LENGTH: 302
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10213

Query Match 13.8%; Score 271.5; DB 4; Length 302;
Best Local Similarity 32.6%; Pred. No. 6.4e-22;
Matches 77; Conservative 51; Mismatches 89; Indels 19; Gaps 5;

QY 45 RDEVQWLAKLYQFNLYPETFALASSLLDRFLATVKAHPKYLSCIAISCFFLAAKTVEE 104
Db 59 RDEVKDLSSLTQFFGFDTEFSLAVNLLDRFLSKMKVQPKHLGCVGLSCFYLAVKSTEE 118
QY 105 DERIPVLKVLARDSCGSSSEILRMERIIIDKLNWDLHTATPLDPLHIFHAIIVSTRPQ 164
Db 119 ERNVPLATDLIRISQYRFTVSDLMRMEKIVLEKVCWKVATTAFOFLQLYYSL----- 171
QY 165 LFLSLP-KLSPSOHLAVLTQKLLHCWACNQLQFSGSMLALAMVLSLEMEKLPDWLSLT 223
Db 172 LQENLPLERRNSINFERLEAQLKACHCRIIFSAKPSVLALSIIALEIQAKCVLFTGI 231
QY 224 ELQK-AQMDSSQLIHCRELVAHHLSTLQ---SLP-----LNSVYVYRPLKHT 268
Db 232 ECLQKHSKINGRDLTFWQELVSKCLTEYSSNCKSPNVQKLKWIIVSGRTARQLKHS 287


```

Qy 224 ELIQ-AQMDSSQLIHCRELVAHSLTLOS---SLP-----LNSVYVVRPLKHT 268
Db 179 ECLQKSHKINGRLDTFWQLSVSKLSEYSSNKKCPNVQKLKWIVSGRTARQLKHS 234

RESULT 12
US-09-092-770-3
; Sequence 3, Application US/09092770
; Patent No. 5973119
; GENERAL INFORMATION:
; APPLICANT: Coats, Steven R.
; APPLICANT: Bass, Michael B.
; APPLICANT: Robinson, Murray O.
; TITLE OF INVENTION: No. 5973119el Cyclin E Genes and Proteins
; FILE REFERENCE: A-524
; CURRENT FILING DATE: 1997-06-05
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin ver. 2.0
; SEQ ID NO 3
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Human
US-09-092-770-3

Query Match 10.4%; Score 204; DB 2; Length 404;
Best Local Similarity 27.7%; Pred. No. 4.6e-14;
Matches 75; Conservative 54; Mismatches 96; Indels 46; Gaps 12

Qy 4 PGLENQRLSFLLEKAITRAQWKNVVRKMP-----NQNVSPQRDEVIOWL 52
Db 99 PSLPDP--LSWGCK-----EVM-LNMLKKESYVHDKHFEVLSDLPEQMSILLDWL 149
Qy 53 AKUKYQFNLYPETFALASSLLDRFLATVK-AHPKYLSCIAISCFFLAAKTVEEDERIPVL 111
Db 150 LEVCEVTLHRETFYLAQDFRPMLTQDKINKMLQIGITSUFIAKSL--EIIYAPKL 207
Qy 112 KVLARISFCCSSSEILRMERIILDKLNWDLTATPLDFLHIFHAI-AVSTRPQLLSLP 170
Db 208 QEPAYVTGACSEEDILRMELIILKALKWELCPVTIISWLNLFQVDALKDAPKVL--LP 265
Qy 171 KLSFQSQHVLAVLTQQLLHCMAQNQLLPQRGSMALAMVSLMEKLI PDWLSL-----TIELL 226
Db 266 QY--SQETFIQIAQLL-----DLCILADSLEFQYRILTAALCHFTSIEW 310
Qy 227 QKAQ-QDSSQLIHCRELVAHSLTLOSLLP 256
Db 311 KKASGLEWDSISECDVMWVPFNVVRKSTSPV 341

RESULT 13
US-09-222-851-3
; Sequence 3, Application US/09222851
; Patent No. 6165753
; GENERAL INFORMATION:
; APPLICANT: Coats, Steven R.
; APPLICANT: Bass, Michael B.
; APPLICANT: Robinson, Murray O.
; TITLE OF INVENTION: No. 6165753el Cyclin E Genes and Proteins
; FILE REFERENCE: A-524
; CURRENT APPLICATION NUMBER: US/09/222,851
; CURRENT FILING DATE: 1998-12-30
; EARLIER APPLICATION NUMBER: 09/092,770
; EARLIER FILING DATE: 1998-06-05
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Human
US-09-222-851-3

Query Match 10.4%; Score 204; DB 3; Length 404;

```

Best Local Similarity 27.7%; Pred. No. 4.6e-14;
Matches 75; Conservative 54; Mismatches 96; Indels 46; Gaps 12;

Qy 4 PGPLENQLSFLEKAITREAOQMKVNRKPS-----NONVSPQRDEVIQWL 52
Db 99 PSPLPD--LSWGCK-----EVM-LNNLKESRYVHDKHFEVLHSDLEPQMRSLLDWL 149

Qy 53 AKLYQFNLYPETFALASSLLDRFLATVK-AHPKYLSCIAISCFPLAAKTVEEDERIPVL 111
Db 150 LEVCEVYTLHRETFFLAQDFDRFMTQDKINKNMQLIGITSLFIASKL--EIIYAPKL 207

Qy 112 KVLARDSFCGSSSEILMERIILDKNWDLHTATPLDFLHIFHAI-AVSTRPQLLSPL 170
Db 208 QEFAYVTDCGACSEEDILRMELIILKALKWELCPVTIISWNLFLQVDALKDAPKVL--LP 265

Qy 171 KLSPSQHLAVLTQKLLHCWACNQQLQFRGSMALAMVSEMEKLIPLDWLSL-----TIELL 226
Db 266 QY--SQETFIQIAQLL-----DICILADSLEFQYRILTAAALCHFTSIEV 310

Qy 227 QKAO-MDSSLHCHRELVAHLSTLQSSLP 256
Db 311 KKASGLEWDSISECVDMVFPVNVKSTSPV 341

RESULT 14

US-09-949-016-11184
; Sequence 11184, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11184
; LENGTH: 407
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11184

Query Match 10.4%; Score 204; DB 4; Length 407;
Best Local Similarity 27.7%; Pred. No. 4.7e-14;
Matches 75; Conservative 54; Mismatches 96; Indels 46; Gaps 12;

Qy 4 PGPLENQLSFLEKAITREAOQMKVNRKPS-----NONVSPQRDEVIQWL 52
Db 102 PSPLPD--LSWGCK-----EVM-LNNLKESRYVHDKHFEVLHSDLEPQMRSLLDWL 152

Qy 53 AKLYQFNLYPETFALASSLLDRFLATVK-AHPKYLSCIAISCFPLAAKTVEEDERIPVL 111
Db 153 LEVCEVYTLHRETFFLAQDFDRFMTQDKINKNMQLIGITSLFIASKL--EIIYAPKL 210

Qy 112 KVLARDSFCGSSSEILMERIILDKNWDLHTATPLDFLHIFHAI-AVSTRPQLLSPL 170
Db 211 QEFAYVTDCGACSEEDILRMELIILKALKWELCPVTIISWNLFLQVDALKDAPKVL--LP 268

Qy 171 KLSPSQHLAVLTQKLLHCWACNQQLQFRGSMALAMVSEMEKLIPLDWLSL-----TIELL 226
Db 269 QY--SQETFIQIAQLL-----DICILADSLEFQYRILTAAALCHFTSIEV 313

Qy 227 QKAO-MDSSLHCHRELVAHLSTLQSSLP 256
Db 314 KKASGLEWDSISECVDMVFPVNVKSTSPV 344

RESULT 15
US-09-092-770-4
; Sequence 4, Application US/09092770
; Patent No. 5973119
; GENERAL INFORMATION:
; APPLICANT: Coats, Steven R.
; APPLICANT: Bass, Michael B.
; APPLICANT: Robinson, Murray O.
; TITLE OF INVENTION: No. 5973119el Cyclin E Genes and Proteins
; FILE REFERENCE: A-524
; CURRENT APPLICATION NUMBER: US/09/092,770
; CURRENT FILING DATE: 1997-06-05
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0.
; SEQ ID NO 4
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Mouse.
US-09-092-770-4

Query Match 10.3%; Score 202; DB 2; Length 403;
Best Local Similarity 25.7%; Pred. No. 7.7e-14;
Matches 83; Conservative 54; Mismatches 126; Indels 60; Gaps 14;

Qy 4 PGPLENQLSFLEKAITREAOQMKVNRK-----MPSNQNVSPSORDEVIOWLA 53
Db 98 PSPLPD-----LSWACSQE--VQNMLOKENRYVHDKHFEVLHSDLEPQMRSLLDWL 149

Qy 54 KLYQFNLYPETFALASSLLDRFLATVK-AHPKYLSCIAISCFPLAAKTVEEDERIPVLK 112
Db 150 EVCEVYTLHRETFFLAQDFDRFMTQDKVNMQLIGITSLFIASKL--EIIYAPKLQ 207

Qy 113 VLARDSFCGSSSEILMERIILDKNWDLHTATPLDFLHIFHAI-AVSTRPQLLSPLK 171
Db 208 EFAYVTDCGACSEVDILKMLNLIKALKWELCPVTIISWNLFLQVDALKDAPKVL--LPQ 265

Qy 172 LSPSOHLAVLTQKLLH-CMACNQQLQFRGSMALA-----MVSLEMEKLIP----- 216
Db 266 Y--SQETFIQIAQLLDLCILADSLEFQYRILAAAALCHFTSIEVKKASGLEWDDISEC 323

Qy 217 -DWL-----SLTIELLQKAMDSSQLIHCRELVHHLSTLOSSLPNVSYYVRP 264
Db 324 VDMVFPVSVVSVKLTFFKIPMED-----RHNIQHTNYLALLNEVYVNIYRK 377

Qy 265 LKHTLVTCDKGVFELHPSVPGP 287
Db 378 GGQLSPVCNGGIM--TPPKSTKPK 399

Search completed: February 11, 2005, 03:06:28
Job time : 32.8184 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 11, 2005, 02:58:24 ; Search time 100.276 Seconds
(without alignments)
1925.221 Million cell updates/sec

Title: US-09-736-250-1

Perfect score: 1962

Sequence: 1 MKFPGLNORLSFLEKAI.....LSROGHASCPPIQPVSV 377

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1962	100.0	377	1 CYCI_HUMAN	Q14094 homo sapien
2	1952	99.5	377	2 Q6FHHO	Q6fhh0 homo sapien
3	1851	94.3	377	2 Q99LF2	Q99lf2 mus musculus
4	1847	94.1	377	1 CYCI_MOUSE	Q922v9 mus musculus
5	1841	93.8	377	2 Q8C7E2	Q8c7e2 mus musculus
6	1325.5	67.6	382	2 Q8P7H3	Q6p7h3 xenopus lae
7	1297.5	66.1	382	2 Q6DQJ8	Q6djg8 xenopus tro
8	1013	51.6	355	2 Q6NUZ7	Q6nuz7 brachydanio
9	1011	51.5	355	2 Q803P0	Q803p0 brachydanio
10	746.5	38.0	359	2 Q661Z0	Q661z0 xenopus lae
11	502.5	25.6	369	2 Q6ZMN8	Q6zmn8 homo sapien
12	327	16.7	344	1 CGS2_MOUSE	Q08918 mus musculus
13	326.5	16.6	344	1 CGG2_HUMAN	Q16589 homo sapien
14	326.5	16.6	344	2 Q8N5D4	Q8n5d4 homo sapien
15	322.5	16.4	356	2 Q6GM00	Q6gm00 xenopus lae
16	320.5	16.3	349	2 Q6NRC3	Q6nrc3 xenopus lae
17	320	16.3	344	2 Q8C9K5	Q8c9k5 mus musculus
18	318.5	16.2	344	2 Q6FGA7	Q6fga7 homo sapien
19	295.5	15.1	299	2 Q6FYI9	Q6fyi9 brachydanio
20	295.5	15.1	299	2 Q6TEN3	Q6ten3 brachydanio
21	295	15.0	295	2 Q802B8	Q802b8 xenopus lae
22	294.5	15.0	295	2 Q6DIY1	Q6diy1 xenopus tro
23	292.5	14.9	299	2 Q72TX1	Q72tx1 brachydanio
24	273.5	13.9	330	2 Q6NZ31	Q6nzz31 brachydanio
25	271.5	13.8	294	1 CGG1_RAT	F39950 rattus norv
26	271.5	13.8	295	1 CGG1_HUMAN	P51959 homo sapien
27	263.5	13.4	294	1 CGG1_MOUSE	P51945 mus musculus
28	229	11.7	171	2 Q6LC40	Q6lc40 mus musculus
29	212	10.8	397	2 Q7ZVC0	Q7zvc0 xenopus lae
30	206.5	10.5	378	2 Q9XG13	Q9xg13 lycopersico
31	204	10.4	300	2 Q9CSV7	Q9csv7 mus musculus

32	204	10.4	374	2	Q8WUE3	Q8wue3 homo sapien
33	204	10.4	404	1	CGE2_HUMAN	Q96020 homo sapien
34	203.5	10.4	410	2	Q9PVT7	Q9pvt7 carassius a
35	202	10.3	404	1	CGE2_MOUSE	Q92238 mus musculus
36	201.5	10.3	410	1	CG1E_BRARE	P47794 brachydanio
37	201	10.2	296	2	Q7Z774	Q7z774 homo sapien
38	197	10.0	407	1	CGE1_CHICK	P49707 gallus gall
39	196	10.0	361	2	Q9SN11	Q9sn11 arabidopsis
40	195	9.9	396	2	Q7PY34	Q7py34 anopheles g
41	192	9.8	311	2	Q95QC1	Q95qc1 caenorhabdi
42	192	9.8	357	2	Q8GVD9	Q8gvd9 helianthus
43	191	9.7	424	1	CG1E_HEMPU	O15995 hemientrot
44	189	9.6	403	2	Q7TW58	Q7tms8 mus musculus
45	188.5	9.6	373	2	Q9ZRX8	Q9zrx8 nicotiana t

ALIGNMENTS

RESULT 1
CYCI_HUMAN
ID CYCI_HUMAN STANDARD; PRT; 377 AA.
AC Q14094;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUN-2004 (Rel. 44, Last annotation update)
DE Cyclin I.
GN Name=CCNI;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Forebrain cortex;
RX MEDLINE=96086776; PubMed=7493655; DOI=10.1006/excr.1995.1406;
RA Nakamura T., Sanokawa R., Sasaki Y.F., Ayusawa D., Oishi M., Mori N.;
RT "Cyclin I: a new cyclin encoded by a gene isolated from human brain.";
RL Exp. Cell Res. 221:534-542(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Chen J.H., Luo W.Q., Zhou Y., Zhou H.J., Huang X.W., Yuan J.G.,
RA Qiang B.Q.;
RT "Isolating a new cDNA coding for human cyclin protein.";
RN Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A., AND VARIANT ILE-207.
RA Rieder M.J., Livingston R.J., Daniels M.R., Montoya M.A., Chung M.-W.,
RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Peel C.L., Robertson P.D.,
RA Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;
RT "NIH-SNPs, environmental genome project, NIHES ES15478, Department
of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).";
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney, and Muscle;
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Griwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalius D.E.,

QJW

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [5]
RP SEQUENCE OF 1-178 FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=98381026; PubMed=9705831; DOI=10.1006/bbrc.1998.9052;
RT Zhu X., Naz R.K.;
RL "Expression of a novel isoform of cyclin D in human testis.";
RL Biochem. Biophys. Res. Commun. 249:56-60 (1998).
CC -!- TISSUE SPECIFICITY: Highest levels in adult heart, brain and
CC skeletal muscle. Lower levels in adult placenta, lung, kidney and
CC pancreas. Also high levels in fetal brain and lower levels in
CC fetal lung, liver and kidney. Also abundant in testis and thyroid.
CC -!- DEVELOPMENTAL STAGE: Expression is independent of the cell cycle
CC in lung fibroblasts.
CC -!- SIMILARITY: Belongs to the cyclin family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D50310; BAA08849.1; -;
DR EMBL; AY207372; NAO313492.1; -;
DR EMBL; BC000420; AAH00420.1; -;
DR EMBL; BC004975; AAH04975.1; -;
DR EMBL; AF135162; AAF43786.1; -;
DR PIR; J02624; J02624.
DR Genew; HGNC:1595; CCNI.
DR H-invDB; HIX0004313; -;
DR GO; GO:0007283; F: spermatogenesis; NAS.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR011028; Cyclin like.
DR InterPro; IPR006671; Cyclin N.
DR Pfam; PF00134; Cyclin N; 1.
DR SMART; SM00385; CYCLIN; 1.
DR PROSITE; PS00292; CYCLINS; FALSE_NEG.
DR Cyclin; Polymorphism.
KW VARIANT 207 207 V -> I (in dbSNP:4252903).
FT CONFLICT 9 9 /FTID=VAR_016312.
FT CONFLICT 58 58 N -> D (in Ref. 5).
FT CONFLICT 75 75 Q -> R (in Ref. 5).
FT CONFLICT 75 75 R -> G (in Ref. 5).
SQ SEQUENCE 377 AA; 42557 MW; 2DE84EFA74698F6C CRC64;

Query Match 100.0%; Score 1962; DB 1; Length 377;
Best Local Similarity 100.0%; Pred. No. 2.1e-152;
Matches 377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKFPGPLENQLSFLLEKAITREAOQMKVNVKMPNSQNVSPSQRDEVIQWLAKLYQFN 60
Db 1 MKFPGPLENQLSFLLEKAITREAOQMKVNVKMPNSQNVSPSQRDEVIQWLAKLYQFN 60

Qy 61 LYPETPALASSLLDRFLATVKAHPKYLSCIAISCFFLAAKTVEDEIPVLKVLARDSFC 120
Db 61 LYPETPALASSLLDRFLATVKAHPKYLSCIAISCFFLAAKTVEDEIPVLKVLARDSFC 120

Qy 121 GCSSEILRMERIIIDKLNWDLHTATPLDFLHIFHAIAVSTRPQLLSPLKLSQHLAV 180
Db 121 GCSSEILRMERIIIDKLNWDLHTATPLDFLHIFHAIAVSTRPQLLSPLKLSQHLAV 180

Qy 181 LTKQLLHMACNQLLOFRGSMALAMVLSLEWEKLI PDWLSLTIELLOKAMDSSQLIHCR 240
Db 181 LTKQLLHMACNQLLOFRGSMALAMVLSLEWEKLI PDWLSLTIELLOKAMDSSQLIHCR 240

Qy 241 ELVAHHLSTLQSSLPVNSVYVYRPLKHTLVTCDKGVFRLHPSSVPGPDFSKDMSKPEVPV 300
Db 241 ELVAHHLSTLQSSLPVNSVYVYRPLKHTLVTCDKGVFRLHPSSVPGPDFSKDMSKPEVPV 300

Qy 301 RGTAAAFVHHLPAASGCKQTSTKRVEMEVDVDFYDGIKRLYNEDNVSENVSVCCTDLRS 360
Db 301 RGTAAAFVHHLPAASGCKQTSTKRVEMEVDVDFYDGIKRLYNEDNVSENVSVCCTDLRS 360

Qy 361 QEGHASPCPPLQPVSV 377
Db 361 QEGHASPCPPLQPVSV 377

Qy 301 RGTAAAFVHHLPAASGCKQTSTKRVEMEVDVDFYDGIKRLYNEDNVSENVSVCCTDLRS 360
Db 301 RGTAAAFVHHLPAASGCKQTSTKRVEMEVDVDFYDGIKRLYNEDNVSENVSVCCTDLRS 360

Qy 361 QEGHASPCPPLQPVSV 377
Db 361 QEGHASPCPPLQPVSV 377

RESULT 2
Q6FHH0 PRELIMINARY; PRT; 377 AA.
AC Q6FHH0; 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE CCNI protein (Fragment).
GN Name=CCNI;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Halleck A., Ebert L., Moundinya M., Schick M., Eisenstein S.,
RA Neubert P., Kstrang-K., Schatten R., Shen B., Henze S., Mar W.,
RA Korn B., Zhang Y., LaBaer J.,
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the cyclin family.
DR EMBL; CR541783; CAG46582.1; -;
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR011028; Cyclin like.
DR InterPro; IPR006671; Cyclin N.
DR Pfam; PF00134; Cyclin N; 1.
DR SMART; SM00385; CYCLIN; 1.
FT NON TER 377 377
SQ SEQUENCE 377 AA; 42486 MW; D950A5CCF0D0F514 CRC64;

Query Match 99.5%; Score 1952; DB 2; Length 377;
Best Local Similarity 99.5%; Pred. No. 1.4e-151;
Matches 375; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKFPGPLENQLSFLLEKAITREAOQMKVNVKMPNSQNVSPSQRDEVIQWLAKLYQFN 60
Db 1 MKFPGPLENQLSFLLEKAITREAOQMKVNVKMPNSQNVSPSQRDEVIQWLAKLYQFN 60

Qy 61 LYPETPALASSLLDRFLATVKAHPKYLSCIAISCFFLAAKTVEDEIPVLKVLARDSFC 120
Db 61 LYPETPALASSLLDRFLATVKAHPKYLSCIAISCFFLAAKTVEDEIPVLKVLARDSFC 120

Qy 121 GCSSEILRMERIIIDKLNWDLHTATPLDFLHIFHAIAVSTRPQLLSPLKLSQHLAV 180
Db 121 GCSSEILRMERIIIDKLNWDLHTATPLDFLHIFHAIAVSTRPQLLSPLKLSQHLAV 180

Qy 181 LTKQLLHMACNQLLOFRGSMALAMVLSLEWEKLI PDWLSLTIELLOKAMDSSQLIHCR 240
Db 181 LTKQLLHMACNQLLOFRGSMALAMVLSLEWEKLI PDWLSLTIELLOKAMDSSQLIHCR 240

Qy 241 ELVAHHLSTLQSSLPVNSVYVYRPLKHTLVTCDKGVFRLHPSSVPGPDFSKDMSKPEVPV 300
Db 241 ELVAHHLSTLQSSLPVNSVYVYRPLKHTLVTCDKGVFRLHPSSVPGPDFSKDMSKPEVPV 300

Qy 301 RGTAAAFVHHLPAASGCKQTSTKRVEMEVDVDFYDGIKRLYNEDNVSENVSVCCTDLRS 360
Db 301 RGTAAAFVHHLPAASGCKQTSTKRVEMEVDVDFYDGIKRLYNEDNVSENVSVCCTDLRS 360

Qy 361 QEGHASPCPPLQPVSV 377
Db 361 QEGHASPCPPLQPVSV 377

```
RESULT 3
Q99LF2 PRELIMINARY; PRT; 377 AA.
ID Q99LF2;
AC Q99LF2;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Cyclin I.
DN
GN Name=Ccni;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Mammary tumor;
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Collins E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Fellings F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Mammary tumor;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the cyclin family.
DR EMBL; BC003290; AA03290.1; -.
DR MGD; MGI:1341077; Ccni.
DR GO; GO:000074; P:regulation of cell cycle; TAS.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR011028; Cyclin_like.
DR Pfam; PF00134; Cyclin_N.
DR SMART; SM00385; CYCLIN; 1.
KW Cyclin.
SQ SEQUENCE 377 AA; 42227 MW; FDA2D896A5366A9F CRC64;
Query Match 94.3%; Score 1851; DB 2; Length 377;
Best Local Similarity 94.2%; Pred. No. 2.7e-143;
Matches 355; Conservative 11; Mismatches 11; Indels 0; Gaps 0;
QY 1 MKFPGPLENORLSLEKAITREAAQMKVNVKMPNSQNSPSORDEVIQWLAKLYQFN 60
DB 1 MKFPGPLENORLSLEKAITREAAQMKVNVKMPNSQNSPSORDEVIQWLAKLYQFN 60
QY 61 LYPETFALLSILDRFLATVKAHPKYLSCIAISCFFLAAKTVEDEIPVLKVLARSFC 120
DB 61 LYPETFALLSILDRFLATVKAHPKYLSCIAISCFFLAAKTVEDEIPVLKVLARSFC 120
QY 121 GCSSEILRMERILDKLNWDLHTATPLDHLHFAIAVSTRPQLLPSLPKSPQHLAV 180
DB 121 GCSSEILRMERILDKLNWDLHTATPLDHLHFAIAVSTRPQLLPSLPKSPQHLAV 180
QY 181 LTKQLLHCWACNQLLOFGKSMALAMVSLMEKLIIPDWLSITIELLOKQAWDSQLIHC 240
DB 181 LTKQLLHCWACNQLLOFGKSMALAMVSLMEKLIIPDWLSITIELLOKQAWDSQLIHC 240

RESULT 4
CYC1 MOUSE
ID CYC1 MOUSE STANDARD; PRT; 377 AA.
AC Q922V9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cyclin I.
DN
GN Name=Ccni;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99172101; PubMed=10072591;
RA Jensen M.R., Audolfsson T., Keck C.L., Zimonjic D.B.,
RA Thorgeirsson S.S.;
RT "Assignment of the cyclin I gene (Ccni) to mouse chromosome 5E3.3-F1.
RT 3 by in situ hybridization."
RL Cytogenet. Cell Genet. 83:242-243 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20509992; PubMed=11054536; DOI=10.1016/S0378-1119(00)00361-9;
RA Jensen M.R., Audolfsson T., Factor V.M., Thorgeirsson S.S.;
RT "In vivo expression and genomic organization of the mouse cyclin I
RT gene (Ccni)."
RL Gene 256:59-67 (2000).
CC -1- SIMILARITY: Belongs to the cyclin family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.ebi.ac.uk/announcements/
CC or send an email to license@sib.ch).
CC EMBL; AF005896; AAD01253.2; -.
DR EMBL; AF228740; AAF43391.1; -.
DR EMBL; AF228739; AAF43391.1; JOINED.
DR MGD; MGI:1341077; Ccni.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR011028; Cyclin_like.
DR Pfam; PF00134; Cyclin_N.
DR SMART; SM00385; CYCLIN; 1.
DR PROSITE; PS00292; CYCLINS; FALSE_NEG.
KW Cyclin.
SQ SEQUENCE 377 AA; 42261 MW; 4151141C6D9AE677 CRC64;
Query Match 94.1%; Score 1847; DB 1; Length 377;
Best Local Similarity 93.9%; Pred. No. 5.7e-143;
Matches 354; Conservative 11; Mismatches 12; Indels 0; Gaps 0;
QY 1 MKFPGPLENORLSLEKAITREAAQMKVNVKMPNSQNSPSORDEVIQWLAKLYQFN 60
DB 1 MKFPGPLENORLSLEKAITREAAQMKVNVKMPNSQNSPSORDEVIQWLAKLYQFN 60
```

```

QY 61 LYPETFALASSLLDRFLATVKAHPKYLSCIAISCFFLAAKTVEDEIPVLKVLARDSFC 120
Db 61 LYPETFALASSLLDRFLATVKAHPKYLNCIAISCFFLAAKTVEDEKIPVLKVLARDSFC 120
QY 121 GCSSEILRMERIIIDKLNWDLHTATPLDFHIFHAIAVSTRPQLLPSLPSQHLAV 180
Db 121 GCSSEILRMERIIIDKLNWDLHTATPLDFHIFHAIAVSTRPQLLPSLPSQHLAV 180
QY 181 LTKQLLHCMAACNQLQFSGMLALAMVLEMEKLIIPDWLSITIELLOKAQWSSQLIHC 240
Db 181 LTKQLLHCMAACNQLQFSGMLALAMVLEMEKLIIPDWLPITIELLOKAQWSSQLIHC 240
QY 241 ELVAHLSTLQSSPLNSVYVYRPLKHTLVTCDKGVFRLHPSVPGPDFSKDNKPEVPV 300
Db 241 ELVAHLSALQSALPLNSVYVYRPLKHTLVTCDKGAFKLHPSVSGPDFSKDNKPEVPV 300
QY 301 RGTAAFYHHLPAASGCKQTSKRKYVEMEVDVFDGIKRLYNEDNNGPENVGSGCTDLSR 360
Db 301 RGTAAFYHHLPAASGCKQTSKRKYVEMEVDVFDGIKRLYNEDNNGPENVGSGCTDLSR 360
QY 361 QEGHASPCLPQPVSM 377
Db 361 QEGHASPCLPQPVSM 377

RESULT 5
Q8C7E2
ID Q8C7E2 PRELIMINARY; PRT; 377 AA.
AC Q8C7E2
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus adult pancreas islet cells cDNA, RIKEN full-length
DE enriched library, clone:C820001G04 product:cyclin I, full insert
DE sequence.
GN Name=Ccni;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=20493174; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=20493174; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.

```

```

RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagao K., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Suni M., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yanamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akashira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the cyclin family.
DR EMBL; AK050465; BAC34271.1; -.
DR MGD; MGI:1341077; Ccni.
DR GO; GO:0000074; P:regulation of cell cycle; TAS.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR011028; Cyclin-like.
DR InterPro; IPR006671; Cyclin_N.
DR Pfam; PF001134; Cyclin_N; 1.
DR SMART; SM00385; CYCLIN; 1.
DR KX
DR KW Cyclin.
SQ SEQUENCE 377 AA; 42206 MW; A1B803BEBE135B0E8 CRC64;

Query Match 93.8%; Score 1841; DB 2; Length 377;
Best Local Similarity 93.6%; Pred. No. 1.8e-142;
Matches 353; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

QY 1 MKFPGPLENORLSPLLEKAITREAOQWKNVVRMPNSQNSQSPQRDEVIQWLAKLYQFN 60
Db 1 MKFPGPLENHRLSLLERALSREAOQWKNVVRMPNSQNSQSPQRDEVIQWLAKLYQFN 60
QY 61 LYPETFALASSLLDRFLATVKAHPKYLSCIAISCFFLAAKTVEDEIPVLKVLARDSFC 120
Db 61 LYPETFALASSLLDRFLATVKAHPKYLNCIAISCFFLAAKTVEDEKIPVLKVLARDSFC 120
QY 121 GCSSEILRMERIIIDKLNWDLHTATPLDFHIFHAIAVSTRPQLLPSLPSQHLAV 180
Db 121 GCSSEILRMERIIIDKLNWDLHTATPLDFHIFHAIAVSTRPQLLPSLPSQHLAV 180
QY 181 LTKQLLHCMAACNQLQFSGMLALAMVLEMEKLIIPDWLSITIELLOKAQWSSQLIHC 240
Db 181 LTKQLLHCMAACNQLQFSGMLALAMVLEMEKLIIPDWLPITIELLOKAQWSSQLIHC 240
QY 241 ELVAHLSTLQSSPLNSVYVYRPLKHTLVTCDKGVFRLHPSVPGPDFSKDNKPEVPV 300
Db 241 ELVAHLSALQSALPLNSVYVYRPLKHTLVTCDKGAFKLHPSVSGPDFSKDNKPEVPV 300
QY 301 RGTAAFYHHLPAASGCKQTSKRKYVEMEVDVFDGIKRLYNEDNNGPENVGSGCTDLSR 360
Db 301 RGTAAFYHHLPAASGCKQTSKRKYVEMEVDVFDGIKRLYNEDNNGPENVGSGCTDLSR 360
QY 361 QEGHASPCLPQPVSM 377
Db 361 QEGHASPCLPQPVSM 377

RESULT 6

```

```

Q6P7H3 ID Q6P7H3 PRELIMINARY; PRT; 382 AA.
AC Q6P7H3
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 28, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE MGC68660 protein.
GN Name=MGC68660;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickinson M.C.,
RA Blakesley R.W., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Klein S., Strausberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the cyclin family.
DR EMBL; BC061670; AAH61670.1; -
DR GO; GO:0007049; P:cell cycle; IEA.
DR GO; GO:0000910; P:cytokinesis; IEA.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR011028; Cyclin like.
DR InterPro; IPR006671; Cyclin N.
DR Pfam; PF00134; Cyclin N; 1.
DR SMART; SM00385; CYCLIN; 1.
DR PROSITE; PS00292; CYCLINS; 1.
KW Cell cycle; Cell division; Cyclin.
SQ SEQUENCE 382 AA; 42913 MW; E19D7C5D8FEC626A CRC64;

Query Match 67.6%; Score 1325.5; DB 2; Length 382;
Best Local Similarity 67.9%; Pred. No. 3.3e-100;
Matches 260; Conservative 48; Mismatches 68; Indels 7; Gaps 4;

QY 1 MKPQPLENQRSLFLEKAITREAAQMKVVRKMPNSQN--VSPQRDEVIQWLAKLYQ 58
Df |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MKFGSPLESQRSLFLLERAVSREAAQMKVYHKTQANDVAVSPQRDEVIQWLAKLYQ 60
QY 59 FNLYPETTALASSLLDRFLATVKAHPKYLSCIAISCFFLAAKTVEEDERIPVLKVLARDS 118

```

```
DR SMART; SM00385; CYCLIN; 1.
KW Cyclin.
SQ SEQUENCE 382 AA; 42919 MW; E1F28D13AFB42CEA CRC64;

Query Match 66.1%; Score 1297.5; DB 2; Length 382;
Best Local Similarity 66.1%; Pred. No. 6.5e-98;
Matches 253; Conservative 54; Mismatches 69; Indels 7; Gaps 4;

QY 1 MKFPGPLENORSLFLEKAITREAOVMKVNVRKMPNSQNV--SPSORDEVITQWLAKLYQ 58
DB 1 MKFPGPLESQRILYFLERAEAGQIKWVYVYKQTOINQDVGISQPRDEVITQWLAKLYQ 60
QY 59 FNLYPETFALASSLLDRFLATVKAHPKYLSCIAISCFFLAAKTVEEDERIPVLKVLARDS 118
DB 61 FRVYPETHALAIISILDRFLAAVKAHPKYLSCIAISCFFLAAKTVEEDERIPVLKVLARDS 120
QY 119 FCGSSSSEILRMERIIIDKLNWDLHTATPLDPLHIFHAIIVSTRPQLLSFSPKLS 178
DB 121 SCGCSPEAEVLRMERIILDKLNWDLHTATPLDPLHIFHAIIVSTRPQLLSFSPKLS 180
QY 179 AVLTKQLLHMACNQLQFRGSMALAMVSLMEKLIIPDWLSLTIELLQKQMDSSQLIH 238
DB 181 ALLTRQLQCNAFHQLQFRGSMALALSLMEKLIIPDWLSLTIELLQKQMDSSQLIF 240
QY 239 CRELVAHLSTLQSSLPNSVYVYRPLKHTLVTCDKGVFRLHPSSVPGPDF--SKDNSKPE 297
DB 241 CREVAHLSLLQPPPLPNAVYISPLKRTLVSYNRGAY--IHPSTVKEPGFHPQNCISG 299
QY 298 VVVRGTAAFYHHLPAASCKQTSTKRKVEEMVEDDFYDGIKRLYNEDNVNENSGV 354
DB 300 ALIKGASVLYOSLAAPVCKQASTKRKVEEMVEDDFYDGIKRLYNEDNVNENSGV 359
QY 355 GTDLRSRQEGHASPCCPLQPVSM 377
DB 360 SSGLRSRSGSLSPCPLQAVSM 382

RESULT 8
Q6NUZ7
ID Q6NUZ7 PRELIMINARY; PRT; 355 AA.
AC Q6NUZ7
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cyclin I.
GN Name=Cni;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitting J., Maman A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human

and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
SEQUENCE FROM N.A.
TISSUE=Embryo;
RC Director MGC Project;
RA Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the cyclin family.
DR EMBL; BC068369; AAH68369.1; -.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR011028; Cyclin like.
DR Pfam; PF00134; Cyclin_N; 1.
DR SMART; SM00385; CYCLIN; 1.
DR PROSITE; PS00292; CYCLINS; UNKNOWN_1.
KW Cyclin.
SQ SEQUENCE 355 AA; 39614 MW; E9D4236191F663BF CRC64;

Query Match 51.6%; Score 1013; DB 2; Length 355;
Best Local Similarity 55.6%; Pred. No. 1.2e-74;
Matches 212; Conservative 56; Mismatches 77; Indels 36; Gaps 8;

QY 1 MKFPGPLENORSLFLEKAITREAOVMKVNVRKMPNSQ--NVSPSORDEVITQWLAKLYQ 58
DB 1 MKFPGPLESQRILYFLERAEAGQIKWVYVYKQTOINQDVGISQPRDEVITQWLAKLYQ 60
QY 59 FNLYPETFALASSLLDRFLATVKAHPKYLSCIAISCFFLAAKTVEEDERIPVLKVLARDS 118
DB 61 LKLYPETCLAIAGLDRLFTIKARPKYLSCIAISCFFLAAKTVEEDERIPSLRELASS 120
QY 119 FCGSSSSEILRMERIIIDKLNWDLHTATPLDPLHIFHAIIVSTRP--QLLSFSLKLS 177
DB 121 KCGCSPSEILRMERIVLDKLNWDLHTATPLDPLHIFHAIIVSTRP--QLLSFSLKLS 180
QY 178 LAVTLKQLLHMACNQLQFRGSMALAMVSLMEKLIIPDWLSLTIELLQKQMDSSQLI 237
DB 181 VALLTQQLFHCIAHALLQVRGSLLSGLITLLEKLCPDWLTALTVDLLHRLQDSSQLI 240
QY 238 HCRELVAHLSTLQSSLPNSVYVYRPLKHTLVTCDKGVFRLHPSSVPGPDFSKDNSKPE 297
DB 241 CCRELVARCISLTHASLPPTVYICRPLPEPR---DEGV---LHVS LAP-----TAPS 287
QY 298 VVVRGTAAFYHHLPAASCKQTSTKRKVEEMVEDDFYDGIKRLYNEDNVNENSGVCGTD 357
DB 288 DP-----NSTHSRSKRKVEEMVEDDFYDGIKRLYNENPQ--GALLCTA 331
QY 358 LSROEGH-----ASPCPLQPV 374
DB 332 QTAGGQGPAGSPCCPLQPV 352

RESULT 9
Q803P0
ID Q803P0 PRELIMINARY; PRT; 355 AA.
AC Q803P0;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2004 (TrEMBLrel. 25, Last annotation update)
DE Cyclin I.
GN Name=Cni;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AB; TISSUE=Whole body;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitting J., Maman A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
```


RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.B., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krywinski M.I., Skalska U., Smallus D.B., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=AB; TISSUE=Whole body;
RA Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the cyclin family.
DR EMBL; BC044400; AAH44400.1; --
DR HSSP; P30274; 1VIN.
DR ZFIN; ZDB-GENE-040426-2898; cnci.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR011028; Cyclin like.
DR InterPro; IPR006671; Cyclin N.
DR Pfam; PF00134; Cyclin_N; 1.
DR SMART; SM00385; CYCLIN; 1.
DR PROSITE; PS00292; CYCLINS; UNKNOWN_1.
KW Cyclin.
SQ SEQUENCE 355 AA; 39517 MW; D2999F2E9812C880 CRC64;

Query Match 51.5%; Score 1011; DB 2; Length 355;
Best Local Similarity 55.6%; Pred. No. 1.8e-74;
Matches 212; Conservative 56; Mismatches 77; Indels 36; Gaps 8;

Qy 1 MKFPGPLENORLSFLLEKAITREAOQMKVNRKPSNQ--NVSPSQRDEVIQWLAKLYQ 58
Db 1 MKFTKPLESRKLSLEKAVSREAKLWKVYVPKPTQDTPDISPEKRDVAVRLRVHSQ 60

Qy 59 FNLYPETFALASSLLDRFLATVKAHPKYLSCIAISCFPLAAKTVEEDERIPVLKVLARDS 118
Db 61 LKLYPETFCLTGAIGLDRFLSTIKARPKYLRCAISCFPLAAKTSEEDERIPSLRELASS 120

Qy 119 FCGSSSEILRMERIILDKLNDLHTATPLDFLHFAIAVSTRP-QLLFSLPKLSPSOH 177
Db 121 KCGSPSEILRMERIILDKLNDLHTATPLDFLHFAIAVSTRP-QLLFSLPKLSPSOH 180

Qy 178 LAVLTQQLLHMACNQLIQFRGSMALAMVLSLEMEKLIIPDWLSLTIELLQKAQMDSSOLI 237
Db 181 VALLITQQLFHCLAHNALLQVRGSLSLGLITLELEKLCPLWALTVDLLHRLQIDSSOLI 240

Qy 238 HCRELVHAHLSTLOSSLPNLYVYRPLKHTLVTCDKGVFRLHPSSVPGPDFSKDNKSKE 297
Db 241 CCRELVARCLSTHTASLPNTVYICRPLPEPR--DEGV--LHVS LAP-----TAPS 287

Qy 298 VPVRGTAFAFHYHLPAAACCKTSTKRYKVEEVDVFDGIKRLYNEDNVSENGVSGCTD 357
Db 288 DP-----NTHSRSAKRKVEQMEVDVFDGIKRLYNEDNVSENGVSGCTD 357

Qy 358 LSRQEGH-----ASPCPPLQPV 374
Db 332 QTAGGGQPNAGSSPCPPLQPV 352

RESULT 10
Q661Z0 PRELIMINARY; PRT; 359 AA.
AC Q661Z0;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)

DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE MGC83953 protein.
GN Name=MGC83953;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Oocytes;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative";
RL Dev. Dyn. 225:384-391(2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Oocytes;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.B., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krywinski M.I., Skalska U., Smallus D.B., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[3]
RP SEQUENCE FROM N.A.
RC TISSUE=Oocytes;
RA Klein S., Gerhard D.S.;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the cyclin family.
DR EMBL; BC081135; AAH81135.1; --
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR011028; Cyclin like.
DR Pfam; PF00134; Cyclin_N; 1.
DR SMART; SM00385; CYCLIN; 1.
KW Cyclin.
SQ SEQUENCE 359 AA; 40577 MW; 230B61BE382A6BC7 CRC64;

Query Match 38.0%; Score 746.5; DB 2; Length 359;
Best Local Similarity 43.4%; Pred. No. 8.9e-53;
Matches 168; Conservative 60; Mismatches 110; Indels 49; Gaps 8;

Qy 1 MKFPGPLENORLSFLLEKAITREAOQMKVNRK--MFSNQVSPSQRDEVIQWLAKLYQ 58
Db 1 MKCFGLSDIQRLMISLENSLQLEDTKWVPVCEGTGLKGTDISLTHYEQAVLWMEVTLR 60

Qy 59 FNLYPETFALASSLLDRFLATVKAHPKYLSCIAISCFPLAAKTVEEDERIPVLKVLARDS 118
Db 61 FHFYPTFGLAVSLNRLILASVKAQVYLRCTVACLFVLAKTSEEDERIPSVKVLAVQS 120

Qy 119 FCGSSSEILRMERIILDKLNDLHTATPLDFLHFAIAVSTRPQLLSPLKSPSOHL 178
Db 121 GCMCSSAEILRMERIILDKLNDLHTATPLDFLHFAIAVSTRPQLLSPLKSPSOHL 180

Qy 179 AVLTQQLLHMACNQLIQFRGSMALAMVLSLEMEKLIIPDWLSLTIELLQKAQMDSSOLI 238

```
Db 181 ALLTRLOQCMACHHLVQFRGSTALVITILELEKLTADWPATITELLKAKVDSAKFIL 240
Qy 239 CRELVAHSLTLOSLPLNSVYVYPLKHTLVTCDKGVRFLHPSPVGP-----DFSKD 292
Db 241 KCLVDQOGLMS-----PPNHVVFISAKR-----DPPAYRKEKSSACSPAGCFQPISMN 292
Qy 293 NSKPEVPVGTAAFYHPLPAASGCKQTSTKRVKVEMEVDFYDGIKRLYNEDNVSEN--- 349
Db 293 TEVPEVL-----SARKQAEIEMETEFYDGFYLYNEESVSDRRI 334
Qy 350 ----VGSVCGTDLRSQRBHAGSPCLQ 372
Db 335 KEMVTGKL-----QEA-SCPCPVQL 353

RESULT 11
Q6ZMN8
ID Q6ZMN8 PRELIMINARY; PRT; 369 AA.
AC Q6ZMN8;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DE 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DT Hypothetical protein FLJ16793.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Breast;
RA Tanigami A., Fujiwara T., Shibahara T., Goto Y., Hirao M., Shimizu F.,
RA Wakebe H., Ono T., Hishigaki H., Watanabe T., Ozaki K., Sugiyama T.,
RA Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J.,
RA Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,
RA Yanashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
RA Wagatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A.,
RA Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahara K.,
RA Masuho Y., Nagai K., Isogai T.;
RA Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the cyclin family.
DR EMBL; AK131553; BAD18687.1; -.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR011028; Cyclin like.
DR Pfam; PF00134; Cyclin N.
DR SMART; SM00385; CYCLIN; 1.
KW Cyclin.
SQ SEQUENCE 369 AA; 40621 MW; 68B887A9C044708 CRC64;

Query Match 25.6%; Score 502.5; DB 2; Length 369;
Best Local Similarity 44.6%; Pred. No. 9.4e-33;
Matches 111; Conservative 44; Mismatches 89; Indels 5; Gaps 1;

Qy 5 GPLENQLRSLLEKAITREAOQWKVVKMPSNQVSPSQDEVIOWIAKLYOFNLYPE 64
Db 115 GDLERRLLCHLQAQDREARLRGG-----KPQDEICDAFEVYVLMRLRLQNTFYFSQS 169
Qy 65 TFALASSLLDRFLATVKAHPKYLSCIAISCFPLAATVEEDERIPVLKVLARDSFQCGSS 124
Db 170 TFLNALTIFGRLLSVKYKYLHCATITSLRLAKVNEEEFIPQVKDFKHGSDYSP 229
Qy 125 SEILRMERIIIDKLNWDLHTATPDLDFHIFHAIAVSTRPQLFLSLPKLSPQHLAVLTQ 184
Db 230 NELLRMELAILDRHLWDLYIGTLPDLFTIFHALVLSWPHVLELLPQRNPSLHVASLTRQ 289
Qy 185 LLHCWACNQLQFRGSMALAWVSLMEKLPDMLSLTIELLOKAQWDSQLIHRELVA 244
Db 290 LQHCWAGHQLQFRGSLTALVITILELERLMPGWCAPISDLRLKKAQWDMQYSCCKELVM 349
Qy 245 HHLSTLQSS 253
Db 350 QQLRSLQSS 358
```

```
RESULT 12
CG2 MOUSE
ID CG2 MOUSE STANDARD; PRT; 344 AA.
AC O08918; O35612;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cyclin G2.
GN Name=Cng2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Thymus;
RA Horne M.C., Donaldson K.L., Goolsby G.L., Tran D., Mulheisen M.,
RA Hell J.W., Wahl A.F.;
RT "Cyclin G2 is up-regulated during growth inhibition and B cell antigen
RT receptor-mediated cell cycle arrest.";
RL J. Biol. Chem. 272:12650-12661(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Liver;
RA MEDLINE=9224097; PubMed=10216255; DOI=10.1016/S0378-1119(99)00057-8;
RA Jensen M.R., Audolfsson T., Keck C.L., Zimonjic D.B.,
RA Thorgeirsson S.S.;
RT "Gene structure and chromosomal localization of mouse cyclin G2
RT (Cng2).";
RN [3]
RP SEQUENCE FROM N.A.
RA Kimura S.H., Nojima H.;
RT "Genomic structure, chromosomal mapping and p53-independent induction
RT of mouse cyclin G2 gene.";
CC Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: May play a role in growth regulation and in negative
CC regulation of cell cycle progression.
CC -1- SUBCELLULAR LOCATION: Primarily cytoplasmic, a minor portion can
CC be detected in some cells in the nucleus.
CC -1- TISSUE SPECIFICITY: Highest levels in intestine. Intermediate
CC levels in spleen, brain and kidney. Low levels in testis, stomach,
CC pancreas, liver, salivary gland and muscle. According to Ref.1
CC also abundant in thymus.
CC -1- DEVELOPMENTAL STAGE: Expression levels oscillate moderately
CC through the cell cycle.
CC -1- INDUCTION: Activated in B-cells by agents causing growth
CC inhibition or growth arrest.
CC -1- SIMILARITY: Belongs to the cyclin family. Cyclin G subfamily.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U95826; AAB58693.1; -.
CC EMBL; AF005885; AAC28496.1; -.
CC EMBL; AF079877; AAC32372.1; -.
CC EMBL; AB035264; BAA87065.1; -.
CC MGD; MGI:1095734; Cng2.
CC InterPro; IPR006670; Cyclin.
CC InterPro; IPR011028; Cyclin like.
CC Pfam; PF00134; Cyclin N.
CC SMART; SM00385; CYCLIN; 1.
KW Cell cycle; Cell division; Cyclin; Mitosis.
SQ SEQUENCE 344 AA; 38847 MW; F6A02698C286D853 CRC64;
```

```
Query Match 16.7%; Score 327; DB 1; Length 344;
Best Local Similarity 29.4%; Pred. No. 2.1e-18;
Matches 113; Conservative 58; Mismatches 107; Indels 106; Gaps 17;

QY 12 LSELLEKAITREAOQWKK-----VNVKQPSNQVPSQ-RDEVIQWLAKLYQFNLYPE 64
DB 21 LNFYLE-----OQORYQPREKGLIIMEATPENDNTLCSRLNAKVEDLRSITNFFGSGTE 75
QY 65 TFLASSLLDRFLATVKAHPKYLSCIALSCFFLAAKTVEEDERIPVLKVLARDSFCGCS 124
DB 76 TFLAVNLDRFLAMKVKPKHLSGIGVCCFLAARLAEEGDPVPTDVRISQCKTA 135
QY 125 SEILRMERIIIDKLNWDHTATPDPLHIFHAI-----VSTRPQLFSLPKLSPQSHLAVL 181
DB 136 SDIKRMKIIIEKHLHYEATLALNFLHVAIVFCHTSEKIL-SLDKLE----- 186
QY 182 TKQLLHMCACNQLQF-----RGSMLALAMVSIEMKLIIPDWLSLTIELQ-----KAQM 231
DB 187 -----AQLKACNCRVVFVKARPSVLACLNLEIETI-----KSVLELEILLVKKHLKL 236
QY 232 DSSQLIHRELVAHLSLTQSSPLNSVYVRPLKHTL-----VTCDKGVFLHPSSVPG 286
DB 237 SDTEFFYRELVSCLAYSF-----RCKPDLKLVIVSRRTAQNLSHYY-- 285
QY 287 PDFSKDNKPEVPVKGTAFFYHULPAAGCKQTSTKRVKMEVDDFYDGKRLYNEDNV 346
DB 286 -----SVPELPT-----IP-EGGC-----PDGSE---SEDS- 307
QY 347 SENVGSVCGTDLRSQEGHASPCCP 370
DB 308 -----GEDMSGEESSLSSPP 323

RESULT 13
CGG2_HUMAN
ID CGG2_HUMAN STANDARD; PRT; 344 AA.
AC Q16589;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cyclin G2.
GN Name=CCNG2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal brain, and Fetal spleen;
RX MEDLINE=96400325; PubMed=8806701;
RA Bates S.A., Rowan S., Voudsen K.H.;
RT "Characterisation of human cyclin G1 and G2: DNA damage inducible
RT genes.";
RL Oncogene 13:1103-1109 (1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=T-cell;
RX MEDLINE=96198057; PubMed=8626390; DOI=10.1074/jbc.271.11.6050;
RA Horne M.C., Goolbsy G.L., Donaldson K.L., Tran D., Neubauer M.,
RA Wahl A.P.;
RT "Cyclin G1 and cyclin G2 comprise a new family of cyclins with
RT contrasting tissue-specific and cell cycle-regulated expression.";
RL J. Biol. Chem. 271:6050-6061 (1996).
RN [3]
RP SEQUENCE FROM N.A., AND VARIANTS VAL-4 AND GLY-28.
RA Rieder M.J., Livingston R.J., Daniels M.R., Montoya M.A., Chung M.-W.,
RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
RA Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;
RT "NIHES-SNPs, environmental genome project, NIHES ES15478, Department
RT of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).";
RT Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: May play a role in growth regulation and in negative
regulation of cell cycle progression.
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- TISSUE SPECIFICITY: High levels in cerebellum, thymus, spleen and
prostate. Low levels in skeletal muscle.
-!- DEVELOPMENTAL STAGE: Expression levels increase through the cell
cycle to peak in the mid/late-S phase and decrease during G2/M
phase.
-!- INDUCTION: Activated by actinomycin-D induced DNA damage.
-!- SIMILARITY: Belongs to the cyclin family. Cyclin G subfamily.
-----
This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (see http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
-----
EMBL; U47414; AAC50689.1; -.
DR EMBL; L49506; AAC41978.1; -.
DR EMBL; AF549495; AAN40704.1; -.
DR Genew; HGNC:1593; CCNG2.
DR MIM; 603203; -.
DR GO; GO:0000075; P:cell cycle checkpoint; TAS.
DR InterPro; IPR011028; Cyclin-like.
DR InterPro; IPR006671; Cyclin_N.
DR Pfam; PF00134; Cyclin_N; 1.
KW Cell cycle; Cell division; Cyclin; Mitosis; Polymorphism.
FT VARIANT 4 4
FT VARIAT 28 28 /FTID=VAR_014333.
FT FTID=VAR_014334.
FT SEQUENCE 344 AA; 38865 MW; D434E0CE92760301 CRC64;
Query Match 16.6%; Score 326.5; DB 1; Length 344;
Best Local Similarity 36.4%; Pred. No. 2.3e-18;
Matches 86; Conservative 44; Mismatches 73; Indels 33; Gaps 7;

QY 31 VRKMPNQ-NVPSQRDEVIQWLAKLYQFNLYPETTALASSLLDRFLATVKAHPKYLSC 89
DB 41 IEATPENDNTLCPGLRNAKVEDLRSANFFGSCCTETFLAVNLDRFLAMKVKPKHLS 100
QY 90 IASCFFLAATVEEDERIPVLKVLARDSFCGSSSEILRMERIIIDKLNWDHTATPLD 149
DB 101 IGVCFFLAARIVVEDCNIPSTHVDVIRISQCKTASDIKRMKIISEKHLHYEATLALN 160
QY 150 FLHIFHAIIV---STRPQLFSLPKLSPQSHLAVLTKQLLHMCACNQLQF---RGSMLA 203
DB 161 FLHYHIIILCHTSEKIL-SLDKLE-----AQLKACNCELIFSKAKPSVLA 207
QY 204 LAMVSLMEKLIIPDWLSLTIELQ-----KAQMSQLIHRELVAHLSLTQSS 252
DB 208 LCLANLEVTI-----KSVLELEILLVKKHSKINDTEFFYRELVSCKLAEYSS 257

RESULT 14
Q8N5D4
ID Q8N5D4 PRELIMINARY; PRT; 344 AA.
AC Q8N5D4;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CCNG2 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
```


Job time : 104.276 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 11, 2005, 02:58:09 ; Search time 107.026 Seconds
(without alignments)
1362.372 Million cell updates/sec

Title: US-09-736-250-1

Perfect score: 1962

Sequence: 1 MKFPGLPQLRSLFLEKAI.....LSRQGHASPCPLPQVSM 377

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1962	100.0	377	2 AAW21965	Aaw21965 Human cyc
2	1962	100.0	377	3 AAY52185	Aay52185 Human cyc
3	1962	100.0	377	6 ABR39934	Abr39934 Human pro
4	1962	100.0	377	8 ADP12615	Adp12615 Protein e
5	1960	99.9	377	8 ABM80569	Abm80569 Tumour-as
6	1713.5	87.3	334	7 RAE37938	Rae37938 Human CGD
7	1529.5	78.0	300	3 AAG01131	Adn01131 Human cel
8	667	34.0	131	3 AAG01903	Aag01903 Human sec
9	502.5	25.6	369	4 ABG18403	Abg18403 Novel hum
10	502.5	25.6	369	8 ADR10466	Adr10466 Human pro
11	326.5	16.6	344	5 ABP65178	Abp65178 Hypoxia-r
12	326.5	16.6	344	8 ADP66631	Adp66631 Human cyc
13	326.5	16.6	344	8 ADO19808	Ado19808 Human pro
14	326.5	16.6	344	8 ADO19317	Ado19317 Human pro
15	326.5	16.6	344	8 ADP54950	Adp54950 Human pro
16	326.5	16.6	344	8 ADP23418	Adp23418 PRO poly
17	326.5	16.6	362	8 ADR66294	Adr66294 Human pro
18	326.5	16.6	362	8 ADR68855	Adr68855 Human pro
19	326.5	16.6	380	8 ADP84518	Adp84518 Human bre
20	326.5	16.6	403	8 ADO19315	Ado19315 Human pro
21	326.5	16.6	403	8 ADP23416	Adp23416 PRO poly
22	271.5	13.8	294	7 ADD46447	Add46447 Rat Prote
23	271.5	13.8	295	7 ADD46449	Add46449 Human pro
24	271.5	13.8	295	8 ABM80697	Abm80697 Tumour-as
25	263.5	13.4	249	5 ABB57103	Abb57103 Mouse isc

26	231	11.8	249	2 AAW24788	Aaw24788 Human cyc
27	218	11.1	88	8 ABO56671	Ab056671 Human gen
28	213.5	10.9	277	8 ABM83893	Abm83893 Human dia
29	213.5	10.9	277	8 ABM83894	Abm83894 Human dia
30	204	10.4	404	2 AAY43173	Aay43173 Human cyc
31	204	10.4	404	3 AAY77483	Aay77483 Human cyc
32	204	10.4	404	4 AAY72462	Aay72462 Human cyc
33	204	10.4	404	7 ADB67893	Adb67893 Human lun
34	204	10.4	404	7 ADF48687	Adf48687 Human cyc
35	204	10.4	404	8 ADI82506	Adi82506 Human mod
36	204	10.4	404	8 ADN05983	Adn05983 Antipsori
37	204	10.4	404	8 ADO19484	Ado19484 Human pro
38	202	10.3	403	2 AAY43174	Aay43174 Mouse cyc
39	202	10.3	403	4 AAY72463	Aay72463 Mouse cyc
40	202	10.3	403	7 ADF48688	Adf48688 Murine cy
41	201	10.2	296	7 ADN95215	Adn95215 Human BEC
42	196	10.0	308	3 AAG07076	Aag07076 Arabidops
43	196	10.0	308	3 AAG53865	Aag53865 Arabidops
44	196	10.0	361	3 AAG53864	Aag53864 Arabidops
45	196	10.0	361	3 AAG07075	Aag07075 Arabidops

ALIGNMENTS

RESULT 1

AAW21965
ID AAW21965 standard; protein; 377 AA.

XX AC AAW21965;

XX DT 02-DEC-1997 (first entry)

XX DE Human cyclin I.

XX KW human; cyclin I; antisense; probe; neurone; cancer; antibody.

XX OS Homo sapiens.

XX PN WO9712973-A1.

XX PD 10-APR-1997.

XX PF 07-OCT-1996; 96WO-JF002905.

XX PR 05-OCT-1995; 95JP-00284663.

XX PA (SUME) SUMITOMO ELECTRIC IND CO.

XX PI Nakamura T;

XX DR WPI; 1997-226217/20.

XX DR N-PSDB; AAT73937.

XX PT Human cyclin I protein and related (anti-sense) DNA - used for neuron labelling method and cancer cell detection.

XX PS Claim 1; Fig 1; 45pp; Japanese.

XX CC This sequence is human cyclin I. Antisense polynucleotides are useful for as probes and can be labelled and used for detection of neurones by hybridisation with mRNA for cyclin I (contained in the neurones and arising by the expression of the cyclin I gene in these cells). The gene can be used for detection of cancer cells by detecting the expression of the cyclin I gene in these cells. Also antibodies specific for the fragments of the protein (especially AAW21966) can be used for detection

XX SQ Sequence 377 AA;

Query Match

Best Local Similarity 100.0%; Score 1962; DB 2; Length 377;

Matches 377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKFPGPLENQLRSLFLEKAITREAOQMKVNRKMPNSQNVSPSQRDEVIOWIAKLKYQFN 60
 DB 1 MKFPGPLENQLRSLFLEKAITREAOQMKVNRKMPNSQNVSPSQRDEVIOWIAKLKYQFN 60
 QY 61 LYPETFALASSLLDRFLATVKAHPKYLSCIAISCFFLAAKTVEEDERIPVLKVLARDSPFC 120
 DB 61 LYPETFALASSLLDRFLATVKAHPKYLSCIAISCFFLAAKTVEEDERIPVLKVLARDSPFC 120
 QY 121 GCSSEILRMERIILDKLNDLHTATPLDFLHIFHAIAVSTRPQLLSPKLSQHLAV 180
 DB 121 GCSSEILRMERIILDKLNDLHTATPLDFLHIFHAIAVSTRPQLLSPKLSQHLAV 180
 QY 181 LTKQLLHCACNQLLQFRGSMALAMVSLMEKLIIPDWLSLTIELLOKQMDSSQLIHCR 240
 DB 181 LTKQLLHCACNQLLQFRGSMALAMVSLMEKLIIPDWLSLTIELLOKQMDSSQLIHCR 240
 QY 241 ELVAHHLSTLQSSLPVNSVYVVRPLKHTLVTCDKGVFRLHPSSVPGDFSKDMSKPEVPV 300
 DB 241 ELVAHHLSTLQSSLPVNSVYVVRPLKHTLVTCDKGVFRLHPSSVPGDFSKDMSKPEVPV 300
 QY 301 RGTAAFYHHLPAASGCKQTSTKRKVEEMVEDDFDGIKRLYNEDNVSNVSGVCGTDLR 360
 DB 301 RGTAAFYHHLPAASGCKQTSTKRKVEEMVEDDFDGIKRLYNEDNVSNVSGVCGTDLR 360
 QY 361 QEGHASPCCPPLQPVSV 377
 DB 361 QEGHASPCCPPLQPVSV 377

RESULT 2

AA152185
 ID AAY52185 standard; protein; 377 AA.
 XX AC AAY52185;

09-FEB-2000 (first entry)

Human cyclin I amino acid sequence.

Cyclin-dependent kinase 2; CDK2; hsReq; hsReq*-1; hsReq*-2; cyclin I; ERH; cell cycle; proliferation; cancer; hyperproliferative disorder; atherosclerosis; tumour.

Homo sapiens.

WO925829-A2.

27-MAY-1999.

12-NOV-1998; 98WO-US024095.

13-NOV-1997; 97US-00969106.

(CURA)-CURAGEN CORP.

Yang M, Nandabalan K, Schulz VP;

WPI; 2000-061923/05.

N-PSDB; AAZ37836.

New complexes of the cyclin-dependent kinase 2 protein with its interacting proteins, used to treat, e.g. atherosclerosis.

Example; Fig 2; 90pp; English.

This is the human Cyclin I amino acid sequence. Cyclin I is expressed at almost constant levels throughout the cell cycle, and is implicated in controlling cell cycle progression and transcriptional control. Cyclins form complexes with cyclin-dependent kinases. CDK2, cyclin-dependent kinase 2, is used in the invention which relates to complexes of the CDK2 protein with other proteins, selected from cyclin I, ERH, hsReq, hsReq*-1 and hsReq*-2 (AAY52185-Y52188). CDK2 is expressed late in G1 or early in S phase of the cell cycle, and is pivotal for G1/S transition.

CC Compositions containing a CDK2 complex, an antibody targeting the complex, and nucleotide sequences encoding CDK2 or its derivatives can be used therapeutically. The complexes and their nucleotide sequences can be used to treat diseases or disorders associated with increased or decreased levels of the complex. Screening the complex, or a derivative or a modulator of the complex for neoplastic activity by measuring the survival or proliferation of cells from a malignant cell line when in contact with the complex can be used to indicate if the the complex has anti-neoplastic activity. Screening for molecules that modulate the formation of the complexes can be used for treating or preventing atherosclerosis or atherosclerosis-associated disease by contacting cells or using a test animal, in which tumour growth or regression is measured to test whether anti-neoplastic activity is displayed. Diseases which can be treated or prevented by molecule/s which modulate the function of the complex include cancer, hyperproliferative disorders and atherosclerosis

XX Sequence 377 AA;

Query Match 100.0%; Score 1962; DB 3; Length 377;

Best Local Similarity 100.0%; Pred. No. 6.7e-197;

Matches 377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKFPGPLENQLRSLFLEKAITREAOQMKVNRKMPNSQNVSPSQRDEVIOWIAKLKYQFN 60

DB 1 MKFPGPLENQLRSLFLEKAITREAOQMKVNRKMPNSQNVSPSQRDEVIOWIAKLKYQFN 60

QY 61 LYPETFALASSLLDRFLATVKAHPKYLSCIAISCFFLAAKTVEEDERIPVLKVLARDSPFC 120

DB 61 LYPETFALASSLLDRFLATVKAHPKYLSCIAISCFFLAAKTVEEDERIPVLKVLARDSPFC 120

QY 121 GCSSEILRMERIILDKLNDLHTATPLDFLHIFHAIAVSTRPQLLSPKLSQHLAV 180

DB 121 GCSSEILRMERIILDKLNDLHTATPLDFLHIFHAIAVSTRPQLLSPKLSQHLAV 180

QY 181 LTKQLLHCACNQLLQFRGSMALAMVSLMEKLIIPDWLSLTIELLOKQMDSSQLIHCR 240

DB 181 LTKQLLHCACNQLLQFRGSMALAMVSLMEKLIIPDWLSLTIELLOKQMDSSQLIHCR 240

QY 241 ELVAHHLSTLQSSLPVNSVYVVRPLKHTLVTCDKGVFRLHPSSVPGDFSKDMSKPEVPV 300

DB 241 ELVAHHLSTLQSSLPVNSVYVVRPLKHTLVTCDKGVFRLHPSSVPGDFSKDMSKPEVPV 300

QY 301 RGTAAFYHHLPAASGCKQTSTKRKVEEMVEDDFDGIKRLYNEDNVSNVSGVCGTDLR 360

DB 301 RGTAAFYHHLPAASGCKQTSTKRKVEEMVEDDFDGIKRLYNEDNVSNVSGVCGTDLR 360

QY 361 QEGHASPCCPPLQPVSV 377

DB 361 QEGHASPCCPPLQPVSV 377

RESULT 3

ABR39934

ID ABR39934 standard; protein; 377 AA.

XX ABR39934;

11-AUG-2003 (first entry)

Human prostate selective polypeptide Pr325.

Prostate; molecular marker; cancer; cytostatic; gene therapy; human.

Homo sapiens.

WO2003014298-A2.

20-FEB-2003.

02-AUG-2002; 2002WO-US024431.

03-AUG-2001; 2001US-0309470P.

30-OCT-2001; 2001US-0330747P.

XX PA (ORIG-) ORIGENE TECHNOLOGIES INC.
 XX PI Sun Z, Li X, Jay G, Kovacs KF, Shu Y, Fan W;
 XX PR WPI; 2003-256562/25.
 XX DR N-PSDB; ACC47339.
 XX XX
 XX PT New polynucleotide, useful for preparing a composition for treating
 XX PT prostate disease, e.g., cancer.
 XX PS Claim 5; Page 147-149; 212pp; English.
 XX XX
 XX CC The invention relates to prostate selective polynucleotides and
 XX CC polypeptides. The polynucleotides are expressed in prostate and are
 XX CC useful as molecular markers, as drug targets, and for detecting,
 XX CC monitoring, preventing or treating diseases and conditions related to
 XX CC prostate, such as prostate cancers. The present sequence represents a
 XX CC prostate specific polypeptide
 XX SQ Sequence 377 AA;
 Query Match 100.0%; Score 1962; DB 6; Length 377;
 Best Local Similarity 100.0%; Pred. No. 6.7e-197;
 Matches 377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKFPGPLENQRSLFLEKAITREAOQMKVNRKMPNSQNVSPQRDEVIQMLAKLYQFN 60
 Db 1 MKFPGPLENQRSLFLEKAITREAOQMKVNRKMPNSQNVSPQRDEVIQMLAKLYQFN 60
 QY 61 LYPETPALASSLLDRFLATVKAHPKYLSCIAISCFFLAAKTVEEDERIPVLKVLARDSFC 120
 Db 61 LYPETPALASSLLDRFLATVKAHPKYLSCIAISCFFLAAKTVEEDERIPVLKVLARDSFC 120
 QY 121 GCSSEILRMERIIIDKLNWDLHTATPLDFLHIFHAIATVSTRPOLLFSLPKLSPSOHLAV 180
 Db 121 GCSSEILRMERIIIDKLNWDLHTATPLDFLHIFHAIATVSTRPOLLFSLPKLSPSOHLAV 180
 QY 181 LTKQLLHMACNQLQFRGSMALAMVSLMEKLI PDWLSLTIELLOKAQMDSSQLIHC 240
 Db 181 LTKQLLHMACNQLQFRGSMALAMVSLMEKLI PDWLSLTIELLOKAQMDSSQLIHC 240
 QY 241 ELVAHHLSTLQSSLPNSVYVYRPLKHTLVTCDKGVFRLHPSSVPGPDFSKDMSKPEVPV 300
 Db 241 ELVAHHLSTLQSSLPNSVYVYRPLKHTLVTCDKGVFRLHPSSVPGPDFSKDMSKPEVPV 300
 QY 301 RGTAAFYHHLPAASGCKQTSTKRVKEEVEDDFYDGIKRLYNEDNVSENVSGVCGTDLRS 360
 Db 301 RGTAAFYHHLPAASGCKQTSTKRVKEEVEDDFYDGIKRLYNEDNVSENVSGVCGTDLRS 360
 QY 361 QEGHASPCCPPLQPVSV 377
 Db 361 QEGHASPCCPPLQPVSV 377
 RESULT 4
 ADP12615
 ID ADP12615 standard; protein; 377 AA.
 XX AC ADP12615;
 XX XX
 XX DT 12-AUG-2004 (first entry)
 XX DE
 XX KW Protein encoded by mRNA of the invention #225.
 XX KW transplant rejection; immune system; rheumatoid arthritis; lupus;
 XX KW inflammatory bowel disease; multiple sclerosis; HIV; AIDS.
 XX OS Homo sapiens.
 XX XX
 XX PN WO2004042346-A2.
 XX XX
 XX PD 21-MAY-2004.

XX PF 24-APR-2003; 2003WO-US012946.
 XX PR 24-APR-2002; 2002US-00131831.
 XX PR 20-DEC-2002; 2002US-00325899.
 XX PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
 XX XX
 XX PI Wohlgenuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;
 XX PI Rosenberg S;
 XX WPI; 2004-400724/37.
 XX XX
 XX PT Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,
 XX PT pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
 XX PT rejection, in an individual, comprises detecting the expression level of
 XX PT the genes.
 XX PS Claim 65; SEQ ID NO 2624; 1762pp; English.
 XX XX
 XX CC The present invention relates to diagnosing or monitoring transplant
 XX CC rejection, e.g. cardiac or kidney transplant rejection, in an individual
 XX CC comprises detecting the expression level of one or more genes. The
 XX CC methods, system and kits are useful in diagnosing or monitoring
 XX CC transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
 XX CC islet, lung, bone marrow or stem cell transplant rejection,
 XX CC xenotransplant rejection or mechanical organ replacement rejection, in an
 XX CC individual. The method is also useful in assessing the immune status of
 XX CC an individual. The methods are also useful in diagnosing and monitoring
 XX CC diseases that involve the immune system, e.g. rheumatoid arthritis,
 XX CC lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
 XX CC viral, bacterial or fungal infection. The present sequence represents a
 XX CC protein that is encoded by the mRNA of the invention.
 XX SQ Sequence 377 AA;
 Query Match 100.0%; Score 1962; DB 8; Length 377;
 Best Local Similarity 100.0%; Pred. No. 6.7e-197;
 Matches 377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKFPGPLENQRSLFLEKAITREAOQMKVNRKMPNSQNVSPQRDEVIQMLAKLYQFN 60
 Db 1 MKFPGPLENQRSLFLEKAITREAOQMKVNRKMPNSQNVSPQRDEVIQMLAKLYQFN 60
 QY 61 LYPETPALASSLLDRFLATVKAHPKYLSCIAISCFFLAAKTVEEDERIPVLKVLARDSFC 120
 Db 61 LYPETPALASSLLDRFLATVKAHPKYLSCIAISCFFLAAKTVEEDERIPVLKVLARDSFC 120
 QY 121 GCSSEILRMERIIIDKLNWDLHTATPLDFLHIFHAIATVSTRPOLLFSLPKLSPSOHLAV 180
 Db 121 GCSSEILRMERIIIDKLNWDLHTATPLDFLHIFHAIATVSTRPOLLFSLPKLSPSOHLAV 180
 QY 181 LTKQLLHMACNQLQFRGSMALAMVSLMEKLI PDWLSLTIELLOKAQMDSSQLIHC 240
 Db 181 LTKQLLHMACNQLQFRGSMALAMVSLMEKLI PDWLSLTIELLOKAQMDSSQLIHC 240
 QY 241 ELVAHHLSTLQSSLPNSVYVYRPLKHTLVTCDKGVFRLHPSSVPGPDFSKDMSKPEVPV 300
 Db 241 ELVAHHLSTLQSSLPNSVYVYRPLKHTLVTCDKGVFRLHPSSVPGPDFSKDMSKPEVPV 300
 QY 301 RGTAAFYHHLPAASGCKQTSTKRVKEEVEDDFYDGIKRLYNEDNVSENVSGVCGTDLRS 360
 Db 301 RGTAAFYHHLPAASGCKQTSTKRVKEEVEDDFYDGIKRLYNEDNVSENVSGVCGTDLRS 360
 QY 361 QEGHASPCCPPLQPVSV 377
 Db 361 QEGHASPCCPPLQPVSV 377
 RESULT 5
 ABM80569
 ID ABM80569 standard; protein; 377 AA.
 XX XX

AC ABM80569;
 XX 18-NOV-2004 (first entry)
 XX Tumour-associated antigenic target (TAT) polypeptide PRO4605, SEQ:1450.
 DE
 XX Tumour-associated antigenic target; TAT; human; overexpression; cancer;
 KW tumour; diagnosis; cell proliferative disorder; breast cancer;
 KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;
 KW central nervous system cancer; bladder cancer; pancreatic cancer;
 KW cervical cancer; melanoma; leukaemia; hybridisation probe;
 KW chromosome identification; chromosome mapping; gene mapping;
 KW gene therapy; cytostatic.
 XX
 XX Homo sapiens.
 XX WO2004030615-A2.
 XX 15-APR-2004.
 XX 29-SEP-2003; 2003WO-US028547.
 XX 02-OCT-2002; 2002US-0414971P.
 XX (GETH) GENENTECH INC.
 XX Wu TD, Zhang Z, Zhou Y;
 XX WPI: 2004-347921/32.
 XX N-PSDB; ACN38124.
 XX
 XX New tumor-associated antigenic target polypeptides and nucleic acids,
 PT useful in preparing a medicament for treating or detecting a
 PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or
 PT prostate cancer or tumor.
 XX
 XX Claim 12; SEQ ID NO 1450; 7273pp; English.
 XX
 XX The invention relates to human tumour-associated antigenic target (TAT)
 CC polypeptides, and their related nucleic acids. The TAT polypeptides are
 CC overexpressed in cancer tissues compared to normal tissues, and may thus
 CC serve as effective targets for the diagnosis and treatment of cancer in
 CC mammals. The invention also relates to nucleic acid and polypeptide
 CC sequences at least 80% identical to the TAT nucleic acids and
 CC polypeptides; expression vectors and host cells comprising a TAT nucleic
 CC acid; an antibody specific for a TAT polypeptide; a peptide or organic
 CC molecule which binds to a TAT polypeptide; fusion proteins comprising a
 CC TAT polypeptide; and methods and compositions for the treatment or
 CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
 CC antibodies, antagonists, binding molecules and compositions are useful
 CC for diagnosing or treating a cell proliferative disorder associated with
 CC increased TAT expression, particularly cancers such as breast cancer,
 CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
 CC cancer, pancreatic cancer, cervical cancer, cancers of the central
 CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be
 CC used as hybridisation probes, in chromosome and gene mapping, in
 CC chromosome identification and in gene therapy. The present sequence
 CC represents a TAT polypeptide of the invention
 XX
 XX Sequence 377 AA;
 SQ
 Query Match 99.9%; Score 1960; DB 8; Length 377;
 Best Local Similarity 99.7%; Pred. NO. 1.1e-196;
 Matches 376; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKPFGPLENQLSFLLEKAITREAOQKYNVRKMPSONVSPQRDEVIOWLAKUKYQFN 60
 DB 1 MKPFGPLENQLSFLLEKAITREAOQKYNVRKMPSONVSPQRDEVIOWLAKUKYQFN 60
 QY 61 LYPETPALASSLLDRFLATVKAHPKYLSCIAISCFFLAAKTVVEEDRIPVLKVLARDSPC 120
 DB 61 LYPETPALASSLLDRFLATVKAHPKYLSCIAISCFFLAAKTVVEEDRIPVLKVLARDSPC 120

121 GCSSEILRMERIIIDKLNWDLHTATPDLDFLHIFHAIAVSTRPQLLFLPKLSQHLAV 180
 121 GCSSEILRMERIIIDKLNWDLHTATPDLDFLHIFHAIAVSTRPQLLFLPKLSQHLAV 180
 181 LTKQLLHCMAQNQLQFRGSMIALAMVSLMEKLIIPDWLSLTIELLOKAQWSSQLIHC 240
 181 LTKQLLHCMAQNQLQFRGSMIALAMVSLMEKLIIPDWLSLTIELLOKAQWSSQLIHC 240
 241 ELVAHHLSTLQSSLPFLNSVYVYRPLKHTLVTCDKGVFRLHPSSVPGDFSKDMSKPEVPV 300
 241 ELVAHHLSTLQSSLPFLNSVYVYRPLKHTLVTCDKGVFRLHPSSVPGDFSKDMSKPEVPV 300
 301 RGTAFAFVHHLPAASGCKQTSTKRVKVEVDDFDGIKRLYNEDNVSENVSGVCGTDL 360
 301 RGTAFAFVHHLPAASGCKQTSTKRVKVEVDDFDGIKRLYNEDNVSENVSGVCGTDL 360
 361 QEGHASPCCPPLQPVSV 377
 361 QEGHASPCCPPLQPVSV 377

RESULT 6
 AAE37938
 ID AAE37938 standard; protein; 334 AA.
 XX
 AC AAE37938;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DE Human CGDD-27 protein.
 XX
 KW Human; cell growth, differentiation and death protein; CGDD; leukaemia;
 KW neurodegenerative disorder; Parkinson's disease; Alzheimer's disease;
 KW muscular disorder; myotonic dystrophy; catatonias; endocrine disorder;
 KW diabetes; Grave's disease; cancer; immunological disorder; scleroderma;
 KW systemic lupus erythematosus; allergy; Crohn's disease; renal disorder;
 KW gastrointestinal disorder; Goodpasture's syndrome; infection; cirrhosis;
 KW cardiovascular disorder; atherosclerosis; hepatic disease; transgenic;
 KW transgenic animal; gene therapy; neuroprotective; relaxant; cytostatic;
 KW dermatological; immunosuppressive; cerebroprotective; anticonvulsant;
 KW antibacterial; antiparasitic; fungicide; virucide; uropathic; cardiant;
 KW protozoacide; nootropic.
 XX
 OS Homo sapiens.
 XX
 PN WO2003050253-A2.
 XX
 PD 19-JUN-2003.
 XX
 PF 04-DEC-2002; 2002WO-US039133.
 XX
 PR 07-DEC-2001; 2001US-0340747P.
 PR 20-DEC-2001; 2001US-0342761P.
 PR 15-JAN-2002; 2002US-0349705P.
 PR 06-FEB-2002; 2002US-0354764P.
 PR 12-FEB-2002; 2002US-0356216P.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 XX
 XX Griffin JA, Ramkumar J, Emerling BM, Kable AE, Elliott VS;
 PI Marquis JP, Baughn MR, Gorvad AE, Yue H, Lee EA, Becha SD, Tang YT;
 PI Tran UK, Swarnakar A, Lee S, Ison CH, Hafalia AJA, Tran B;
 PI Sprague WW, Lee SY, Khare R, Gandhi AR, Gietzen KU, Bhatia U;
 PI Burrill JD, Blake JU, Ho A, Zheng W;
 XX
 DR WPI: 2003-532903/50.
 DR N-PSDB; AAD57247.
 XX
 PT New CGDD polypeptides, useful for diagnosing, preventing, and treating
 PT disorders associated with an abnormal expression or activity of CGDD,
 PT e.g. neuromuscular, immunological, cardiovascular disorders, cancer
 PT and/or infections.

PS Claim 1; Page 250; 299pp; English.

XX The present invention relates to novel cell growth, differentiation and
 XX death (CGDD) proteins and polynucleotides encoding them. The sequences of
 CC the invention are useful in diagnosing, preventing and treating disorders
 CC associated with an abnormal expression or activity of CGDD such as
 CC neurodegenerative disorders (e.g. Parkinson's disease, Alzheimer's
 CC disease), muscular disorders (e.g. myotonic dystrophy, catatonial),
 CC endocrine disorders (e.g. diabetes, Grave's disease), cancers (e.g.
 CC leukaemia, cervical or breast cancers), immunological disorders (e.g.
 CC scleroderma, systemic lupus erythematosus, allergies), gastrointestinal
 CC disorders (e.g. Crohn's disease), renal disorders (e.g. Goodpasture's
 CC syndrome), infections (e.g. viral, bacterial, fungal, parasitic,
 CC protozoal, helminthic), cardiovascular disorders (e.g. atherosclerosis)
 CC and hepatic diseases (e.g. cirrhosis). The polynucleotides can be used to
 CC create humanised animals or transgenic animals to model human diseases.
 CC The invention is also used in gene therapy. The present sequence is human
 CC CGDD-27 protein

XX Sequence 334 AA;

Query Match 87.3%; Score 1713.5; DB 7; Length 334;
 Best Local Similarity 88.6%; Pred. No. 7.3e-171;
 Matches 334; Conservative 0; Mismatches 0; Indels 43; Gaps 1;

QY 1 MKPPGPLENORLSFLEKAITREAOQWKVNVKRMPSNQNVSPSQRDEVIOQLAKLYQFN 60
 DB 1 MKPPGPLENORLSFLEKAITREAOQWKVNVKRMPSNQNVSPSQRDEVIOQLAKLYQFN 38

QY 61 LYPETALASSLLDRFLATVKAHPKYLSCIAISCFPLAAKTVEEDRIPVLKVLARDSPC 120
 DB 39 -----AHPKYLSCIAISCFPLAAKTVEEDRIPVLKVLARDSPC 77

QY 121 GCSSEILRMERIIIDKLNWDLHTATPLDFLHIFHAIAVSTRPQLFLSLPKLSPSOHLAV 180
 DB 78 GCSSEILRMERIIIDKLNWDLHTATPLDFLHIFHAIAVSTRPQLFLSLPKLSPSOHLAV 137

QY 181 LTKQLLHCWACNQLQFRGSMALANVSLMEKLPDWLSLTIELLOKQAMDSSQLIHCN 240
 DB 138 LTKQLLHCWACNQLQFRGSMALANVSLMEKLPDWLSLTIELLOKQAMDSSQLIHCN 197

QY 241 ELVAHHLSTLQSSLPNSVYVTRPLKHTLVTCDKGVFRLHPSPVPGDFSKNSKPEVPV 300
 DB 198 ELVAHHLSTLQSSLPNSVYVTRPLKHTLVTCDKGVFRLHPSPVPGDFSKNSKPEVPV 257

QY 301 RGTAAFYHHLPAASGCKQSTTKRKVEEMEVDDFYDGIKELYNEDNVSENVGSCGTDLSR 360
 DB 258 RGTAAFYHHLPAASGCKQSTTKRKVEEMEVDDFYDGIKELYNEDNVSENVGSCGTDLSR 317

QY 361 QEGHASPCCPPLQPVSM 377
 DB 318 QEGHASPCCPPLQPVSM 334

RESULT 7
 ADN01131
 ID ADN01131 standard; protein; 300 AA.
 XX
 AC ADN01131;
 XX
 DT 01-JUL-2004 (first entry)
 XX
 DE Human cell growth, differentiation, and death-associated protein #15.
 XX
 KW human; cell growth; cell differentiation; cell death; CGDD;
 KW cell proliferative disorder; arteriosclerosis; atherosclerosis; bursitis;
 KW cirrhosis; hepatitis; polycythaemia vera; psoriasis; cancer;
 KW developmental disorder; Cushing's syndrome; hypothyroidism;
 KW neurological disorder; epilepsy; stroke; Alzheimer's disease;
 KW Pick's disease; Huntington's disease; Parkinson's disease;
 KW multiple sclerosis; autoimmune disorder; inflammatory disorder; AIDS;
 KW allergy; anaemia; asthma; contact dermatitis; diabetes mellitus;
 KW reproductive disorder; infertility; endometriosis; uterine fibroid.

XX Homo sapiens.

XX WO2004031364-A2.

XX 15-APR-2004.

XX 03-OCT-2003; 2003WO-US031441.

XX 03-OCT-2002; 2002US-0416205P.

XX 25-OCT-2002; 2002US-0421521P.

XX 21-NOV-2002; 2002US-0428376P.

XX 23-DEC-2002; 2002US-0436258P.

XX 10-JAN-2003; 2003US-0439292P.

XX 13-FEB-2003; 2003US-0447578P.

XX (INCY-) INCYTE CORP.

XX (BURR/) BURRILL J D.

XX Elliott VS, Swarnakar A, Tang YT, Yue H, Lu DM, Khare R;
 PI Chawla NK, Richardson TW, Marquis JP, Lal PG, Nguyen DB, Lee SY;
 PI Tran UK, Bhatia UG, Lee S, Blake JJ, Ho A, Zheng W, Gao J, Tran B;
 PI Yang YG, Gietzen KJ, Hafalia AJA;

DR WPI: 2004-330172/30.
 DR N-PSDB; ADN01156.

XX New isolated polypeptides associated with cell growth, differentiation
 PT and death, useful for diagnosing, treating or preventing e.g.
 PT atherosclerosis, psoriasis, cancers, Alzheimer's disease, AIDS, anemia,
 PT diabetes mellitus or infertility.

XX Claim 1; SEQ ID NO 15; 213pp; English.

XX The invention comprises the amino acid and coding sequences of human
 CC proteins that are associated with cell growth, differentiation, and death
 CC (CGDD). The DNA and protein sequences of the invention are useful for
 CC diagnosing, treating or preventing disorders associated with aberrant
 CC expression of CGDD, such as: cell proliferative disorders (e.g.
 CC arteriosclerosis, atherosclerosis, bursitis, cirrhosis, hepatitis,
 CC polycythaemia vera, psoriasis and cancers), developmental disorders (e.g.
 CC Cushing's syndrome and hypothyroidism), neurological disorders (e.g.
 CC epilepsy, stroke, Alzheimer's disease, Pick's disease, Huntington's
 CC disease, Parkinson's disease and multiple sclerosis),
 CC autoimmune/inflammatory disorders (e.g. AIDS, allergies, anaemia, asthma,
 CC contact dermatitis and diabetes mellitus), and reproductive disorders
 CC (e.g. infertility, endometriosis and uterine fibroid). The present amino
 CC acid sequence represents a human CGDD-associated protein of the
 CC invention.

XX Sequence 300 AA;

Query Match 78.0%; Score 1529.5; DB 8; Length 300;
 Best Local Similarity 79.6%; Pred. No. 1.4e-151;
 Matches 300; Conservative 0; Mismatches 0; Indels 77; Gaps 1;

QY 1 MKPPGPLENORLSFLEKAITREAOQWKVNVKRMPSNQNVSPSQRDEVIOQLAKLYQFN 60
 DB 1 MKPPGPLENORLSFLEKAITREAOQWKVNVKRMPSNQNVSPSQRDEVIOQLAKLYQFN 60

QY 61 LYPETALASSLLDRFLATVKAHPKYLSCIAISCFPLAAKTVEEDRIPVLKVLARDSPC 120
 DB 61 LYPETALASSLLDRFLATVKAHPKYLSCIAISCFPLAAKTVEEDRIPVLKVLARDSPC 120

QY 121 GCSSEILRMERIIIDKLNWDLHTATPLDFLHIFHAIAVSTRPQLFLSLPKLSPSOHLAV 180
 DB 121 GCSSEILRMERIIIDKLNWDLHTATPLDFLHIFHAIAVSTRPQLFLSLPKLSPSOHLAV 153

QY 181 LTKQLLHCWACNQLQFRGSMALANVSLMEKLPDWLSLTIELLOKQAMDSSQLIHCN 240
 DB 154 -----MDSQLIHCN 163

QY 241 ELVAHHLSTLQSSLPNSVYVTRPLKHTLVTCDKGVFRLHPSPVPGDFSKNSKPEVPV 300

Db 164 ELVAHSLTQSSLPNSVYVRPLKHTLVTCGKGVRLHPSVPGPDFSKNSRPEV 223
QY 301 RGTAAFYHLPAASGCKQTSTKRKVEEMVDDFYDGIKELYNEDNVSENVSGVCGTDLR 360
Db 224 RGTAAFYHLPAASGCKQTSTKRKVEEMVDDFYDGIKELYNEDNVSENVSGVCGTDLR 283
QY 361 QEGHASPCCPPLQPVSV 377
Db 284 QEGHASPCCPPLQPVSV 300

RESULT 8
AAG01903
ID AAG01903 standard; protein; 131 AA.
XX
AC AAG01903;
XX
DT 06-OCT-2000 (first entry)
XX
DE Human secreted protein, SEQ ID NO: 5984.
XX
KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping.
XX
OS Homo sapiens.
XX
PN EP1033401-A2.
XX
PD 06-SEP-2000.
XX
PF 21-FEB-2000; 2000EP-00200610.
XX
PR 26-FEB-1999; 99US-0122487P.
XX
PA (GEST) GENSET.
XX
PI Dumas Milne Edwards J, Duclert A, Giordano J;
XX
DR WPI; 2000-500381/45.
DR N-PSDB; AAC01909.
XX
PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX
PS Claim 13; SEQ ID NO 5984; 71pp + Sequence Listing; English.

XX
CC The present sequence is a polypeptide encoded by one of a large number of
CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were
CC prepared from total human RNAs or polyA+ RNAs derived from 30 different
CC tissues. EST sequences usually correspond mainly to the 3' untranslated
CC region (UTR) of the mRNA because they are often obtained from oligo-dT
CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA
CC sequences derived from the 5' ends of mRNAs and even in those cases where
CC longer cDNA sequences have been obtained, the full 5' UTR is rarely
CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can
CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs
CC are also used in diagnostic, forensic, gene therapy and chromosome
CC mapping procedures. They are used to obtain upstream regulatory sequences
CC and to design expression and secretion vectors

XX
SQ Sequence 131 AA;
Query Match 34.0%; Score 667; DB 3; Length 131;
Best Local Similarity 100.0%; Pred. No. 1.8e-61; Mismatches 0; Indels 0; Gaps 0;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 130 MERIILDKLNDLHTATPLDFLHFAIAVSTRPQLLSPLKLSPSQHLAVLTQLLHGM 189
Db 1 MERIILDKLNDLHTATPLDFLHFAIAVSTRPQLLSPLKLSPSQHLAVLTQLLHGM 60
QY 190 ACNQLQFRGSMALAMVSLMEKLIPLDWLSLTIELLOKAQMDSSQLIHCRELVAHLS 249

Db 61 ACNQLQFRGSMALAMVSLMEKLIPLDWLSLTIELLOKAQMDSSQLIHCRELVAHLS 120
QY 250 LQSSLPNSVY 260
Db 121 LQSSLPNSVY 131
RESULT 9
ABG18403
ID ABG18403 standard; protein; 369 AA.
XX
AC ABG18403;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #18394.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR N-PSDB; AAS82590.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 20; SEQ ID NO 48762; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 369 AA;

Query Match 25.6%; Score 502.5; DB 4; Length 369;
Best Local Similarity 44.6%; Pred. No. 1.7e-43;
Matches 111; Conservative 44; Mismatches 89; Indels 5; Gaps 1;

PT Identifying a gene involved in disease for treating hypoxia-regulated
 PT conditions, comprises comparing the transcriptome/proteome of two cell
 PT types under different conditions and identifying a differentially
 PT regulated gene.

XX Claim 35; Page 374; 538pp; English.

XX The present invention relates to methods for identifying genes and
 CC proteins that are implicated in a specific disease or physiological
 CC condition. The method comprises comparing the transcriptome/proteome of a
 CC specialised cell type implicated in a disease or condition with that of a
 CC second specialised cell type, under two experimental conditions, and
 CC identifying a gene that is differentially regulated in the two
 CC specialised cell types under experimental conditions. ABV7873-ABV78116
 CC and ABP65061-ABP65257 were identified using the methods of the invention.
 CC The coding sequences and proteins are useful for treating a disease in a
 CC patient, for manufacture of a medicament for treating hypoxia-regulated
 CC conditions, and for regulating tumorigenesis, angiogenesis, apoptosis,
 CC biological response to hypoxia conditions, or hypoxic-associated
 CC pathology in a patient. The coding sequences and proteins are also useful
 CC for monitoring the therapeutic treatment of a disease or physiological
 CC condition, such as cancer, ischaemic conditions, reperfusion injury,
 CC retinopathy, neonatal stress, pre-eclampsia, atherosclerosis, inflammatory
 CC conditions, wound healing, inflammation, erythropoiesis or hair loss

XX Sequence 344 AA;

Query Match 16.6%; Score 326.5; DB 5; Length 344;

Best Local Similarity 36.4%; Pred. No. 4.7e-25;

Matches 86; Conservative 44; Mismatches 73; Indels 33; Gaps 7;

QY 31 VRKMPSON-VSPSORDEVIOWLAKLYQFNLYPETFALASSLLDRFLATVKAHPKYLSC 89
 DB 41 IEATPNDNTLCFGRNAKVEDLRSLANFFGSCSTETFLAVNLDRFLAMKVKPKHLSC 100
 QY 90 IAISCFFLAAKTVEEDERIPVLKVLARDSFCGSCSSSEILRMERIIDKLNWDLHTATPLD 149
 DB 101 IGVCSFLAARIVEEDCNIPSTHDVIRISQCKTASDIKRMKEIISEKLYHELEATTALN 160
 QY 150 FLHIFHAIIV--STRPQLLSLPKLSPOHLAVLTQKLLHMACNQLLOF---RGSMLA 203
 DB 161 FLHYHTIILCHTSEKIL-SLDKLE-----AQLKACNCRLIIFSKAKPSVLA 207

204 LAMVSEMEKLIPOWLSLTIELQ-----KAQDSSQLIHCRELVAHLSTLOS 252

208 LCLLNLEVTI-----KSVELLEILLVKKHKSINDTEFFYRWELVSKLAEYSS 257

RESULT 12

ADF66631

XX ADF66631 standard; protein; 344 AA.

XX ADF66631;

XX 12-FEB-2004 (first entry)

XX Human cyclin G2 protein.

XX apoptosis inducer; cyclin G2; cyclin box; cytostatic;

XX antineoplastic drug; cancer; human.

XX Homo sapiens.

XX JP2003238591-A.

XX 27-AUG-2003.

XX 21-FEB-2002; 2002JP-00044335.

XX 21-FEB-2002; 2002JP-00044335.

XX (OOSA-) ZH OOSAKA SANGYO SHINKO KIKO.

XX

DR WPI; 2004-065215/07.

XX Apoptosis inducer comprising polypeptide which consists of amino acid
 PT sequence which is one or all part of cyclin G2, sequence in which 1 or
 PT more amino acid has deletion, substitution or addition in the amino acid
 PT sequence.

XX Disclosure; SEQ ID NO 1; 15pp; Japanese.

XX The invention relates to a novel apoptosis inducer consisting of a
 CC polypeptide comprising an amino acid sequence which is part or all of
 CC cyclin G2 and contains at least a cyclin box and a polypeptide which
 CC consists of an amino acid sequence from which 1 or more amino acid is
 CC deleted, substituted or added in this amino acid sequence and has an
 CC apoptosis induction activity. The polypeptide of the invention
 CC demonstrates cytostatic activity and may be useful for screening
 CC antineoplastic drugs, as well as for treating cancer. The current
 CC sequence is that of the human cyclin G2 protein of the invention.

XX Sequence 344 AA;

Query Match 16.6%; Score 326.5; DB 8; Length 344;

Best Local Similarity 36.4%; Pred. No. 4.7e-25;

Matches 86; Conservative 44; Mismatches 73; Indels 33; Gaps 7;

QY 31 VRKMPSON-VSPSORDEVIOWLAKLYQFNLYPETFALASSLLDRFLATVKAHPKYLSC 89
 DB 41 IEATPNDNTLCFGRNAKVEDLRSLANFFGSCSTETFLAVNLDRFLAMKVKPKHLSC 100
 QY 90 IAISCFFLAAKTVEEDERIPVLKVLARDSFCGSCSSSEILRMERIIDKLNWDLHTATPLD 149
 DB 101 IGVCSFLAARIVEEDCNIPSTHDVIRISQCKTASDIKRMKEIISEKLYHELEATTALN 160
 QY 150 FLHIFHAIIV--STRPQLLSLPKLSPOHLAVLTQKLLHMACNQLLOF---RGSMLA 203
 DB 161 FLHYHTIILCHTSEKIL-SLDKLE-----AQLKACNCRLIIFSKAKPSVLA 207
 QY 204 LAMVSEMEKLIPOWLSLTIELQ-----KAQDSSQLIHCRELVAHLSTLOS 252
 DB 208 LCLLNLEVTI-----KSVELLEILLVKKHKSINDTEFFYRWELVSKLAEYSS 257

RESULT 13

ADO19808

ID ADO19808 standard; protein; 344 AA.

XX ADO19808;

XX 12-AUG-2004 (first entry)

XX Human PRO polypeptide #366.

XX Human; PRO; immune related disorder; systemic lupus erythematosus;
 KW rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis;
 KW systemic sclerosis; Sjogren's syndrome; vasculitis; sarcoidosis;
 KW autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroiditis;
 KW diabetes mellitus; renal disease; demyelinating disease;
 KW central nervous system; peripheral nervous system;
 KW demyelinating polyneuropathy; Guillain-Barre syndrome;
 KW chronic inflammatory demyelinating polyneuropathy.

XX Homo sapiens.

XX WO2004043361-A2.

XX 27-MAY-2004.

XX 06-NOV-2003; 2003WO-US035268.

XX 08-NOV-2002; 2002US-0425235P.

XX (GETH) GENENTECH INC.

XX

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 11, 2005, 07:36:40 ; Search time 947.803 Seconds
(without alignments)
2354.648 Million cell updates/sec

Title: US-09-736-250-1

Perfect score: 377

Sequence: 1 MKFPCPLENQLSLLEKAI.....LSROEGHASPCLPQPVSVM 377

Scoring table:

OLIGO	Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 4390206 seqs, 2959870667 residues

Word size: 1

Total number of hits satisfying chosen parameters: 8776198

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US09736250/runat_07022005_154941_20640/app_query.fasta_1.718
-DB=N_Geneseq_16Dec04 -QWMT=fastap -SUFFIX=oligo.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=1000 -DOCALLIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09736250@cgn 1 1 586 @runat_07022005_154941_20640 -NCPU=6 -ICPU=3
-NO_MMAP -LARGQUERY -NEG_SCORE=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : N_Geneseq_16Dec04:*

1:	geneseqn1980s:*
2:	geneseqn1990s:*
3:	geneseqn2000s:*
4:	geneseqn2001as:*
5:	geneseqn2001bs:*
6:	geneseqn2002as:*
7:	geneseqn2002bs:*
8:	geneseqn2003as:*
9:	geneseqn2003bs:*
10:	geneseqn2003cs:*
11:	geneseqn2003ds:*
12:	geneseqn2004as:*
13:	geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	377	100.0	1260	3	Aa237836 Human cDN
2	377	100.0	1260	6	ABK83672 Human cDN
3	377	100.0	1260	10	ADK61064 Ovarian c
4	377	100.0	1260	11	ADI31573 Human cDN
5	377	100.0	1260	13	ADR25465 Breast ca

6	377	100.0	1328	2	AAT73937	Aat73937 DNA encod
7	377	100.0	1384	8	ACC47339	Acc47339 Human pro
8	377	100.0	1889	6	ABL87929	AbL87929 Human ova
9	377	100.0	1890	12	ADP10653	Adp10653 Reference
10	377	100.0	1890	13	ACN38124	Acn38124 Tumour-as
11	296	78.5	1651	9	AAD57247	Aad57247 Human CGD
12	266	70.6	2755	5	ADL63374	AdL63374 Human ova
13	153	40.6	903	12	ADN01156	Adn01156 Human cel
14	144	38.2	444	3	AAC01909	Aac01909 Human sec
15	129	34.2	804	2	AAX40003	Aax40003 Prostate
16	123	32.6	2146	5	ADL63082	AdL63082 Human ova
17	90	23.9	392	2	AAQ61358	AaQ61358 Human bra
18	90	23.9	536	10	ADF82253	Adf82253 Leukaemia
19	88	23.3	1493	2	AZA41284	Aza41284 Human nor
20	84	22.3	409	10	ADF80870	Adf80870 Leukaemia
21	75	19.9	486	5	ADL43407	AdL43407 Human ova
22	66	17.5	329	2	AAT23729	Aat23729 Human gen
23	65	17.2	447	4	AAS25071	Aas25071 Human ova
24	65	17.2	447	5	AAH83716	AaH83716 Human ova
25	62	16.4	889	6	ABL87928	AbL87928 Human ova
26	51	13.5	597	10	ADK61065	Adk61065 Ovarian c
27	49	13.0	426	5	ADL37023	AdL37023 Human ova
28	49	13.0	426	5	ADI71872	Adi71872 Human ova
29	44	11.7	417	2	AAT26236	Aat26236 Human gen
30	41	10.9	389	10	ADK61066	Adk61066 Ovarian c
31	40	10.6	477	5	ADI72632	Adi72632 Human ova
32	40	10.6	477	5	ADL37771	AdL37771 Human ova
33	40	10.6	516	5	ADL44155	AdL44155 Human ova
34	38	10.1	136	2	AAQ76921	AaQ76921 Human gen
35	37	9.8	444	6	ABK45862	AbK45862 cDNA enco
36	34	9.0	304	3	AAC25819	Aac25819 Human sec
37	34	9.0	388	4	AAI91566	Aai91566 Human pol
38	30	8.6	247	6	ABV89029	Abv89029 Human col
39	25	6.6	351	8	ABV81549	Abv81549 Human BCA
40	25	6.6	469	9	ACH26661	Ach26661 Human adu
41	24	6.4	420	4	ABX44645	Abx44645 Bovine ES
42	22	5.8	183	2	AAQ76715	AaQ76715 Human gen
43	21	5.6	298	8	ABZ19815	Abz19815 Group III
44	21	5.0	60	6	ABN40110	Abn40110 Human spl
45	18	4.8	348	6	ABSG9603	Absg9603 Novel mur
46	14	3.7	65	6	ABN55748	Abn55748 Mouse spl
47	13	3.4	135	2	AAQ76716	AaQ76716 Human gen
48	10	2.7	50	6	ABZ00749	Abz00749 Human leu
49	9	2.4	28	12	ADP11644	Adp11644 Tagman pr
50	9	2.4	1643	2	AAK08522	Aak08522 NBP46 (ro
51	9	2.4	1643	6	ABK11098	Abk11098 DNA encod
52	9	2.4	6265	2	AAK08523	Aak08523 NBP46 (ro
53	9	2.4	24389	4	ABL29006	AbL29006 Drosophil
54	9	2.4	16382	13	ABD32659	Abd32659 Human can
55	8	2.1	267	7	ADS65315	Ads65315 Corn seed
56	8	2.1	277	10	ABX81638	Abx81638 Corn ear-
57	8	2.1	279	3	AAC28555	Aac28555 Human sec
58	8	2.1	400	2	AAV75840	Aav75840 Staphyloc
59	8	2.1	435	10	ADF80883	Adf80883 Leukaemia
60	8	2.1	483	8	ABZ53075	Abz53075 Aspergill
61	8	2.1	494	13	ACN56052	Acn56052 Cotton an
62	8	2.1	551	6	ABQ55991	Abq55991 Human ova
63	8	2.1	554	6	ABT10393	Abt10393 Human bre
64	8	2.1	573	13	ADQ55289	Adq55289 Novel can
65	8	2.1	578	13	ADQ79216	Adq79216 Novel can
66	8	2.1	738	13	ADR26517	Adr26517 Breast ca
67	8	2.1	744	3	AAA44975	Aaa44975 Human sec
68	8	2.1	791	6	ABQ37048	Abq37048 Oligonuc
69	8	2.1	791	6	ABQ37049	Abq37049 Oligonuc
70	8	2.1	796	6	ABQ34158	Abq34158 Oligonuc
71	8	2.1	796	6	ABQ34159	Abq34159 Oligonuc
72	8	2.1	809	10	ADH44941	Adh44941 Murine TC
73	8	2.1	852	4	AAH05379	Aah05379 Human cDN
74	8	2.1	871	13	ADRG3643	Adrg3643 Cotton cD
75	8	2.1	909	10	ADP41724	Adp41724 Bacillus
76	8	2.1	912	6	AAD28484	Aad28484 Bacillus
77	8	2.1	1053	10	ACC60670	Acc60670 Gene sequ
78	8	2.1	1053	10	ADK62087	Adk62087 Disease t

79	8	2.1	1089	6	ABK24365	152	8	2.1	3486	13	AD889002	Ad889002 Human CDK
80	8	2.1	1099	4	AAH00430	153	8	2.1	3568	2	AAH82180	Ad889002 Human p27
c 81	8	2.1	1099	13	AD896675	154	8	2.1	3568	2	AAH74231	Ad889002 Human p27
c 82	8	2.1	1110	8	ACA44674	155	8	2.1	3578	2	AAH05819	Ad889002 Human p27
c 83	8	2.1	1119	8	ABZ71977	156	8	2.1	3706	4	AAH12100	Ad889002 Human p27
c 84	8	2.1	1119	10	ADD14654	157	8	2.1	3819	4	AAH18644	Ad889002 Human p27
c 85	8	2.1	1125	10	ADF00364	158	8	2.1	4003	12	ADQ22240	Ad889002 Human p27
c 86	8	2.1	1176	6	ABK24364	159	8	2.1	4230	10	AD831378	Ad889002 Human p27
c 87	8	2.1	1233	12	ADL03978	160	8	2.1	4284	13	AD806868	Ad889002 Human p27
c 88	8	2.1	1242	12	ADO30250	161	8	2.1	4286	12	ADL12903	Ad889002 Human p27
c 89	8	2.1	1248	10	ADH44926	162	8	2.1	4336	5	AAH64328	Ad889002 Human p27
c 90	8	2.1	1268	10	ADH44939	163	8	2.1	4388	8	ABX34490	Ad889002 Human p27
c 91	8	2.1	1294	6	ABL53778	164	8	2.1	4434	8	ACA22280	Ad889002 Human p27
c 92	8	2.1	1332	4	ABL23349	165	8	2.1	4750	6	ABL68819	Ad889002 Human p27
c 93	8	2.1	1355	12	ADN96037	166	8	2.1	4902	4	ABL20352	Ad889002 Human p27
c 94	8	2.1	1356	9	ACD06214	167	8	2.1	5091	4	ABL07051	Ad889002 Human p27
c 95	8	2.1	1374	6	ABK65337	168	8	2.1	5091	13	ADQ89687	Ad889002 Human p27
c 96	8	2.1	1401	13	ADT45098	169	8	2.1	6201	4	ABL14030	Ad889002 Human p27
c 97	8	2.1	1527	10	ADC92050	170	8	2.1	6428	4	AAK78562	Ad889002 Human p27
c 98	8	2.1	1550	5	ADL62569	171	8	2.1	6539	10	AD857349	Ad889002 Human p27
c 99	8	2.1	1557	10	AAH57653	172	8	2.1	6669	6	ABL32193	Ad889002 Human p27
c 100	8	2.1	1637	3	AAH48042	173	8	2.1	6669	6	ABL92197	Ad889002 Human p27
c 101	8	2.1	1654	4	ABL10415	174	8	2.1	6669	6	ABL49306	Ad889002 Human p27
c 102	8	2.1	1699	4	AAH14082	175	8	2.1	8285	6	AAK98916	Ad889002 Human p27
c 103	8	2.1	1703	6	ABL90390	176	8	2.1	8285	10	ADG90365	Ad889002 Human p27
c 104	8	2.1	1715	2	AAZ24887	177	8	2.1	8522	8	AAH50016	Ad889002 Human p27
c 105	8	2.1	1715	8	ADA39843	178	8	2.1	8541	4	ABL07050	Ad889002 Human p27
c 106	8	2.1	1715	8	ACC50456	179	8	2.1	9299	6	ABL33724	Ad889002 Human p27
c 107	8	2.1	1715	8	ABZ71255	180	8	2.1	9352	6	ABL32103	Ad889002 Human p27
c 108	8	2.1	1715	10	ADC73523	181	8	2.1	9905	4	ABL28652	Ad889002 Human p27
c 109	8	2.1	1719	8	ADA70078	182	8	2.1	10274	4	ABL06514	Ad889002 Human p27
c 110	8	2.1	1771	10	ADF82265	183	8	2.1	10918	5	ABA09581	Ad889002 Human p27
c 111	8	2.1	1790	12	ADQ17542	184	8	2.1	10920	6	ABN60009	Ad889002 Human p27
c 112	8	2.1	1831	4	AAH44676	185	8	2.1	10942	4	ABL29604	Ad889002 Human p27
c 113	8	2.1	1831	12	ADI29374	186	8	2.1	11827	6	ABK87610	Ad889002 Human p27
c 114	8	2.1	1907	3	AAH79848	187	8	2.1	11827	10	ADH00899	Ad889002 Human p27
c 115	8	2.1	1962	13	ADS56130	188	8	2.1	12099	4	ABL16890	Ad889002 Human p27
c 116	8	2.1	1986	8	ACA20539	189	8	2.1	12099	6	ABL33718	Ad889002 Human p27
c 117	8	2.1	1989	4	ABL20305	190	8	2.1	17934	6	ABL33718	Ad889002 Human p27
c 118	8	2.1	1992	9	ADA31028	191	8	2.1	19311	13	AD836463	Ad889002 Human p27
c 119	8	2.1	2000	8	ADA72978	192	8	2.1	20001	13	ACN37212	Ad889002 Human p27
c 120	8	2.1	2000	8	ADA72978	193	8	2.1	20512	6	AAH38339	Ad889002 Human p27
c 121	8	2.1	2001	2	AAH05858	194	8	2.1	21840	11	ACN44054	Ad889002 Human p27
c 122	8	2.1	2007	4	AAH51625	195	8	2.1	26071	13	ABD33438	Ad889002 Human p27
c 123	8	2.1	2007	8	ACF74655	196	8	2.1	27310	11	ACN44622	Ad889002 Human p27
c 124	8	2.1	2010	4	AAH54599	197	8	2.1	32220	8	AAH37568	Ad889002 Human p27
c 125	8	2.1	2010	8	ACA20319	198	8	2.1	32220	8	ABX60556	Ad889002 Human p27
c 126	8	2.1	2021	6	ABK73866	199	8	2.1	32220	12	ADJ31306	Ad889002 Human p27
c 127	8	2.1	2071	12	ADQ64086	200	8	2.1	32829	13	ABD33037	Ad889002 Human p27
c 128	8	2.1	2114	6	ABQ54834	201	8	2.1	35651	4	AAH57595	Ad889002 Human p27
c 129	8	2.1	2161	2	AAQ58742	202	8	2.1	36176	11	ACN45126	Ad889002 Human p27
c 130	8	2.1	2161	9	ADA02835	203	8	2.1	39827	12	ADN98979	Ad889002 Human p27
c 131	8	2.1	2161	10	AD872573	204	8	2.1	43572	12	ADQ97861	Ad889002 Human p27
c 132	8	2.1	2161	10	ADC55314	205	8	2.1	48680	11	ACN45210	Ad889002 Human p27
c 133	8	2.1	2161	12	ADH74430	206	8	2.1	50781	11	ACN44360	Ad889002 Human p27
c 134	8	2.1	2165	6	ABK24363	207	8	2.1	55996	9	ADA02741	Ad889002 Human p27
c 135	8	2.1	2165	12	ADL06480	208	8	2.1	55996	10	AD872479	Ad889002 Human p27
c 136	8	2.1	2187	10	ADC91237	209	8	2.1	55996	12	AD872479	Ad889002 Human p27
c 137	8	2.1	2287	12	ADQ63099	210	8	2.1	55996	12	AD872479	Ad889002 Human p27
c 138	8	2.1	2304	4	ABA08970	211	8	2.1	70768	6	AAH41152	Ad889002 Human p27
c 139	8	2.1	2464	4	ABA08691	212	8	2.1	72149	10	AD881173	Ad889002 Human p27
c 140	8	2.1	2496	6	ABA05022	213	8	2.1	72352	12	ADQ97067	Ad889002 Human p27
c 141	8	2.1	2644	10	ADA30486	214	8	2.1	74037	6	ABK94412	Ad889002 Human p27
c 142	8	2.1	2790	2	AAV28916	215	8	2.1	85680	3	AAH22299	Ad889002 Human p27
c 143	8	2.1	2800	11	ADM01338	216	8	2.1	88607	12	ADQ97648	Ad889002 Human p27
c 144	8	2.1	2986	8	ACF62754	217	8	2.1	96591	10	AD85301	Ad889002 Human p27
c 145	8	2.1	3275	5	ABV23844	218	8	2.1	96592	9	ADA02822	Ad889002 Human p27
c 146	8	2.1	3387	12	ADO84890	219	8	2.1	96592	10	AD872560	Ad889002 Human p27
c 147	8	2.1	3394	4	ABL23348	220	8	2.1	96592	12	AD872560	Ad889002 Human p27
c 148	8	2.1	3432	2	AAV28915	221	8	2.1	110000	3	AAH22299	Ad889002 Human p27
c 149	8	2.1	3486	8	ABZ09880	222	8	2.1	115780	13	ABD32303	Ad889002 Human p27
c 150	8	2.1	3486	10	AD853961	223	8	2.1	119211	4	AAH28553	Ad889002 Human p27
c 151	8	2.1	3486	10	ADE84022	224	8	2.1	121160	12	ADQ97870	Ad889002 Human p27
c 152	8	2.1	3486	10	ADE84022	225	8	2.1	130207	11	ACN44762	Ad889002 Human p27

225	8	2.1	133632	11	ACN45054	Acn45054 Human gen	C 298	7	1.9	261	4	ABA38513	AbA38513 Probe #16
226	8	2.1	166910	12	ADN01278	Adn01278 Human end	C 299	7	1.9	261	4	AAK47547	AAk47547 Human bon
227	8	2.1	174600	12	ADQ97520	Adq97520 Mouse can	C 300	7	1.9	261	4	AAK21386	AAk21386 Human bra
228	8	2.1	312477	12	ADP69744	Adp69744 Human ROC	C 301	7	1.9	261	4	ABSA47282	ABs47282 Human liv
C 229	8	2.1	339234	12	ADQ59437	Adq59437 Human can	C 302	7	1.9	261	6	ABSA21644	ABs21644 Human gen
230	8	2.1	349980	6	ABQ81844	Abq81844 Bifidobac	C 303	7	1.9	262	5	ABV56933	ABv56933 Human pro
231	7	1.9	21	12	ADP11892	Adp11892 Set 2 lef	C 304	7	1.9	266	6	ABK93405	ABk93405 Human bre
C 232	7	1.9	22	4	AAF60112	Aaf60112 Human ATM	C 305	7	1.9	266	6	AAK60188	AAk60188 Human imm
233	7	1.9	25	2	AAQ80095	Aaq80095 ADPGPP gl	C 306	7	1.9	268	9	ADA59392	AdA59392 Soybean t
234	7	1.9	25	2	AAQ74550	Aaq74550 Respirato	C 307	7	1.9	268	12	ADP60686	ADp60686 Soybean c
235	7	1.9	25	2	AAQ74552	Aaq74552 Respirato	C 308	7	1.9	273	3	ADF56911	ADf56911 Urogenita
C 236	7	1.9	25	2	AAV03257	Aav03257 Homo eapi	C 309	7	1.9	273	5	ABV60028	ABv60028 Human pro
237	7	1.9	25	9	ACI29910	ACi29910 Human mic	C 310	7	1.9	274	6	ABL69662	ABl69662 Prostate
C 238	7	1.9	25	13	ADR56654	Adr56654 Drug ther	C 311	7	1.9	274	6	ABN93815	ABn93815 Gene #313
239	7	1.9	30	2	AAV03258	Aav03258 Homo sapi	C 312	7	1.9	277	5	ABAL4893	ABaL4893 Human ner
240	7	1.9	33	2	AAQ73938	Aaq73938 Primer fo	C 313	7	1.9	281	10	ABX87275	ABx87275 Corn ear-
C 241	7	1.9	35	2	AAQ74555	Aaq74555 Respirato	C 314	7	1.9	283	9	ADA59389	ADa59389 Soybean t
242	7	1.9	41	4	AAH44336	Aah44336 Human pro	C 315	7	1.9	283	12	ADP60683	ADp60683 Soybean c
C 243	7	1.9	41	6	ABZ44564	Abz44564 Human ATP	C 316	7	1.9	284	10	ADG37661	ADg37661 Aspergill
C 244	7	1.9	41	6	ABZ447352	Abz447352 Human ATP	C 317	7	1.9	285	10	ABX88348	ABx88348 Corn ear-
C 245	7	1.9	49	2	AAQ80484	Aaq80484 Hepatoma	C 318	7	1.9	287	5	ABV59696	ABv59696 Human pro
246	7	1.9	60	13	ADS52932	Ads52932 Eucalyptu	C 319	7	1.9	291	6	ABL71676	ABl71676 Corn tass
C 247	7	1.9	61	2	AAV38265	Aav38265 Murine li	C 320	7	1.9	291	8	ACA44850	ACa44850 Prokaryot
C 248	7	1.9	65	6	ABN54061	ABn54061 Mouse spl	C 321	7	1.9	292	6	ABZ78070	ABz78070 Human bre
C 249	7	1.9	65	12	ADP97797	Adp97797 C. albica	C 322	7	1.9	293	4	AAAS27973	AAa27973 Novel CDN
250	7	1.9	84	2	AAV50396	Aav50396 Obesity p	C 323	7	1.9	293	6	ABL70921	ABl70921 Corn tass
C 251	7	1.9	105	5	AAQ88481	Aaq88481 Target se	C 324	7	1.9	293	6	ABL72651	ABl72651 Corn tass
C 252	7	1.9	109	3	AAQ25321	Aaq25321 Human sec	C 325	7	1.9	293	10	ADG40877	ADg40877 Human res
253	7	1.9	135	4	AAI26119	AAi26119 Probe #16	C 326	7	1.9	293	11	ADI96651	ADi96651 Human res
254	7	1.9	135	4	ABA73477	ABa73477 Human foe	C 327	7	1.9	293	12	ADQ19591	ADq19591 Human sof
255	7	1.9	135	4	AAI53913	AAi53913 Probe #22	C 328	7	1.9	298	6	ABN16401	ABn16401 Human ORF
256	7	1.9	135	4	ABA38781	ABa38781 Probe #17	C 329	7	1.9	298	10	ADK53642	ADk53642 Plant DNA
257	7	1.9	135	4	AAK48084	AAk48084 Human bon	C 330	7	1.9	299	10	ADL24571	ADl24571 Intestina
258	7	1.9	135	4	AAK21920	AAk21920 Human bra	C 331	7	1.9	299	13	ADS50728	ADs50728 Bacterial
259	7	1.9	135	4	ABSA47798	ABs47798 Human liv	C 332	7	1.9	300	2	AAZ14572	Aaz14572 Human gen
260	7	1.9	135	6	ABS22005	ABs22005 Human gen	C 333	7	1.9	300	2	AAZ13463	Aaz13463 Human gen
261	7	1.9	138	6	ABQ94367	ABq94367 Tumour su	C 334	7	1.9	300	5	ABV59677	ABv59677 Human pro
262	7	1.9	154	5	AAI61603	AAi61603 Soybean 3	C 335	7	1.9	300	6	ABL72270	ABl72270 Corn tass
263	7	1.9	156	4	AAI26013	AAi26013 Probe #15	C 336	7	1.9	302	2	ABL72622	ABl72622 Human gen
264	7	1.9	156	4	ABA73082	ABa73082 Human foe	C 337	7	1.9	303	3	AAA82177	AAa82177 N. mening
265	7	1.9	156	4	AAI53511	AAi53511 Probe #22	C 338	7	1.9	303	4	AAAL25149	AAl25149 Human bre
266	7	1.9	156	4	ABA38580	ABa38580 Probe #17	C 339	7	1.9	303	10	ADL24580	ADl24580 Intestina
267	7	1.9	156	4	AAK47677	AAk47677 Human bon	C 340	7	1.9	305	4	AAK58245	AAk58245 Human imm
268	7	1.9	156	4	AAK21515	AAk21515 Human bra	C 341	7	1.9	307	8	ABX54191	ABx54191 Bovine ES
269	7	1.9	156	4	ABSA47412	ABs47412 Human liv	C 342	7	1.9	308	5	ABV02252	ABv02252 Human pro
270	7	1.9	156	6	ABS21732	ABs21732 Human gen	C 343	7	1.9	312	6	ABN17494	ABn17494 Human ORF
C 271	7	1.9	201	13	ADS41108	ADs41108 Human aut	C 344	7	1.9	313	6	ABN75549	ABn75549 Human ORF
C 272	7	1.9	201	13	ADS41115	ADs41115 Human aut	C 345	7	1.9	313	5	ABV59563	ABv59563 Human pro
C 273	7	1.9	201	13	ADS41111	ADs41111 Human aut	C 346	7	1.9	315	4	ABL22863	ABl22863 Drosophil
C 274	7	1.9	206	5	AAF92541	Aaf92541 Rat T2R14	C 347	7	1.9	315	6	ABQ98980	ABq98980 Human ORF
C 275	7	1.9	206	13	ADR29165	Adr29165 Taste rec	C 348	7	1.9	317	5	ADL71329	ADl71329 Human ova
C 276	7	1.9	212	10	ABX88942	ABx88942 Corn ear-	C 349	7	1.9	317	5	ADL36488	ADl36488 Human ova
C 277	7	1.9	216	10	ABX07022	ABx07022 S. pneumo	C 350	7	1.9	318	5	AAAS34533	AAa34533 Human DNA
C 278	7	1.9	221	3	AAI61671	AAi61671 Human sec	C 351	7	1.9	321	12	ADN98601	ADn98601 Novel hum
279	7	1.9	222	2	AAI12223	AAi12223 Human bia	C 352	7	1.9	321	12	ADO00170	ADo00170 Novel hum
280	7	1.9	222	2	AAI12224	AAi12224 Human bia	C 353	7	1.9	324	4	AAAL16306	AAaL16306 Human bre
C 281	7	1.9	231	5	ABV59872	ABv59872 Human pro	C 354	7	1.9	324	5	AAAS40074	AAaS40074 DNA encod
C 282	7	1.9	234	6	ABL38031	ABl38031 Human col	C 355	7	1.9	324	6	ABN18826	ABn18826 Human ORF
C 283	7	1.9	240	6	ABN75948	ABn75948 Human ORF	C 356	7	1.9	324	11	ADJ09069	ADj09069 Human pro
C 284	7	1.9	245	5	AAAS78156	AAa78156 DNA encod	C 357	7	1.9	330	5	ADL36584	ADl36584 Human ova
285	7	1.9	245	9	ADA59388	ADa59388 Soybean t	C 358	7	1.9	330	5	ADL71426	ADl71426 Human ova
286	7	1.9	245	12	ADP60682	ADp60682 Soybean c	C 359	7	1.9	330	10	ABT41116	ABt41116 Toxicity
287	7	1.9	246	9	ACH44024	ACH44024 Human foe	C 360	7	1.9	330	12	ADP28773	ADp28773 Human sec
C 288	7	1.9	248	6	ABL82550	ABl82550 Human ova	C 361	7	1.9	331	8	ACC60033	ACC60033 Rice leaf
C 289	7	1.9	251	3	AAI12254	AAi12254 Human sec	C 362	7	1.9	333	5	AAAS33551	AAa33551 Human CDN
C 290	7	1.9	255	5	AAH81835	Aah81835 Rat diffe	C 363	7	1.9	333	10	ADF01017	ADf01017 Bacterial
C 291	7	1.9	256	12	ADQ06443	ADq06443 Soybean t	C 364	7	1.9	333	11	ACH95909	ACH95909 Klebsiell
C 292	7	1.9	257	8	ABZ73190	ABz73190 Rice leaf	C 365	7	1.9	333	12	ADO00101	ADo00101 Novel hum
293	7	1.9	258	10	ADF03777	ADf03777 Bacterial	C 366	7	1.9	333	12	ADN98532	ADn98532 Novel hum
294	7	1.9	260	4	AAK77126	AAk77126 Human imm.	C 367	7	1.9	335	6	ABN19642	ABn19642 Human ORF
C 295	7	1.9	261	4	AAI25973	AAi25973 Probe #15	C 368	7	1.9	338	3	AAAC26641	AAa26641 Human sec
C 296	7	1.9	261	4	ABR72355	ABa72355 Human foe	C 369	7	1.9	338	3	ABAL12454	ABaL12454 Human ner
C 297	7	1.9	261	4	AAI53379	AAi53379 Probe #22	C 370	7	1.9	339	3	AAAC56289	AAc56289 Pinus rad

371	7	1.9	341	4	AAI80247	AAI80247 Human pol	c 444	7	1.9	407	4	AAK38822	AAK38822 Human bon
372	7	1.9	342	2	ADT67714	Aat67714 H. pylori	c 445	7	1.9	407	4	AAK13094	AAK13094 Human bra
373	7	1.9	342	8	ACD05602	ACD05602 cDNA enco	c 446	7	1.9	407	4	ABS38407	ABS38407 Human liv
374	7	1.9	342	9	ADB12224	ADB12224 Alloiococ	c 447	7	1.9	407	5	RAI05349	RAI05349 Probe #53
375	7	1.9	345	2	AAQ04582	Aaq04582 Translate	c 448	7	1.9	407	5	ABA13888	ABA13888 Human ner
376	7	1.9	347	3	AAAC19786	AAc19786 Human sec	c 449	7	1.9	407	6	ABS12903	ABS12903 Human gen
377	7	1.9	347	6	ABN95719	ABn95719 Gene #221	450	7	1.9	408	2	AAAX22311	AAx22311 Human Tan
378	7	1.9	348	8	ABX40729	ABx40729 Bovine ES	451	7	1.9	411	3	AAA77900	AAa77900 cDNA enco
379	7	1.9	350	9	ADA01647	Ada01647 Mouse Cct	452	7	1.9	411	3	AAI28638	AAi28638 Colon tum
380	7	1.9	350	10	ADB171386	Adb171386 Mouse car	453	7	1.9	411	8	ABZ32824	ABz32824 Human col
381	7	1.9	351	5	ADI67925	Adi67925 Human ova	c 454	7	1.9	411	11	ABDI5173	ABd15173 Pseudomon
382	7	1.9	351	6	ADI74301	ADI74301 Human ova	c 455	7	1.9	412	6	ABN23489	ABn23489 Human ORF
383	7	1.9	351	6	ABN75387	ABn75387 Human ORF	456	7	1.9	412	9	ACH15795	ACH15795 Human adu
384	7	1.9	352	6	ABV77970	ABv77970 Hypoxia-r	c 457	7	1.9	413	8	ABX50478	ABx50478 Bovine ES
385	7	1.9	355	8	ABX40295	ABx40295 Bovine ES	458	7	1.9	413	11	ACN86250	ACn86250 Breast ca
386	7	1.9	357	2	AAQ90416	Aaq90416 Anti-idio	459	7	1.9	415	8	ABZ55892	ABz55892 Aspergill
387	7	1.9	357	6	ABN21278	ABn21278 Human ORF	c 460	7	1.9	416	9	ACH46178	ACH46178 Human inf
388	7	1.9	358	10	ACD95887	ACd95887 Human col	c 461	7	1.9	417	8	ACA25770	ACA25770 Prokaryot
389	7	1.9	363	2	AAT67949	Aat67949 H. pylori	462	7	1.9	421	4	ABA08282	ABa08282 Human phe
390	7	1.9	364	5	ABV06784	ABv06784 Human pro	463	7	1.9	421	8	ACD05890	ACd05890 Novel hum
391	7	1.9	366	12	ADJ40403	Adj40403 Plant CDN	c 464	7	1.9	423	5	ABV00616	ABv00616 Human pro
392	7	1.9	367	5	ABV03385	ABv03385 Human pro	c 465	7	1.9	423	8	ABX52708	ABx52708 Bovine ES
393	7	1.9	369	2	AAQ59659	Aaq59659 Human bra	c 466	7	1.9	425	5	ABV09785	ABv09785 Human pro
394	7	1.9	369	13	ADS45423	Ads45423 Bacterial	467	7	1.9	425	6	ABN63474	ABn63474 Human can
395	7	1.9	371	4	AAI84375	AAi84375 Human pol	468	7	1.9	426	4	AAK55615	AAk55615 Human imm
396	7	1.9	371	9	ACL15554	ACL15554 DNA clone	c 469	7	1.9	426	12	ADO76027	ADg76027 Murine GM
397	7	1.9	372	8	ABX38062	ABx38062 Bovine ES	470	7	1.9	427	4	AAI13726	AAi13726 Probe #36
398	7	1.9	373	6	ABL67565	ABl67565 Oesophagu	471	7	1.9	427	4	ABA55438	ABa55438 Human foe
399	7	1.9	373	6	ABL64867	ABl64867 Lung canc	472	7	1.9	427	4	RAI35084	RAi35084 Probe #37
400	7	1.9	375	4	AAI14769	AAi14769 Human ins	473	7	1.9	427	4	ABA44962	ABa44962 Human bre
401	7	1.9	375	4	AAI14767	AAi14767 Human IGF	474	7	1.9	427	4	ABA25160	ABa25160 Probe #36
402	7	1.9	375	5	AA565869	AA565869 DNA enco	475	7	1.9	427	4	AAK29135	AAk29135 Human bon
403	7	1.9	375	10	ADI60316	Adi60316 Secreted	476	7	1.9	427	4	AAK03677	AAk03677 Human bra
404	7	1.9	375	10	ADK41560	Adk41560 Anti-cell	477	7	1.9	427	5	RAI03604	RAi03604 Probe #35
405	7	1.9	375	10	ADK41562	Adk41562 Anti-cell	478	7	1.9	427	6	ABS03688	ABs03688 Human gen
406	7	1.9	377	2	AAQ60973	Aaq60973 Human bra	479	7	1.9	429	4	AAAL06799	AAa106799 Human rep
407	7	1.9	377	5	AA592520	AA592520 DNA enco	480	7	1.9	429	4	AAAL06797	AAa106797 Human rep
408	7	1.9	380	4	AAI89106	AAi89106 Human pol	481	7	1.9	429	4	AAAL06798	AAa106798 Human rep
409	7	1.9	381	8	ABX47046	ABx47046 Bovine ES	482	7	1.9	429	4	ABA08071	ABa08071 Human ova
410	7	1.9	383	9	ACH31119	ACH31119 Human bon	483	7	1.9	429	4	ABA08072	ABa08072 Human ova
411	7	1.9	384	4	AAF72002	Aaf72002 Corynebac	484	7	1.9	429	4	ABA08073	ABa08073 Human ova
412	7	1.9	384	4	AAF72194	Aaf72194 Corynebac	485	7	1.9	429	6	ABT03068	ABt03068 Human bre
413	7	1.9	384	4	AAF71325	Aaf71325 Corynebac	c 486	7	1.9	429	8	ABX54173	ABx54173 Bovine ES
414	7	1.9	384	5	AAV15276	AAv15276 Human pro	c 487	7	1.9	430	13	ADQ54156	ADq54156 Novel can
415	7	1.9	386	6	ABQ85205	ABq85205 Arabidops	c 488	7	1.9	432	9	ACH47302	ACH47302 Human inf
416	7	1.9	386	11	ADI31366	Adi31366 Human CDN	c 489	7	1.9	432	9	ABV41491	ABv41491 Human pro
417	7	1.9	387	5	AA585155	AA585155 DNA enco	490	7	1.9	433	5	ABV32566	ABv32566 Human pro
418	7	1.9	388	5	AAF64808	AAf64808 Novel hum	491	7	1.9	436	9	ACL13362	ACL13362 DNA clone
419	7	1.9	390	4	AAI81259	AAi81259 Human pol	492	7	1.9	437	4	AAAL02250	AAa102250 Human rep
420	7	1.9	390	9	ADA49159	Ada49159 Maize gen	493	7	1.9	437	4	ABA07622	ABa07622 Human ova
421	7	1.9	390	10	ADB51050	Adb51050 Primary r	c 494	7	1.9	437	13	ADRI4935	ADr14935 Rosa sp K
422	7	1.9	390	11	ADT95801	Adt95801 Colon can	c 495	7	1.9	438	5	AA580906	AA580906 DNA enco
423	7	1.9	390	12	ADJ44295	Adj44295 Plant CDN	c 496	7	1.9	439	10	ADD16090	ADD16090 cDNA (Seq
424	7	1.9	392	4	AAK84890	AAk84890 Human imm	497	7	1.9	439	10	ABX61036	ABx61036 Arabidops
425	7	1.9	399	2	AAQ90425	Aaq90425 DNA enco	c 498	7	1.9	441	9	ACH49658	ACH49658 Human leu
426	7	1.9	399	5	ADL42968	ADl42968 Human ova	499	7	1.9	443	9	ACH49855	ACH49855 Human leu
427	7	1.9	399	8	ABX41703	ABx41703 Bovine ES	500	7	1.9	445	5	ABV11421	ABv11421 Human pro
428	7	1.9	400	2	AAV75163	AAv75163 Staphyloc	501	7	1.9	449	4	AAI12248	AAi12248 Probe #21
429	7	1.9	400	5	ADL42872	ADl42872 Human ova	502	7	1.9	449	4	ABA53951	ABa53951 Human foe
430	7	1.9	402	2	AAQ90426	Aaq90426 DNA enco	503	7	1.9	449	4	AAI33603	AAi33603 Probe #22
431	7	1.9	402	2	AAV75593	AAv75593 Staphyloc	504	7	1.9	449	4	ABA43502	ABa43502 Human bre
432	7	1.9	402	12	ADP93228	ADp93228 Cotton ex	505	7	1.9	449	4	ABA23702	ABa23702 Probe #21
433	7	1.9	403	6	ABN23600	ABn23600 Human ORF	506	7	1.9	449	4	AAK27668	AAk27668 Human bon
434	7	1.9	403	10	ADD45829	Add45829 Rat gene	507	7	1.9	449	4	AAK02221	AAk02221 Human bra
435	7	1.9	403	10	ADE60275	Ade60275 Rat gene	508	7	1.9	449	4	AB27240	ABe27240 Human liv
436	7	1.9	404	6	ABL81522	ABl81522 Human ova	509	7	1.9	449	5	AAI02162	AAi02162 Probe #21
437	7	1.9	404	9	ACH31539	ACH31539 Human bon	510	7	1.9	449	6	ABS02129	ABs02129 Human gen
438	7	1.9	406	5	AAH42811	AAh42811 Nucleotid	511	7	1.9	450	6	ABZ08415	ABz08415 Human leu
439	7	1.9	407	4	AAI19630	AAi19630 Probe #95	c 512	7	1.9	451	3	ACH28063	ACH28063 Human adu
440	7	1.9	407	4	ABA64656	ABa64656 Human foe	c 513	7	1.9	452	3	AA55932	AA55932 Euclalyptu
441	7	1.9	407	4	AAI44826	AAi44826 Probe #13	c 514	7	1.9	452	4	ABA58691	ABa58691 Human foe
442	7	1.9	407	4	AA46776	AA46776 Human bre	515	7	1.9	452	4	AAI38370	AAi38370 Probe #70
443	7	1.9	407	4	ABA31781	ABa31781 Probe #10	516	7	1.9	452	4	AAK32544	AAk32544 Human bon

517	7	1.9	452	4	AAK06826	Aak06826 Human bra	c 590	7	1.9	501	6	ABL80020	AbL80020 Human ova
518	7	1.9	452	4	ABS32255	AbS32255 Human liv	c 591	7	1.9	503	10	ABE81605	Abe81605 Arabidops
519	7	1.9	452	6	ABE07334	AbE07334 Human gen	c 592	7	1.9	505	4	ABL28019	AbL28019 Drosophil
520	7	1.9	453	6	ABQ58127	AbQ58127 Human col	c 593	7	1.9	505	6	ABV87781	AbV87781 Human col
521	7	1.9	454	4	AAK66418	Aak66418 Human imm	c 594	7	1.9	505	10	ADD48316	Add48316 Human gen
c 522	7	1.9	455	9	ACH34588	Ach34588 Human end	c 595	7	1.9	505	10	ADD48680	Add48680 Human gen
c 523	7	1.9	456	4	AAAL12180	AaL12180 Human bre	c 596	7	1.9	506	8	AAAS1602	AaA51602 Human lif
c 524	7	1.9	456	5	ABAI3783	AbA13783 Human ner	c 597	7	1.9	506	8	ABZ73143	AbZ73143 Rice leaf
c 525	7	1.9	456	9	ACH39713	Ach39713 Human foe	c 598	7	1.9	507	5	AAAS92128	AaA92128 DNA encod
c 526	7	1.9	456	10	ADC19743	AdC19743 H. influe	c 599	7	1.9	507	6	ABL37469	AbL37469 Human col
c 527	7	1.9	457	10	ADF80960	AdF80960 Leukemia	c 600	7	1.9	512	11	ACN88132	AcN88132 Breast ca
c 528	7	1.9	458	9	ACH41606	Ach41606 Human foe	c 601	7	1.9	513	10	ADSE1651	Ade61651 Rat gene
c 529	7	1.9	459	9	ACH39977	Ach39977 Human foe	c 602	7	1.9	513	13	ADQ52500	AdQ52500 Novel can
c 530	7	1.9	460	5	ABV09637	AbV09637 Human pro	c 603	7	1.9	514	8	ADT23525	AdT23525 Cellobioh
c 531	7	1.9	460	5	ABV36071	AbV36071 Human pro	c 604	7	1.9	514	12	ADJ10792	Adj10792 Recombina
c 532	7	1.9	460	6	ABL93667	AbL93667 Arabidops	c 605	7	1.9	515	12	ACH75341	Ach75341 Human gen
c 533	7	1.9	460	10	ADE85381	Ade85381 Farnesyl	c 606	7	1.9	515	8	ABX73133	AbX73133 Metabolic
c 534	7	1.9	461	5	ABV39780	AbV39780 Human pro	c 607	7	1.9	519	10	ADE81284	Ade81284 Arabidops
c 535	7	1.9	461	5	ABV30812	AbV30812 Human pro	c 608	7	1.9	519	13	ACN55312	AcN55312 Cotton an
c 536	7	1.9	461	6	ABL93657	AbL93657 Arabidops	c 609	7	1.9	520	9	ACH41144	Ach41144 Human foe
c 537	7	1.9	464	3	AAAC41326	AaC41326 Zea mays	c 610	7	1.9	520	12	ACH77657	Ach77657 Human gen
c 538	7	1.9	464	4	AAI15538	AaI15538 Probe #54	c 611	7	1.9	522	6	ABK79326	AbK79326 Bacillus
c 539	7	1.9	464	4	ABA57441	Aba57441 Human foe	c 612	7	1.9	523	4	ABAL01862	Al01862 Human rep
c 540	7	1.9	464	4	AAI36989	AaI36989 Probe #56	c 613	7	1.9	523	4	ABAL01862	Al01862 Human tes
c 541	7	1.9	464	4	ABA26946	Aba26946 Probe #54	c 614	7	1.9	523	12	ADP91511	AdP91511 Cotton ex
c 542	7	1.9	464	4	AAK31080	Aak31080 Human bon	c 615	7	1.9	523	13	ADRG2200	AdRG2200 Cotton cd
c 543	7	1.9	464	4	AAK05479	Aak05479 Human bra	c 616	7	1.9	524	2	AAAX30891	AaX30891 Streptoco
c 544	7	1.9	464	4	ABS30759	AbS30759 Human liv	c 617	7	1.9	524	13	ACN59855	AcN59855 Cotton gy
c 545	7	1.9	464	6	ABS05831	AbS05831 Human gen	c 618	7	1.9	525	11	ACN90721	AcN90721 Breast ca
c 546	7	1.9	467	5	ABV30959	AbV30959 Human pro	c 619	7	1.9	525	13	ACN55620	AcN55620 Cotton an
c 547	7	1.9	468	4	AAI16073	AaI16073 Probe #60	c 620	7	1.9	528	4	AAK60038	Aak60038 Human imm
c 548	7	1.9	468	4	ABA58604	Aba58604 Human foe	c 621	7	1.9	529	4	AAI16929	AaI16929 Probe #68
c 549	7	1.9	468	4	ABA73901	AbA73901 Human foe	c 622	7	1.9	529	4	ABA60951	Aba60951 Human foe
c 550	7	1.9	468	4	AAI54349	AaI54349 Probe #23	c 623	7	1.9	529	4	AAI40848	AaI40848 Probe #95
c 551	7	1.9	468	4	AAI39273	AaI39273 Probe #69	c 624	7	1.9	529	4	ABA28912	AbA28912 Probe #73
c 552	7	1.9	468	4	ABA27615	Aba27615 Probe #60	c 625	7	1.9	529	4	AAK35131	Aak35131 Human bon
c 553	7	1.9	468	4	AAK48520	Aak48520 Human bon	c 626	7	1.9	529	4	AAK09241	Aak09241 Human bra
c 554	7	1.9	468	4	AAK32436	Aak32436 Human bon	c 627	7	1.9	529	4	ABK34883	AbK34883 Human liv
c 555	7	1.9	468	4	AAK22352	Aak22352 Human bra	c 628	7	1.9	529	6	ABK77577	AbK77577 Bacillus
c 556	7	1.9	468	4	AAK06731	Aak06731 Human bra	c 629	7	1.9	529	13	ACN59582	AcN59582 Human gen
c 557	7	1.9	468	4	ABS32142	AbS32142 Human liv	c 630	7	1.9	529	13	ACN59618	AcN59618 Cotton gy
c 558	7	1.9	468	6	ABS07220	AbS07220 Human gen	c 631	7	1.9	530	13	ACN59899	AcN59899 Cotton gy
c 559	7	1.9	469	12	ADO55031	AdO55031 Gene #128	c 632	7	1.9	531	5	ADL39151	AdL39151 Human ova
c 560	7	1.9	470	12	ADP94395	AdP94395 Cotton ex	c 633	7	1.9	531	5	ADL45379	AdL45379 Human ova
c 561	7	1.9	471	5	AA572725	Aa572725 DNA encod	c 634	7	1.9	534	2	AAAX22309	AaX22309 Human Tan
c 562	7	1.9	471	3	AA27922	Aa27922 Human int	c 635	7	1.9	535	13	ACN46743	AcN46743 Cotton pr
c 563	7	1.9	474	9	ACH34675	Ach34675 Human end	c 636	7	1.9	536	12	ADO35883	AdO35883 Novel mou
c 564	7	1.9	474	9	ACH13231	Ach13231 Human adu	c 637	7	1.9	538	13	ADR64047	AdR64047 Cotton cd
c 565	7	1.9	474	9	ACH37923	Ach37923 Human end	c 638	7	1.9	539	10	ADK71789	AdK71789 Rice endo
c 566	7	1.9	475	10	ADD33286	Add33286 Mouse mit	c 639	7	1.9	539	12	ACH77687	Ach77687 Human gen
c 567	7	1.9	477	3	AAA62522	Aaa62522 Human sec	c 640	7	1.9	542	6	ABK77577	AbK77577 Bacillus
c 568	7	1.9	477	4	AAH22696	Aah22696 Human sec	c 641	7	1.9	542	9	ACL15549	AcL15549 DNA clone
c 569	7	1.9	477	9	ACH39326	Ach39326 Human foe	c 642	7	1.9	542	13	ADO31087	AdO31087 Novel can
c 570	7	1.9	477	10	ADB50879	AdB50879 Primary r	c 643	7	1.9	542	4	AAH07228	Aah07228 Human cdn
c 571	7	1.9	480	5	ABV59672	AbV59672 Human pro	c 644	7	1.9	547	4	AAF75084	Aaf75084 Human col
c 572	7	1.9	481	9	ACH45615	Ach45615 Human foe	c 645	7	1.9	547	5	ABV27247	AbV27247 Human pro
c 573	7	1.9	481	10	ACD97344	AcD97344 Human col	c 646	7	1.9	547	5	ABV21429	AbV21429 Human pro
c 574	7	1.9	482	6	ABL87814	AbL87814 Human ova	c 647	7	1.9	549	5	AAAS86439	AaA86439 DNA encod
c 575	7	1.9	487	6	ABN64706	Abn64706 Human can	c 648	7	1.9	549	6	ABN68972	Abn68972 Streptoco
c 576	7	1.9	487	12	ADP91540	AdP91540 Cotton ex	c 649	7	1.9	549	12	ADJ44635	Adj44635 Plant CDN
c 577	7	1.9	488	9	ACH39832	Ach39832 Human foe	c 650	7	1.9	549	12	ACH75752	Ach75752 Human gen
c 578	7	1.9	492	6	ABL82980	AbL82980 Human ova	c 651	7	1.9	549	12	ACH75813	Ach75813 Human gen
c 579	7	1.9	494	9	ACH50815	Ach50815 Human mam	c 652	7	1.9	550	12	ADN13574	AdN13574 Human pro
c 580	7	1.9	495	5	ADL39538	AdL39538 Human ova	c 653	7	1.9	551	4	AAH35458	Aah35458 Human col
c 581	7	1.9	495	6	AA622778	Aa622778 CDNA sequ	c 654	7	1.9	551	4	AAAS28307	AaA28307 Genomic s
c 582	7	1.9	496	5	ABV36730	AbV36730 Human pro	c 655	7	1.9	551	4	AAAS28308	AaA28308 Genomic s
c 583	7	1.9	497	5	ABV59612	AbV59612 Human pro	c 656	7	1.9	551	10	ADGA1504	AdG41504 Human res
c 584	7	1.9	498	9	ACH15614	Ach15614 Human'adu	c 657	7	1.9	551	10	ADGA1503	AdG41503 Human res
c 585	7	1.9	498	13	ADO54525	AdO54525 Novel can	c 658	7	1.9	551	11	ADI97277	AdI97277 Human res
c 586	7	1.9	500	3	AAQ94167	Aaq94167 Cat flea	c 659	7	1.9	551	11	ADI97278	AdI97278 Human res
c 587	7	1.9	500	3	ACL15565	AcL15565 DNA clone	c 660	7	1.9	552	12	ADJ43263	AdJ43263 Plant CDN
c 588	7	1.9	501	2	AAAX22310	AaX22310 Human Tan	c 661	7	1.9	553	8	ABZ76797	AbZ76797 Nicotiana
c 589	7	1.9	501	5	ADL40459	AdL40459 Human ova	c 662	7	1.9	554	4	AAAL21110	AaL21110 Human bre

c 663	7	1.9	554	4	AAH11992	Aah11992 Human cDN	c 736	7	1.9	584	3	AAA46489	Aaa46489 cDNA enco
c 664	7	1.9	556	2	AX33953	Aax33953 Human HCM	c 737	7	1.9	585	13	ACN45563	Acn45563 Cotton pr
c 665	7	1.9	556	8	ABZ54243	Abz54243 Aspergill	c 738	7	1.9	585	9	ACL13285	ACL13285 DNA clone
c 666	7	1.9	556	10	ADB55637	Adb55637 Toxicity-	c 739	7	1.9	586	12	ACH78948	Ach78948 Human gen
c 667	7	1.9	556	10	ADB50202	Adb50202 Primary r	c 740	7	1.9	589	4	AK65258	Aak65258 Human imm
c 668	7	1.9	557	5	ADI73914	Adi73914 Human ova	c 741	7	1.9	589	13	ACN60788	Acn60788 Cotton gy
c 669	7	1.9	557	5	ADI67525	Adi67525 Human ova	c 742	7	1.9	590	4	AAH04344	Aah04344 Human cDN
c 670	7	1.9	557	9	ACH39700	Ach39700 Human foe	c 743	7	1.9	590	5	ABV58632	Abv58632 Human pro
c 671	7	1.9	557	13	ADQ54826	Adq54826 Novel can	c 744	7	1.9	590	12	ACH87126	Ach87126 Human gen
c 672	7	1.9	559	4	RAI44261	RAI44261 Probe #12	c 745	7	1.9	591	3	AAF08818	Aaf08818 Fusarium
c 673	7	1.9	559	12	ADN12578	Adn12578 Human pro	c 746	7	1.9	591	6	ABN67375	Abn67375 Streptoco
c 674	7	1.9	559	13	ADQ54088	Adq54088 Novel can	c 747	7	1.9	592	13	ACN56853	Acn56853 Cotton gy
c 675	7	1.9	561	3	AAA51603	Aaa51603 Human IL-	c 748	7	1.9	593	5	ABV56007	Abv56007 Human pro
c 676	7	1.9	561	13	ACN62192	Acn62192 Cotton gy	c 749	7	1.9	593	10	ADG37982	Adg37982 Aspergill
c 677	7	1.9	563	13	ADS54336	Ads54336 Bacterial	c 750	7	1.9	594	3	AAA51361	Aaa51361 Streptoco
c 678	7	1.9	563	13	ACN61910	Acn61910 Cotton gy	c 751	7	1.9	594	3	AAA27921	Aaa27921 Human int
c 679	7	1.9	564	5	ABV60508	Abv60508 Human pro	c 752	7	1.9	594	4	AAH22755	Aah22755 Human sec
c 680	7	1.9	564	10	ADK56162	Adk56162 Plant DNA	c 753	7	1.9	598	2	AAV69356	Aav69356 Wheat gly
c 681	7	1.9	565	4	AAI19210	AAI19210 Probe #91	c 754	7	1.9	598	4	AAO92556	Aao92556 Wheat wat
c 682	7	1.9	565	4	ABL19203	Ab119203 Drosophil	c 755	7	1.9	598	6	ABK15097	Abk15097 cDNA enco
c 683	7	1.9	565	4	ABA64219	Aba64219 Human foe	c 756	7	1.9	598	10	AAK58846	Aak58846 Wheat gly
c 684	7	1.9	565	4	ABA31364	Aba31364 Probe #98	c 757	7	1.9	599	3	AAC01514	Aac01514 Human sec
c 685	7	1.9	565	6	ABS12473	Abs12473 Human gen	c 758	7	1.9	600	4	AAS54035	Aas54035 Klebsiell
c 686	7	1.9	566	5	ABV50387	Abv50387 Human pro	c 759	7	1.9	600	12	ADQ84110	Adq84110 Human tum
c 687	7	1.9	567	4	AAH02883	Aah02883 Human she	c 760	7	1.9	601	9	ACL15555	ACL15555 DNA clone
c 688	7	1.9	567	13	ADS50706	Ads50706 Bacterial	c 761	7	1.9	604	5	AAS72939	Aas72939 DNA enco
c 689	7	1.9	569	4	AAH22954	Aah22954 Human tes	c 762	7	1.9	606	3	AAC43625	Aac43625 Arabidops
c 690	7	1.9	569	4	ABA61403	Aba61403 Human foe	c 763	7	1.9	606	5	AAS66222	Aas66222 DNA enco
c 691	7	1.9	569	4	RAI41311	RAI41311 Probe #99	c 764	7	1.9	606	13	ADQ57641	Adq57641 Novel can
c 692	7	1.9	569	4	AAK35595	Aak35595 Human bon	c 765	7	1.9	606	13	ACN53150	Acn53150 Cotton an
c 693	7	1.9	569	4	AAK09701	Aak09701 Human bra	c 766	7	1.9	607	9	ACL15560	ACL15560 DNA clone
c 694	7	1.9	569	6	AAD37357	Aad37357 R7 adeny1	c 767	7	1.9	607	12	ADQ36603	Ado36603 Isoquinol
c 695	7	1.9	569	6	AAD37356	Aad37356 R8 adeny1	c 768	7	1.9	609	13	ACN62482	Acn62482 Cotton de
c 696	7	1.9	570	6	ABN69480	Abn69480 Streptoco	c 769	7	1.9	610	9	ACL15547	ACL15547 DNA clone
c 697	7	1.9	570	6	ABN69479	Abn69479 Streptoco	c 770	7	1.9	610	13	ADQ52192	Adq52192 Novel can
c 698	7	1.9	570	9	ACL15548	ACL15548 DNA clone	c 771	7	1.9	611	4	ABL17811	Ab117811 Drosophil
c 699	7	1.9	571	3	AAFI1446	Aafi1446 Aspergill	c 772	7	1.9	613	6	ABQ35544	Abq35544 Oligonucl
c 700	7	1.9	572	10	ADC72409	Adc72409 DNA Seq I	c 773	7	1.9	613	6	ABQ35545	Abq35545 Oligonucl
c 701	7	1.9	572	10	ADC75507	Adc75507 DNA homol	c 774	7	1.9	614	13	ADR59299	Adr59299 Cotton cD
c 702	7	1.9	573	6	ABT07883	Abt07883 Human lun	c 775	7	1.9	616	3	AAC39314	Aac39314 Arabidops
c 703	7	1.9	573	11	ACH98095	Ach98095 Klebsiell	c 776	7	1.9	624	8	ACF74964	Acf74964 Staphyloc
c 704	7	1.9	574	4	AAI16778	AAI16778 Probe #67	c 777	7	1.9	625	10	ADFI13344	Adfi13344 Human 3-h
c 705	7	1.9	574	4	ABA60416	Aba60416 Human foe	c 778	7	1.9	625	12	ADJ84429	Adj84429 Human phe
c 706	7	1.9	574	4	AAI40300	AAI40300 Probe #89	c 779	7	1.9	626	3	AAA51601	Aaa51601 Human IL-
c 707	7	1.9	574	4	ABA28636	Aba28636 Probe #71	c 780	7	1.9	627	5	ABV53042	Abv53042 Human pro
c 708	7	1.9	574	4	AKA34581	Aak34581 Human bon	c 781	7	1.9	627	10	ADQ333423	Adq333423 Mouse mit
c 709	7	1.9	574	4	RAK08694	Rak08694 Human bra	c 782	7	1.9	629	3	AAA51594	Aaa51594 Human IL-
c 710	7	1.9	574	4	ABS34354	Abs34354 Human liv	c 783	7	1.9	629	13	ACN54253	Acn54253 Cotton an
c 711	7	1.9	574	6	ABS09212	Abs09212 Human liv	c 784	7	1.9	630	5	AAC84317	Aac84317 Human EXC
c 712	7	1.9	574	12	ACH73401	Ach73401 Human gen	c 785	7	1.9	630	12	ADL66931	Adl66931 Human ext
c 713	7	1.9	576	4	AAI16818	AAI16818 Probe #67	c 786	7	1.9	632	5	AAH42815	Aah42815 Nucleotid
c 714	7	1.9	576	4	ABA60543	Aba60543 Human foe	c 787	7	1.9	633	10	ADFI13345	Adfi13345 Human 3-h
c 715	7	1.9	576	4	RAI40432	RAI40432 Probe #91	c 788	7	1.9	633	10	ABX95401	Abx95401 cDNA enco
c 716	7	1.9	576	4	ABA28703	Aba28703 Probe #71	c 789	7	1.9	633	12	ADFS3256	Adfs3256 Human pro
c 717	7	1.9	576	4	AAK34711	Aak34711 Human bon	c 790	7	1.9	634	6	ABL63301	Ab163301 Breast ca
c 718	7	1.9	576	4	AAH55621	Aah55621 Human bre	c 791	7	1.9	634	6	ABL62874	Ab162874 Breast ca
c 719	7	1.9	576	4	AAK08823	Aak08823 Human bra	c 792	7	1.9	634	6	ABL63092	Ab163092 Breast ca
c 720	7	1.9	576	4	ABS34484	Abs34484 Human liv	c 793	7	1.9	634	6	ABK35563	Abk35563 Gene ISG1
c 721	7	1.9	576	6	ABS09300	Abs09300 Human gen	c 794	7	1.9	634	6	ABT10900	Abt10900 Human bre
c 722	7	1.9	576	10	ABX56863	Abx56863 Arabidops	c 795	7	1.9	634	6	ABZ35078	Abz35078 Human gen
c 723	7	1.9	576	12	ADN40391	Adn40391 Human bre	c 796	7	1.9	634	6	ABK83926	Abk83926 Human cDN
c 724	7	1.9	578	12	ACH79716	Ach79716 Human gen	c 797	7	1.9	634	8	ACC51007	Acc51007 Human bla
c 725	7	1.9	579	3	AAA27918	Aaa27918 Human int	c 798	7	1.9	634	8	ACC50195	Acc50195 Breast ca
c 726	7	1.9	579	8	ACA49968	Aca49968 Prokaryot	c 799	7	1.9	634	8	ACC51210	Acc51210 Human plk
c 727	7	1.9	579	10	ADC76945	Adc76945 DNA homol	c 800	7	1.9	634	10	ADD19019	Add19019 Human dis
c 728	7	1.9	579	12	ADN05879	Adn05879 Antipsori	c 801	7	1.9	634	10	ADF76521	Adf76521 Novel hum
c 729	7	1.9	581	9	ACL15550	ACL15550 DNA clone	c 802	7	1.9	634	10	ACC72677	Acc72677 Human can
c 730	7	1.9	581	10	ACD94462	Acd94462 Human col	c 803	7	1.9	634	11	ADN95888	Adn95888 Human BEC
c 731	7	1.9	582	5	ABV39927	Abv39927 Human pro	c 804	7	1.9	634	11	ADN95816	Adn95816 Human BEC
c 732	7	1.9	582	12	ACH72109	Ach72109 Human gen	c 805	7	1.9	634	12	ADJ74815	Adj74815 Marker ge
c 733	7	1.9	582	13	ACN45993	Acn45993 Cotton pr	c 806	7	1.9	634	12	ADL83099	Adl83099 Human PRO
c 734	7	1.9	582	13	ACN55807	Acn55807 Cotton an	c 807	7	1.9	634	12	ADN04149	Adn04149 Antipsori
c 735	7	1.9	583	4	AAK70689	Aak70689 Human imm	c 808	7	1.9	634	12	ADO24416	Ado24416 Human PRO

809	7	1.9	634	13	ADR14230	Adi14230 Human NF-	c 882	7	1.9	706	12	ADJ42232	Adj42232 Plant cDN
810	7	1.9	634	13	ADP56303	Adp56303 Human PRO	883	7	1.9	708	2	AAT68277	Aat68277 H. pylori
811	7	1.9	634	13	ADR52863	Adr52863 Drug ther	884	7	1.9	710	4	AH06458	Ah06458 Human cDN
812	7	1.9	634	13	ADP23872	Adp23872 PRO poly	c 885	7	1.9	710	4	AAH08141	Aah08141 Human cDN
813	7	1.9	634	13	ADP64440	Adp64440 Human int	c 886	7	1.9	711	12	ACH91585	Ach91585 Human gen
814	7	1.9	635	5	ABV271143	Abv271143 Human pro	c 887	7	1.9	716	11	ACN91844	Acn91844 Breast ca
815	7	1.9	635	5	ABV21124	Abv21124 Human pro	c 888	7	1.9	717	6	ABK74060	Abk74060 Bacillus
816	7	1.9	635	5	ADL62343	Adl62343 Human ova	889	7	1.9	719	3	AAF12941	Aaf12941 Aspergill
817	7	1.9	636	11	ACN90695	Acn90695 Breast ca	890	7	1.9	719	4	AAH99862	Aah99862 Human pro
818	7	1.9	636	3	ADAO0211	Adao0211 Human zil	891	7	1.9	720	6	ABQ51364	Abq51364 Oligonuc1
819	7	1.9	636	10	ADH89069	Adh89069 DNA encod	c 892	7	1.9	720	6	ABQ51365	Abq51365 Oligonuc1
820	7	1.9	636	10	ADH83044	Adh83044 Enterococ	c 893	7	1.9	722	12	ADO24382	Ado24382 Human PRO
c 821	7	1.9	638	6	ABN62368	Abn62368 Human can	c 894	7	1.9	729	6	ABN68013	Abn68013 Streptoco
c 822	7	1.9	639	4	AAI21063	Aai21063 Human bre	895	7	1.9	729	8	ABZ36826	Abz36826 Human GEN
c 823	7	1.9	640	3	AAF14923	Aaf14923 Trichoder	896	7	1.9	729	12	ADQ37046	Adq37046 Cell prol
824	7	1.9	641	13	ACN46548	Acn46548 Cotton pr	897	7	1.9	730	2	AAQ05940	Aaq05940 Complete
825	7	1.9	642	8	ABX63536	Abx63536 Human cDN	c 898	7	1.9	730	13	ADQ55259	Adq55259 Novel can
c 826	7	1.9	643	4	AAH05305	Aah05305 Human cDN	c 899	7	1.9	731	3	AAC36471	Aac36471 Arabidops
c 827	7	1.9	650	2	AAH19258	Aah19258 Alfalfa d	c 900	7	1.9	731	4	AAI23532	Aai23532 Human bre
c 828	7	1.9	650	3	AAH15592	Aah15592 Human il-	c 901	7	1.9	737	4	AAH04385	Aah04385 Human cDN
c 829	7	1.9	651	13	ADT46877	Adt46877 Bacterial	c 902	7	1.9	739	4	AAH08552	Aah08552 Influenza
830	7	1.9	652	9	ACL15546	Act15546 DNA clone	c 903	7	1.9	740	12	ADO15236	Ado15236 Plant tra
831	7	1.9	652	9	ACL15558	Act15558 DNA clone	c 904	7	1.9	741	12	ADI42544	Adi42544 Plant tra
832	7	1.9	655	5	ABV24354	Abv24354 Human pro	c 905	7	1.9	741	12	ADO02873	Ado02873 Corn orth
833	7	1.9	657	3	ADAO0212	Adao0212 Human zil	c 906	7	1.9	744	4	AAH04493	Aah04493 Human cDN
834	7	1.9	657	3	AAA08513	Aaa08513 Primate i	c 907	7	1.9	744	10	ADD33422	Add33422 Mouse mit
835	7	1.9	657	3	AAH27920	Aah27920 Human int	908	7	1.9	745	2	AAZ16327	Aaz16327 Human gen
836	7	1.9	657	6	ABK93116	Abk93116 Human pro	909	7	1.9	747	4	AAK67494	Aak67494 Human imm
837	7	1.9	657	10	ADH89074	Adh89074 DNA encod	910	7	1.9	747	4	AAK67493	Aak67493 Human imm
838	7	1.9	657	12	ADJ88305	Adj88305 Human int	911	7	1.9	747	4	AAK67492	Aak67492 Human imm
839	7	1.9	657	12	ADL15867	Adl15867 Human int	c 912	7	1.9	747	12	ADI57648	Adi57648 Human bre
840	7	1.9	657	12	ADAO4678	Adao4678 Human int	913	7	1.9	750	2	AAH15255	Aah15255 DNA encod
c 841	7	1.9	659	4	AAH99340	Aah99340 Human pro	914	7	1.9	750	4	AAH15255	Aah15255 DNA encod
842	7	1.9	660	2	AAV90532	Aav90532 EST clone	c 915	7	1.9	750	12	ADQ26699	Adq26699 PCNA ali
c 843	7	1.9	663	3	AAH46399	Aah46399 Arabidops	c 916	7	1.9	753	10	ACF67085	Acf67085 Phototrab
c 844	7	1.9	663	9	ADA30546	Ada30546 DNA encod	917	7	1.9	754	3	AAH51593	Aah51593 Processed
845	7	1.9	663	10	ADD33693	Add33693 Mouse mit	918	7	1.9	754	4	AAH51593	Aah51593 Processed
846	7	1.9	663	10	ADL13944	Adl13944 Osteoarth	919	7	1.9	754	6	ABH74448	Abh74448 Human cDN
847	7	1.9	664	10	ADL18461	Adl18461 Human pro	920	7	1.9	754	8	ACA91234	Ac91234 Novel hum
848	7	1.9	668	2	AAZ277534	Aaz277534 Human ova	921	7	1.9	754	8	ACD81611	Acd81611 Human cDN
849	7	1.9	669	2	AAH30436	Aah30436 H. pylori	922	7	1.9	754	8	ACA60433	Ac60433 Novel hum
850	7	1.9	669	10	ABZ83065	Abz83065 Toxicolog	923	7	1.9	754	8	ACA58880	Ac58880 CDNA enco
851	7	1.9	670	2	AAZ33612	Aaz33612 Human bre	924	7	1.9	754	8	ACA64056	Ac64056 CDNA enco
852	7	1.9	671	2	AAT64341	Aat64341 Human sma	925	7	1.9	754	8	ACA91320	Ac91320 CDNA enco
c 853	7	1.9	671	3	AAH44260	Aah44260 Arabidops	926	7	1.9	754	8	ACD45219	Acd45219 Human sec
854	7	1.9	675	6	AAH21054	Aah21054 Isolated	927	7	1.9	754	8	ACA93767	Ac93767 Human cDN
c 855	7	1.9	676	3	AAH11973	Aah11973 Aspergill	928	7	1.9	754	8	ACA67341	Ac67341 cDNA enco
856	7	1.9	678	12	ADQ17878	Adq17878 Human sof	929	7	1.9	754	8	ACH66314	Ach66314 Novel hum
857	7	1.9	681	10	ADG84255	Adg84255 Human TMD	930	7	1.9	754	8	ACH66314	Ach66314 Novel hum
858	7	1.9	681	12	ADJ43202	Adj43202 Plant cDN	931	7	1.9	754	8	ACH66314	Ach66314 Novel hum
c 859	7	1.9	681	13	ADR59475	Adr59475 Cotton cD	932	7	1.9	754	8	ACA89359	Ac89359 Novel hum
860	7	1.9	682	13	ADQ49828	Adq49828 Novel can	933	7	1.9	754	8	ACA68996	Ac68996 Novel hum
c 861	7	1.9	685	3	AAH18131	Aah18131 Lung canc	934	7	1.9	754	9	ACA98518	Ac98518 Human PRO
c 862	7	1.9	685	10	ACF66159	Acf66159 Phototrab	935	7	1.9	754	9	ACA63443	Ac63443 cDNA enco
c 863	7	1.9	686	6	ABH77078	Abh77078 Frog embr	936	7	1.9	754	9	ADB17198	Adb17198 Human cDN
c 864	7	1.9	687	5	ABA18465	Abal8465 Human ner	937	7	1.9	754	9	ACH03646	Ach03646 Human sec
865	7	1.9	687	5	AAH76180	Aah76180 DNA encod	938	7	1.9	754	9	ADA20003	Ada20003 Novel hum
866	7	1.9	687	5	AAH77047	Aah77047 DNA encod	939	7	1.9	754	9	ADB17386	Adb17386 Human cDN
867	7	1.9	687	5	AAH76262	Aah76262 DNA encod	940	7	1.9	754	9	ADA20175	Ada20175 Novel hum
c 868	7	1.9	687	5	AAH91886	Aah91886 DNA encod	941	7	1.9	754	9	ACD82160	Acd82160 Human sec
c 869	7	1.9	687	12	ADL81821	Adl81821 P. aerugi	942	7	1.9	754	9	ADA00472	Ada00472 Human sec
c 870	7	1.9	689	4	AAK55189	Aak55189 Human imm	943	7	1.9	754	9	ADB85714	Adb85714 Novel hum
c 871	7	1.9	689	5	ABA12883	Abal2883 Human ner	944	7	1.9	754	10	ADB68200	Adb68200 Human PRO
c 872	7	1.9	692	4	AAH06066	Aah06066 Human cDN	945	7	1.9	754	10	ADB91017	Adb91017 Novel hum
c 873	7	1.9	700	4	AAH92694	Aah92694 Human inf	946	7	1.9	754	10	ADC07097	Adc07097 Human PRO
874	7	1.9	700	4	AAH93213	Aah93213 Human inf	947	7	1.9	754	10	ADC17276	Adc17276 cDNA sequ
c 875	7	1.9	700	13	ACN56525	Acn56525 Cotton gy	948	7	1.9	754	10	ADC14974	Adc14974 Novel hum
c 876	7	1.9	701	3	AAH34778	Aah34778 Arabidops	949	7	1.9	754	10	ADC52469	Adc52469 Novel hum
877	7	1.9	702	6	ABK78598	Abk78598 Bacillus	950	7	1.9	754	10	ADG01146	Adg01146 Novel hum
878	7	1.9	703	12	ADQ20103	Adq20103 Human sof	951	7	1.9	754	10	ADG01146	Adg01146 Novel hum
c 879	7	1.9	703	13	ADR5925	Adr5925 Breast ca	952	7	1.9	754	10	ADG08699	Adg08699 Novel hum
c 880	7	1.9	705	8	ACA33296	Ac33296 Prokaryot	953	7	1.9	754	10	ADP95320	Adp95320 Novel hum
881	7	1.9	705	8	ACA33296	Ac33296 Prokaryot	954	7	1.9	754	10	ADH24173	Adh24173 Novel hum

955 7 1.9 754 10 ADH34199 Novel hum
 956 7 1.9 754 10 ADH30032 Novel hum
 957 7 1.9 754 10 ADH24003 Novel hum
 958 7 1.9 754 10 ADG85407 Novel hum
 959 7 1.9 754 10 ADH24683 Novel hum
 960 7 1.9 754 10 ADH37539 Human sec
 961 7 1.9 754 10 ADH02128 Human PRO
 962 7 1.9 754 10 ADH37709 Human sec
 963 7 1.9 754 10 ADG85747 Novel hum
 964 7 1.9 754 10 ADH24343 Novel hum
 965 7 1.9 754 10 ADH38637 Novel hum
 966 7 1.9 754 10 ADH383758 Human PRO
 967 7 1.9 754 10 ADH29566 Novel hum
 968 7 1.9 754 10 ADH27682 Novel hum
 969 7 1.9 754 10 ADH37879 Human sec
 970 7 1.9 754 10 ADH38056 Human sec
 971 7 1.9 754 10 ADH57476 Novel hum
 972 7 1.9 754 10 ADH53618 Novel hum
 973 7 1.9 754 10 ADH53788 Novel hum
 974 7 1.9 754 10 ADH52124 Novel hum
 975 7 1.9 754 10 ADH49979 Novel hum
 976 7 1.9 754 10 ADI25489 Novel hum
 977 7 1.9 754 10 ADH90282 Novel hum
 978 7 1.9 754 10 ADI25659 Novel hum
 979 7 1.9 754 10 ADH97833 Novel hum
 980 7 1.9 754 10 ADI03681 Novel hum
 981 7 1.9 754 10 ADI12038 Human PRO
 982 7 1.9 754 10 ADH90112 Novel hum
 983 7 1.9 754 10 ADH98513 Novel hum
 984 7 1.9 754 10 ADI11188 Human PRO
 985 7 1.9 754 10 ADI11698 Human PRO
 986 7 1.9 754 10 ADH98343 Novel hum
 987 7 1.9 754 10 ADH98683 Novel hum
 988 7 1.9 754 10 ADH98173 Novel hum
 989 7 1.9 754 10 ADI05161 Novel hum
 990 7 1.9 754 10 ADI03511 Novel hum
 991 7 1.9 754 10 ADI04906 Novel hum
 992 7 1.9 754 10 ADH78360 Human PRO
 993 7 1.9 754 10 ADI19704 Novel hum
 994 7 1.9 754 10 ADH90452 Novel hum
 995 7 1.9 754 10 ADI03171 Novel hum
 996 7 1.9 754 10 ADH78020 Human PRO
 997 7 1.9 754 10 ADH98003 Novel hum
 998 7 1.9 754 10 ADI01388 Novel hum
 999 7 1.9 754 10 ADI02083 Novel hum
 1000 7 1.9 754 10 ADI03341 Novel hum

ALIGNMENTS

RESULT 1
 AAZ37836
 ID AAZ37836 standard; DNA; 1260 BP.

XX AC AAZ37836;

XX DT 09-FEB-2000 (first entry)

XX DE Human cyclin I nucleotide sequence.

XX KW Cyclin-dependent kinase 2; CDK2; hsReq; hsReq*-1; hsReq*-2; cyclin I;
 KW ERH; cell cycle; proliferation; cancer; hyperproliferative disorder;
 KW atherosclerosis; tumour; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
 XX CDS 1..1134
 XX FT /*tag= a
 XX FT /product= "Cyclin_I"

XX PN WO9925829-A2.

XX

Adh34199 Novel hum
 Adh30032 Novel hum
 Adh24003 Novel hum
 Adg85407 Novel hum
 Adh24683 Novel hum
 Adh37539 Human sec
 Adh02128 Human PRO
 Adh37709 Human sec
 Adg85747 Novel hum
 Adh24343 Novel hum
 Adh38637 Novel hum
 Adg83758 Human PRO
 Adh29566 Novel hum
 Adh27682 Novel hum
 Adh37879 Human sec
 Adh38056 Human sec
 Adh57476 Novel hum
 Adh53618 Novel hum
 Adh53788 Novel hum
 Adh52124 Novel hum
 Adh49979 Novel hum
 Adi25489 Novel hum
 Adh90282 Novel hum
 Adi25659 Novel hum
 Adh97833 Novel hum
 Adi03681 Novel hum
 Adi12038 Human PRO
 Adh90112 Novel hum
 Adh98513 Novel hum
 Adi11188 Human PRO
 Adi11698 Human PRO
 Adh98343 Novel hum
 Adh98683 Novel hum
 Adh98173 Novel hum
 Adi05161 Novel hum
 Adi03511 Novel hum
 Adi04906 Novel hum
 Adh78360 Human PRO
 Adi19704 Novel hum
 Adh90452 Novel hum
 Adi03171 Novel hum
 Adh78020 Human PRO
 Adh98003 Novel hum
 Adi01388 Novel hum
 Adi02083 Novel hum
 Adi03341 Novel hum

PD 27-MAY-1999.
 XX 12-NOV-1998; 98WO-US024095.
 XX 13-NOV-1997; 97US-00969106.
 XX (CURA-) CURAGEN CORP.
 XX Yang M, Nandabalan K, Schulz VP;
 DR WPI; 2000-061923/05.
 DR P-PSDB; AAY52185.

New complexes of the cyclin-dependent kinase 2 protein with its
 interacting proteins, used to treat, e.g. atherosclerosis.

Example; Fig 2; 90pp; English.

This sequence is the human Cyclin I nucleotide sequence. Cyclin I is
 expressed at almost constant levels throughout the cell cycle, and is
 implicated in controlling cell cycle progression and transcriptional
 control. Cyclins form complexes with cyclin-dependent kinases. CDK2,
 cyclin-dependent kinase 2, is used in the invention which relates to
 complexes of the CDK2 protein with other proteins, selected from cyclin
 I, ERH, hsReq, hsReq*-1 and hsReq*-2 (AAY52185-Y52188). CDK2 is expressed
 late in G1 or early in S phase of the cell cycle, and is pivotal for G1/S
 transition. Compositions containing a CDK2 complex, an antibody targeting
 the complex, and nucleotide sequences encoding CDK2 or its derivatives
 can be used therapeutically. The complexes and their nucleotide sequences
 can be used to treat diseases or disorders associated with increased or
 decreased levels of the complex. Screening the complex, or a derivative
 or a modulator of the complex for neoplastic activity by measuring the
 survival or proliferation of cells from a malignant cell line when in
 contact with the complex can be used to indicate if the the complex has
 anti-neoplastic activity. Screening for molecules that modulate the
 formation of the complexes can be used for treating or preventing
 atherosclerosis or other atherosclerosis-associated disease by contacting cells
 or using a test animal, in which tumour growth or regression is measured
 to test whether anti-neoplastic activity is displayed. Diseases which can
 be treated or prevented by molecule/s which modulate the function of the
 complex include cancer, hyperproliferative disorders and atherosclerosis

Sequence 1260 BP; 352 A; 283 C; 274 G; 351 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 0 Length: 1260
 Score: 377.00 Matches: 377
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 3 Gaps: 0

US-09-736-250-1 (1-377) x AAZ37836 (1-1260)

Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuGluLysAlaIle 20
 Db 1 ATCAAGTTTCAGGGCCCTTGGAAAACACAGAGATTGCTTCTCTGTGGAAAGCGCAATC 60
 Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnAsnVal 40
 Db 61 ACTAGGGAAGACAGATGTGAAGTGAATGTCGGAAATGCCTTCAATACAGAAATGTT 120
 Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTrpGlnPheAsn 60
 Db 121 TCTCCATCCACAGAGATGAAGTAATTCATGGCTGGCCAAACTCAAGTACCAATTCAAC 180
 Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
 Db 181 CTTTACCACAGAAACATTGTCTCTGGCTAGCAGTCTTTTGGTAGTGTATTTAGCTACCCTA 240
 Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaTleSerCysPhePheLeuAlaAlaLys 100
 Db 241 AAGGCTCATCAAAATACTGAGTTGATTGCAATCAGCTGTTTTTCTAGCTGCCAAG 300


```
Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle 20
Db 1 ATGAAGTTTCAGGGCCCTTCGAAAACCCAGAGATTGCTTTCCTGTTGGAAAAGGCAATC 60

Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 61 ACTAGGGAAGCACAGATGTGGAAGTGAATGTGGGAAAATGCCTTCAAAATCAGAAATGTT 120

Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTrpGlnPheAsn 60
Db 121 TCTCCATCCAGAGAGATGAAGTAAATCAATGGCTGGCCAAACTCAAGTACCAATTCAC 180

Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 181 CTTTACCAGAAACATTTGCTCTGGCTAGCAGTCTTTGGATAGTGTTTTAGCTACCGTA 240

Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaAlaLys 100
Db 241 AAGGCTCATCCAAAATACTTGAGTTGTATTGCAATCAGCTGTTTTCCTAGCTGCCAAG 300

Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 301 ACTGTTGAGGAAGATGAGAAATTCAGTACTAAGGTAATGGCAAGACAGATTCTGT 360

Qy 121 GlyCysSerSerSerGluIleLeuArgMetGluArgIleLeuLeuAspLysLeuAsnTrp 140
Db 361 GGATGTTCTCATCTGAATTTTGAGATGGAGAGAAATATTCTGGATAAGTGAATGG 420

Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 421 GATCTTCACACAGCCACACCATGGAATTTCTTCATATTTTCCATGTCATGCGAGTCA 480

Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 481 ACTAGGCTCTAGTACTTTTCAGTTTGGCCAAATGGAGCCCATCTCAACATTTGGCAGTC 540

Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgLys 200
Db 541 CTTACCAAGCAACTACTTCACTGTATGGCTGCAACCAACTCTGCAATTCAGAGGATCC 600

Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
Db 601 ATGCTTGCTCTGGCCATGTTAGTGTGGAATGAGAAACTCAATTCCTGATTGGCTTCT 660

Qy 221 LeuThrIleGluLeuGluLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
Db 661 CTTACAAATTGAACCTCTTCAGAAAGCACAGATGATAGCTCCAGTTGATCCATTTGCGG 720

Qy 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
Db 721 GAGCTTGTGGCACATCACCTTTCTACTCTGCAGTCTTCCCTGCTCTGAATTCGGTTAT 780

Qy 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db 781 GTCTACCGTCCCTCAAGCACACCCCTGGTGACCTGTGCACAAAGGAGTGTTCAGATTACAT 840

Qy 281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
Db 841 CCTTCTCTGTCCAGGCCCGAGCTTCTCCAGGACACACAGCCAGAGTGCAGTC 900

Qy 301 ArgGlyThrAlaAlaPheTyrHisLeuProAlaHisLeuProAlaHisLeuGlnThrSer 320
Db 901 AGAGTACAGCAGCCTTTTACCATCATCTCCAGCTGCCAGTGGGTGCAAGCAGACCTCT 960

Qy 321 ThrLysArgLysValGluGluMetGluValAspAspPheTyrAspGlyIleLysArgLeu 340
Db 961 ACTAAACCAAGTAGAGAAATGGAAGTGATGACCTTCTATGATGGAATCAAAACGGCTC 1020

Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValGlySerGlyThrAspLeuSerArg 360
Db 1021 TATATGAGATATATGTTCTAGAAAATATGTTGGTCTCTGTGTGGCAGCTGATTTATCAGA 1080
```

```
Qy 361 GlnGluGlyHisAlaSerProCysProLeuGlnProValSerValMet 377
Db 1081 CAAGAGGGACATGCTTCCCTTGTCCACCTTTGCAGCTGTTTCTGTCAATG 1131

RESULT 5
ADR25465
ID ADR25465 standard; DNA; 1260 BP.
XX
AC ADR25465;
XX
DT 21-OCT-2004 (first entry)
XX
DE Breast cancer prognosis marker #1326.
XX
KW ds; breast cancer; prognosis; gene expression; diagnosis.
XX
OS Homo sapiens.
XX
FN WO2004065545-A2.
XX
PD 05-AUG-2004.
XX
PF 15-JAN-2004; 2004WO-US001100.
XX
PR 15-JAN-2003; 2003US-00342887.
XX
PA (ROSE-) ROSETTA INPHARMATICS LLC.
PA (NECA-) NETHERLANDS CANCER INST.
XX
PI Van't Veer LJ, He Y;
XX
DR WPI; 2004-593473/57.
XX
```

Classifying a breast cancer patient according to prognosis comprises determining the similarity between the level of expression of each of five genes in a cell sample taken from patient, to control levels.

Disclosure; SEQ ID NO 1326; 226bp; English.

The invention relates to a method of classifying a breast cancer patient according to prognosis by determining the similarity between the level of expression of each of five genes for which markers are listed in the specification, in a cell sample taken from the breast cancer patient, to control levels of expression for each respective five genes to obtain a patient similarity value. The methods are useful for classifying a breast cancer patient according to prognosis. Kits and computer program products are useful for data analysis using the diagnostic, prognostic and statistical methods of the invention. This sequence corresponds to a marker used in the method of the invention.

Sequence 1260 BP; 352 A; 283 C; 274 G; 351 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	0	Length:	1260
Score:	377.00	Matches:	377
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	13	Gaps:	0

US-09-736-250-1 (1-377) x ADR25465 (1-1260)

```
Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuGluLysAlaIle 20
Db 1 ATGAAGTTTCAGGGCCCTTCGAAAACCCAGAGATTGCTTTCCTGTTGGAAAAGGCAATC 60

Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 61 ACTAGGGAAGCACAGATGTGGAAGTGAATGTGGGAAAATGCCTTCAAAATCAGAAATGTT 120

Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTrpGlnPheAsn 60
Db 121 TCTCCATCCAGAGAGATGAAGTAAATCAATGGCTGGCCAAACTCAAGTACCAATTCAC 180
```

```

Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 181 CTTTACCAGAAACATTTGCTCGGTAGCAGTCTTTGGATAGTGTTCCTAGTACCGTA 240
Qy 81 LysAlaHisProLysTyrLeuSerCysAlaIleLeuSerCysPhePheLeuAlaAlaLys 100
Db 241 AAGGCTCATCCAAATACCTGAGTGTATTCGAATCAGCTGTTTTCTAGTGCACAAG 300
Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 301 ACTGTTGAGGAGAGATGAGAGATTCAGTACTAAGGTATTTGGCAAGACAGATTTCTGT 360
Qy 121 GlyCysSerSerSerGluLeuLeuArgMetGluArgIleLeuLeuAspLysLeuAsnTrp 140
Db 361 GGATGTTCTCATCTGAAATTTTGAGATGAGAGATTTATTCGGATAGTGAATGG 420
Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 421 GATCTTCACAGCCACACCATTGATTTCTTCATATTTTCCATGTCATTCGAGTGTCA 480
Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 481 ACTAGGCTCAGTTACTTTTCAGTTGGCCAAATGAGCCCATCTCAACATTTGCGAGTC 540
Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
Db 541 CTTACCAAGCAACTACTTCTGATGATGCGCTGCAACCAACTCTGCAATTCAGAGGATCC 600
Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
Db 601 ATGCTTGCTCGGCCATGTTAGTGTGGAATGAGAACTCAATTCCTGATGCTTCT 660
Qy 221 LeuThrIleGluLeuGlnLysAlaGlnMetAspSerSerGlnLeuLeuHisCysArg 240
Db 661 CTTCAATGTAACCTCTCAGAAAGCAGATGATAGCTCCAGTTGATCATTTGTCGG 720
Qy 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
Db 721 GAGCTTGTGGCACATCCTTTCTACTCTGCGCTCTCCCTGCTGCAATTCGCTTTAT 780
Qy 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db 781 GTCTACCGTCCCTCAAGCACACCCCTGCTGACCTGTGCAAAAGGAGTGTTCAGATTAAT 840
Qy 281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
Db 841 CCTCCTCTGTCAGGCCAGACTTCTCAGGACAAAGCAGCAAGCCCAAGTGCAGTC 900
Qy 301 ArgGlyThrAlaAlaPheTyrHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
Db 901 AGAGTACAGCAGCGCTTTTACCATCATCTCCAGCTGCGAGTGGTGCAGCAGACCTCT 960
Qy 321 ThrLysArgLysValGluGluMetGluValAspAspPheTyrAspGlyIleLysArgLeu 340
Db 961 ACTAAACCAAGTAGAGGAAATGGAAGTGAATGATCTTCTATGATGGAATCAAAAGGCTC 1020
Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
Db 1021 TATATGAGATAATGTTCTCAGAAATGTTGGTCTGTGTGGCAGCTGATTTATCAAGA 1080
Qy 361 GlnGluGlyHisAlaSerProCysProLeuGlnProValSerValMet 377
Db 1081 CAAGAGGCAGATGCTTCCCTTGTCCACCTTTGCGACCTGTTCTGTCTCATG 1131

```

RESULT 6

AAT73937

ID AAT73937 standard; DNA; 1328 BP.

XX AC

XX AAT73937;

XX DT

02-DEC-1997 (first entry)

XX

```

DE DNA encoding human cyclin I.
XX human; cyclin I; antisense; probe; neurone; cancer; antibody; ds.
XX Homo sapiens.
XX Key Location/Qualifiers
XX CDS 69..1202
XX /*tag= a
XX
XX W09712973-A1.
XX PN 10-APR-1997.
XX PD
XX PF 07-OCT-1996; 96WO-JP002905.
XX PR 05-OCT-1995; 95JP-00284663.
XX (SUME ) SUMITOMO ELECTRIC IND CO.
XX Nakamura T;
XX WPI; 1997-226217/20.
XX P-PSDB; AAW21965.
XX
XX Human cyclin I protein and related (anti:sense) DNA - used for neuron
XX labelling method and cancer cell detection.
XX Example 1; Fig 1; 45pp; Japanese.
XX
XX This sequence encodes human cyclin I. Antisense polynucleotides are
XX useful for as probes and can be labelled and used for detection of
XX neurones by hybridisation with mRNA for cyclin I (contained in the
XX cells). The gene can be used for detection of cancer cells by detecting
XX the expression of the cyclin I gene in these cells. Also antibodies
XX specific for the fragments of the protein (especially AAW21966) can be
XX used for detection
XX
XX Sequence 1328 BP; 376 A; 292 C; 302 G; 358 T; 0 U; 0 Other;

```

Alignment Scores:

```

Pred. NO.: 0 Length: 1328
Score: 377.00 Matches: 377
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

```

US-09-736-250-1 (1-377) x AAT73937 (1-1328)

```

Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuGluLysAlaIle 20
Db 69 ATGAAGTTTCAGAGGCCCTTTGGAAACACAGAGATGCTTCTTCCTGTTGGAAAGGCAATC 128
Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 129 ACTAGGGAAGCACAGATGTGGAAGTGAATGTGCGGAAATGCCTTCAATCAGAAATGTT 188
Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn 60
Db 189 TCTCCATCCCAGAGAGATGAAGTAATTCAATGGTGGCCCAACTCAAGTACCAATTCAAC 248
Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 249 CTTTACCAGAAACATTTGCTCGTAGCAGTCTTTTGGATAGTGTTCCTAGTACCGTA 308
Qy 81 LysAlaHisProLysTyrLeuSerCysAlaIleLeuSerCysPhePheLeuAlaAlaLys 100
Db 309 AAGGCTCATCCAAATACCTGAGTTGATTTGCAATCAGCTGTTTTTCTAGTGCACAAG 368
Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120

```

```
Db 369 ACTGTTAGGAGATGAGAGAAATCCAGTACTAAAGGTATTGGCAAGACAGATTTCTGT 428
Qy 121 GlyCysSerSerGluLeuLeuArgMetGluArgGilelleLeuAspLysLeuAsnTrp 140
Db 429 GGATGTTCTCATCTGAATTTTGGATGAGAGAAATATTCTGGATAAGTTGATGG 488
Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 489 GATCTTCACAGCCACACCATGATTTCTTCATATTTTCCATGTCATTCAGTGTC 548
Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 549 ACTAGGCTCAGTTACTTTTCTGTTGCCCCAAATGAGCCCATCTCAACATTTGGCAGTC 608
Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
Db 609 CTTACCAAGCACTACTTTCATGTATGCTGCTGCAACCACTTCTGCAATTCAGAGGATCC 668
Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
Db 669 ATGCTTGCTCTGGCCATGCTTAGTCTGGAATGGAGAACTCATTCCTGATTGGCTTCT 728
Qy 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuLeuHisCysArg 240
Db 729 CTTCAATTTGAATGCTTTTCAGAAAGCACAGATGATAGTCTCCAGTTGATCCATTTGCGG 788
Qy 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
Db 789 GAGCTTGCGGCATCATCTTCTACTCTGCTGAGTCTTCCCTGCTCTGAATTCGGTTAT 848
Qy 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db 849 GTCTACCGTCCCTCAAGCACACCTGCTGACCTGTGACAAAGGAGTCTTCAGATTACAT 908
Qy 281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
Db 909 CCTTCCTCTGTCAGGCGCAGACTTCTCCAAAGACACACAGCAAGCCAGAGTGCAGTC 968
Qy 301 ArgGlyThrAlaAlaPheTyrHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
Db 969 AGAGTCACAGCAGCCTTTTACCATCATCTCCAGCTGCCAGTGGTGCACAGACCTCT 1028
Qy 321 ThrLysArgLysValGluGluMetGluValAspAspPheTyrAspGlyIleLysArgLeu 340
Db 1029 ACTAAACCAAGATAGAGAAATGAGTGGATGACTTCTATGATGGAATCAAAACGGCTC 1088
Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
Db 1089 TATTAATGAAGATAATGCTCAGAAATGTGGTCTCTGTGTGGCAGTATTTATCAAGA 1148
Qy 361 GlnGluGlyHisAlaSerProCysProProLeuGlnProValSerValMet 377
Db 1149 CAAGAGGACATGCTTCCCTTGTCCACCTTTGAGCCTGTTCTGTGTCATG 1199
```

RESULT 7

ACC47339
ID ACC47339 standard; cDNA; 1384 BP.

XX AC
XX AC
XX ACC47339;

DT 11-AUG-2003 (first entry)

DE Human prostate selective polynucleotide Pr325.

XX KW Prostate; molecular marker; cancer; cytostatic; gene therapy; human;
XX KW gene; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
XX CDS 200..1333
/*tag= a

FN WO2003014298-A2.
XX 20-FEB-2003.
XX 02-AUG-2002; 2002WO-US024431.
XX 03-AUG-2001; 2001US-0309470P.
PR 30-OCT-2001; 2001US-0330747P.
XX (ORIG-) ORIGENE TECHNOLOGIES INC.
XX Sun Z, Li X, Jay G, Kovacs KF, Shu Y, Fan W;
FI WPI; 2003-256562/25.
DR P-PSDB; ABR39934.
XX New polynucleotide, useful for preparing a composition for treating
PT prostate disease, e.g., cancer.
XX Claim 1; Page 147-149; 212pp; English.
XX The invention relates to prostate selective polynucleotides and
CC polypeptides. The polynucleotides are expressed in prostate and are
CC useful as molecular markers, as drug targets, and for detecting,
CC monitoring, preventing or treating diseases and conditions related to
CC prostate, such as prostate cancers. Sequences ACC47325-356 represent
CC specific examples of prostate specific polynucleotides
XX
SQ Sequence 1384 BP; 364 A; 329 C; 324 G; 367 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0 Length: 1384
Score: 377.00 Matches: 377
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-09-736-250-1 (1-377) x ACC47339 (1-1384)

Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuGluLysAlaIle 20
Db 200 ATGAAGTTTCAGGGCCTTTGGAAACACAGAGATTGCTTTCCCTGTGGAAAGCGCAATC 259
Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 260 ACTAGGAGACACAGATGTGGAAGTCAATGTGGGAAATGCCTTCAATCAGATGTT 319
Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn 60
Db 320 TCTCCATCCCAGAGAGATGAATTAATCAATGGCTGGCCAAACTCAAGTACCAATTCAAC 379
Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 380 CTTTACCAGAAACATTTGCTTGGCTAGCAGTCTTTTGGATAGTGTTTTAGCTACCGTA 439
Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaAlaLys 100
Db 440 AAGGCTCATCCAAATACTTGGATTGTATTGCAATCAGCTGTTTTTCTAGTGCCCAAG 499
Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 500 ACTGTTGAGGAAGATGAGAGAAATTCAGTACTAAAGGTATTGGCAAGAGACAGATTTCTGT 559
Qy 121 GlyCysSerSerGluIleLeuArgMetGluArgIleIleLeuAspLysLeuAsnTrp 140
Db 560 GGATGTTCTCATCTGAAATTTTGGAAATGAGAGAAATATTCTGGATAAGTTGAAATGG 619
Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 620 GATCTTCACAGCCACACCATGATTTCTTCATATTTTCCATGTCATTTGCAAGTGTCA 679
Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180

Db 680 ACTAGGCTCAGTACTTTTTCAGTTTGCCAAATAGCCCATCTCAACATTTGGCAGTC 739
Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgLysSer 200
Db 740 CTTACCAAGCAACTACTTCTACCTGTATGCGCTGCAACCAACTTCTGCAATTCAGAGGATCC 799
Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuLeuPheAspTrpLeuSer 220
Db 800 ATGCTTGCTCTGGCCATGCTGTAGTCTGGAAATGGAGAAACTCATTCCTGATTTGGCTTTCT 859
Qy 221 LeuThrLysGlnLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuLeuHisCysArg 240
Db 860 CTTACAATGAACTGCTTCAGAACACAGATGATGATCTCCAGTTGATCATTTGTCGG 919
Qy 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
Db 920 GAGCTTGTGGCACATCACCTTTCTACTCTGCAGTCTTCCCTGCCTCTGAATTCGGTTTAT 979
Qy 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db 980 GTCTACCGTCCCTCAAGCACACCCCTGTGTGACCTGTGACAAAGGAGTCTTCAGATTACAT 1039
Qy 281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
Db 1040 CCTCTCTCTGCCAGGCCAGACTTCTCCAGGACAAACAGCAAGCCAGAAAGTGCAGTC 1099
Qy 301 ArgGlyThrAlaAlaPheTyrHisHisLeuProAlaLaserGlyCysLysGlnThrSer 320
Db 1100 AGAGGTACAGCAGCCTTTTACCATCATCTCCAGCTGCCAGTGGTGCAAGCAGACCTCT 1159
Qy 321 ThrLysArgLysValGluGluMetGluValAspAspPheTyrAspGlyLysLysArgLeu 340
Db 1160 ACTAAACGCAAGTAGAGGAAATGGAAGTGGATGACTTCTATGATGGAATCAAAACGGCTC 1219
Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
Db 1220 TATAATGAAGATAATGTCTCGAAATAATGGGTTCTGTGTGGCAGCTGTTCTGTCTCATG 1279
Qy 361 GlnGluGlyHisAlaSerProCysProProLeuGlnProValSerValMet 377
Db 1280 CAAGAGGACATGCTTCCCTTGTCCACTTTCAGCTTTCAGCTTTCAGCTTTCAGT 1330

RESULT 8

ID ABL87929
XX ABL87929 standard; DNA; 1889 BP.
XX AC ABL87929;
XX DT 17-MAY-2002 (first entry)
XX DE Human ovarian cancer related DNA clone SEQ ID NO:10907.
XX DE Human; ovarian cancer; ovarian tumour; cytostatic; gene; ds.
XX OS Homo sapiens.
XX PN WO200192581-A2.
XX PD 06-DEC-2001.
XX PF 29-MAY-2001; 2001WO-US017756.
XX PR 26-MAY-2000; 2000US-0207484P.
XX PA (CORI-) CORIXA CORP.
XX PI Algate PA, Harlocker SL, Jones R;
XX DR WPI; 2002-122075/16.
XX PT Composition for therapy and diagnosis of ovarian cancer comprising polypeptide of a ovarian tumor polypeptide, polynucleotide encoding

PT polypeptide, antibody specific to polypeptide or T cell expressing polypeptide.

XX Claim 1; SEQ ID NO 10907; 489pp; English.

XX The present invention describes a composition (I) comprising: carriers and immunostimulants; and a polypeptide (II) of an ovarian tumour polypeptide encoded by a polynucleotide (III) having a cDNA sequence (S1) from the 10912 nucleotide sequences as given in ABL77023 to ABL87934, (III) encoding (II) having a sequence (S2), a T cell population of (II), or antigen presenting cells that express (II). (I) has cytostatic activity. An oligonucleotide (IV) that hybridises to (S1) can be used for detecting ovarian cancer in a patient's biological sample preferably serum or ovarian tissue. The method comprises contacting a biological sample from a patient with (IV), detecting the amount of polynucleotide hybridising to (IV) and comparing the amount to a predetermined cutoff value and thereby detecting ovarian cancer in the patient, where the amount of polynucleotide hybridising to (IV) is detected preferably by polymerase chain reaction (PCR). (I) comprising (III) and/or (II) is useful for stimulating and/or expanding T cells specific for an ovarian tumour protein comprising contacting T cells with (III) or (II). (III) is useful in design and preparation of ribozyme molecules for inhibiting expression of the tumour polypeptides and proteins in tumour cells; and to isolate a full length gene from a suitable library e.g., a tumour cDNA library using well known techniques

SQ Sequence 1889 BP; 473 A; 501 C; 436 G; 479 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0 Length: 1889
Score: 377.00 Matches: 377
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-736-250-1 (1-377) x ABL87929 (1-1889)

Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuGluLysAlaIle 20
Db 544 ATGAAGTTTCAGGGCCTTTGGAAACACAGAGATTGCTTCTTCTGTTGAAAGGCAATC 603
Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 604 ACTAGGGAAGCACAGATGTGGAAAGTGAATGTGGGAAAATGSCCTTCAATCAGAATGTT 663
Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn 60
Db 664 TCTCCATCCCAGAGAGATGAAGTAATTCATGGCTGGCCAAACTCAAGTCAATTCAC 723
Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 724 CTTTACCAGAAACATTTGCTCTGGCTAGCAGTCTTTTGGATAGTGTTCAGTACCGTA 783
Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaLys 100
Db 784 AAGGCTCATCCAAATACTTTCAGTTGTATTTCATCAATCAGCTGTTTTTCTAGTGCACAG 843
Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 844 ACTGTTGAGGAAGATGAGAGAAATTCAGATCTAAGGTAATTTGGCAAGAGACAGTTTCTGT 903
Qy 121 GlyCysSerSerSerGluIleLeuArgMetGluArgIleIleLeuAspLysLeuAsnTrp 140
Db 904 GGATGTTCTCATCTGAAATTTTGGAAATGAGAGAAATTTCTGGATAGTTGATTTGG 963
Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 964 GATCTTCACAGCAGCCACCATTTGATTTCTTCATATTTTCCATTTTCCATGTCAGTGCA 1023
Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 1024 ACTAGGCTCAGTTACTTTTTCAGTTTGGCCAAATTTGAGCCCATCTCAACATTTGGCAGTC 1083

```
QY 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgLysSer 200
DB 1084 CTTACCAAGCAACTACTTCACTGATGATGCGTCCACCAACTCTGCAATTCAGAGGATCC 1143
QY 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuLeuProAspTrpLeuSer 220
DB 1144 ATGCTTGCTGCGCATGTTAGTCTGGAATGGAGAACTCAATTCCTGATGGCTTCT 1203
QY 221 LeuThrLleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuLleHisCysArg 240
DB 1204 CTTCAATTTGAATGCTTTCAAGAAACAGATGGATAGTCTCCAGTTGATCCATTTGTCGG 1263
QY 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
DB 1264 GAGCTTGTGGACATCACTTTCTACTCTGAGCTTCCCTGCCCTCGAATTCGGTTAT 1323
QY 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
DB 1324 GTCTACCGTCCCTCAAGCACACCCCTGGTGCACCTGTGACAAAGGAGTGTTCAGATTACAT 1383
QY 281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
DB 1384 CCCTCTCTGTCGCCAGGCCGAGACTTCTCCAGGACAAACAGACCCAGAGTCCAGTCC 1443
QY 301 ArgGlyThrAlaAlaPheTyrHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
DB 1444 AGAGGTACAGCAGCTTTTACCATCATCTCCAGCTGCAGTGGGTGCAAGCAGACTCT 1503
QY 321 ThrLysArgLysValGluGluMetGluValAspAspPheTyrAspGlyLleLysArgLeu 340
DB 1504 ACTAAACGCAAAAGTAGAGAAATGGAAGTGGATGATCTTCTATGATGGAATCAAACGGCTC 1563
QY 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLysSerArg 360
DB 1564 TATATGAGGATAATGTCTCAAGAAATGTGGTCTCTGTGTGGCAGCTGATTTATCAAGA 1623
QY 361 GlnGluGlyHisAlaSerProCysProLeuGlnProValSerValMet 377
DB 1624 CAAGAGGACATGCTTCCCTTGTCACCTTTGACAGCTGTTCTGTGTCATG 1674

RESULT 9
ADP10653
ID ADP10653 standard; DNA; 1890 BP.
AC ADP10653;
XX
XX
DT 12-AUG-2004 (first entry)
XX
DE Reference mRNA sequences for marker probe #330.
XX
KW transplant rejection; immune system; rheumatoid arthritis; lupus;
XX inflammatory bowel disease; multiple sclerosis; HIV; AIDS; ss.
XX
OS Homo sapiens.
XX
PN WO2004042346-A2.
XX
PD 21-MAY-2004.
XX
PF 24-APR-2003; 2003WO-US012946.
XX
XX 24-APR-2002; 2002US-00131831.
PR 20-DEC-2002; 2002US-00325899.
XX
XX (EXPR-) EXPRESSION DIAGNOSTICS INC.
PA
XX Wohlgenuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;
PI Rosenberg S;
PI
DR WPI; 2004-400724/37.
XX
PT Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,
```

```
PT pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
PT rejection, in an individual, comprises detecting the expression level of
PT the genes.
XX
PS Claim 80; SEQ ID NO 662; 1762pp; English.
XX
XX The present invention relates to diagnosing or monitoring transplant
CC rejection, e.g. cardiac or kidney transplant rejection, in an individual
CC comprises detecting the expression level of one or more genes. The
CC methods, system and kits are useful in diagnosing or monitoring
CC transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
CC islet, lung, bone marrow or stem cell transplant rejection,
CC xenotransplant rejection or mechanical organ replacement rejection, in an
CC individual. The method is also useful in assessing the immune status of
CC diseases that involve the immune system, e.g. rheumatoid arthritis,
CC lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
CC viral, bacterial or fungal infection. The present sequence represents a
CC mRNA reference sequence for a 50 mer oligonucleotide marker for diagnosis
CC and monitoring of allograft rejection and other disorders.
XX
SQ Sequence 1890 BP; 473 A; 501 C; 436 G; 480 T; 0 U; 0 Other;
```

```
Alignment Scores:
Pred. NO.: 0 Length: 1890
Score: 377.00 Matches: 377
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0
```

US-09-736-250-1 (1-377) x ADP10653 (1-1890)

```
QY 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuGluLysAlaIle 20
DB 545 ATGAAGTTTCAGGGCCTTTGGAAACACAGAGATTGCTTTCCCTGTTGGAAAGCGCAATC 604
QY 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
DB 605 ACTAGGAGNAGCACAGATGTGGAAAGTGAATGTGGGAAATGCCTTCAATCAGATGTT 664
QY 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn 60
DB 665 TCTCCATCCCAGAGAGATGAATTAATCAATGGCTGGCCAACTCAAGTACCAATTCAC 724
QY 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
DB 725 CTTTACCCAGAAACATTTGCTCTGGCTAGCAGTCTTTTGGATAGGTTTTTAGCTACCGTA 784
QY 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaAlaLys 100
DB 785 AAGGCTCATCCAAATACTTGGATTGTATTGCATCAGCTGTTTTTCTAGCTGCCAAG 844
QY 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
DB 845 ACTGTTGAGGAAGATGAGAGAAATCCAGTACTAAAGGTATTGGCAAGAGACAGATTTCTGT 904
QY 121 GlyCysSerSerSerGluLleLeuArgMetGluArgIleIleLeuAspLysLeuAsnTrp 140
DB 905 GGATGTTCTCATCTGAAATTTTGAGAAATGGAGAAATATTCTGGATAAGTTGAATTTGG 964
QY 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
DB 965 GATCTTCACACAGCCACACCATTTGATTTCTTCATATTTTCCATGTCATTCAGTGTCA 1024
QY 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
DB 1025 ACTAGGCTCAGTTACTTTTTCAGTTTGCCTTGCCTTGCCTTGCCTTGCCTTGCCTTGC 1084
QY 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgLysSer 200
DB 1085 CTTACCAAGCAACTACTTCACTGATGCTTGCCTTGCCTTGCCTTGCCTTGCCTTGCCTTGC 1144
```


Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuLeuProAspTrpLeuSer 220
Db |||||
1145 ATGCTTGCTCTGGCCATGGTAGTCTGGAATGGAGAAACCATCTCCGATGGCTTTCT 1204
Qy 221 LeuThrIleGluLeuGlnLysAlaGlnMetAspSerSerGlnLeuLeuHisCysArg 240
Db |||||
1205 CTTACAAATGAACGTCTTCAGAAAGCAGATGGATAGTCCAGTTGATCCATTTGCGG 1264
Qy 241 GluLeuValAlaHisHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
Db |||||
1265 GAGCTTGTGGCACATCACCCTTCTACTCTGCAGTCTCCCTGCCTCTGAATTCGGTTAT 1324
Qy 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db |||||
1325 GTCTACCTGCCCCCTCAACACACCCCTGTGTGACCTGTGACAAAGGAGTGTTCAGATTAT 1384
Qy 281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
Db |||||
1385 CCTCTCTGTCCAGGCCAGACTTCTCCAAAGCACAACAGCCAGAGTGCAGTC 1444
Qy 301 ArgGlyThrAlaAlaPheTyrHisHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
Db |||||
1445 AGAGGTACAGCAGCCCTTTTACCATCATCTCCAGCTGCAGTGGGTGCAAGCAGACCTCT 1504
Qy 321 ThrLysArgLysValGluGluMetGluValAspPheTyrAspGlyLysArgLeu 340
Db |||||
1505 ACTAAACCAAGTAGAGAAATGGAAGTGATGACTTCTATGATGGAAATCAACGGGCTC 1564
Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLysSerArg 360
Db |||||
1565 TATATGAAGATAATGCTTCAGAAATGTGGTCTGTGTGGCACTGATTTATCAAGA 1624
Qy 361 GlnGluGlyHisAlaSerProCysProProLeuGlnProValSerValMet 377
Db |||||
1625 CAAGAGGACATGCTTCCCTTGTCCACCTTTGCACCTTGTTCGATGTCATG 1675

RESULT 10

ACN38124
ID ACN38124 standard; cDNA; 1890 BP.
AC ACN38124;
XX
XX 18-NOV-2004 (first entry)
XX
XX Tumour-associated antigenic target (TAT) cDNA DNA324488, SEQ ID NO:1449.
DE
XX Tumour-associated antigenic target; TAT; human; overexpression; cancer;
KW tumour; diagnosis; cell proliferative disorder; breast cancer;
KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;
KW central nervous system cancer; bladder cancer; pancreatic cancer;
KW cervical cancer; melanoma; leukaemia; hybridisation probe;
KW chromosome identification; chromosome mapping; gene mapping;
KW gene therapy; cytostatic; gene; ss.
XX
OS Homo sapiens.
XX
XX WO2004030615-A2.
XX
XX 15-APR-2004.
XX
XX 29-SEP-2003; 2003WO-US028547.
XX
XX 02-OCT-2002; 2002US-0414971P.
XX
XX (GETH) GENENTECH INC.
XX
XX Wu TD, Zhang Z, Zhou Y;
XX WPI; 2004-347921/32.
XX P-PSDB; ABM80569.
XX
XX New tumor-associated antigenic target polypeptides and nucleic acids,
PT useful in preparing a medicament for treating or detecting a

PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or
PT prostate cancer or tumor.

FS Claim 1; SEQ ID NO 1449; 7273pp; English.

XX The invention relates to human tumour-associated antigenic target (TAT)
CC polypeptides, and their related nucleic acids. The TAT polypeptides are
CC overexpressed in cancer tissues compared to normal tissues, and may thus
CC serve as effective targets for the diagnosis and treatment of cancer in
CC mammals. The invention also relates to nucleic acid and polypeptide
CC sequences at least 80% identical to the TAT nucleic acids and
CC polypeptides; expression vectors and host cells comprising a TAT nucleic
CC acid; an antibody specific for a TAT polypeptide; a peptide or organic
CC molecule which binds to a TAT polypeptide; fusion proteins comprising a
CC TAT polypeptide; and methods and compositions for the treatment or
CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
CC antibodies, antagonists, binding molecules and compositions are useful
CC for diagnosing or treating a cell proliferative disorder associated with
CC increased TAT expression, particularly cancers such as breast cancer,
CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
CC cancer, pancreatic cancer, cervical cancer, cancers of the central
CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be
CC used as hybridisation probes, in chromosome and gene mapping, in
CC chromosome identification and in gene therapy. The present sequence
CC represents a TAT nucleic acid of the invention

SQ Sequence 1890 BP; 473 A; 501 C; 436 G; 480 T; 0 U; 0 Other;

Alignment Scores:

Pred No.: 0 Length: 1890
Score: 377.00 Matches: 377
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-09-736-250-1 (1-377) x ACN38124 (1-1890)

Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle 20
Db 545 ATGAAGTTTCAGGGCCCTTTGGAAACACAGAGATTGCTTTCTCTGTGGAAAGGCAATC 604
Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGluAsnVal 40
Db 605 ACTAGGAAGACACAGATGTGGAAAGTGAATGTGGCAAAATGCCTTCAATCAGAAATGTT 664
Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn 60
Db 665 TCTCATCCACAGAGATGAAGTAAATTCATGGTGGCCAAACTCAAGTACCAATTCAC 724
Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 725 CTTTACCAGAAACATTTGCTCTGGTAGCAGTCTTTGGATAGTGTTTTAGCTACCGTA 784
Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaLys 100
Db 785 AAGCTCATCCAAATATCTTGAGTTGATTGCAATCAGCTGTTTTTCTAGCTGCCAAG 844
Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 845 ACTGTTGAGGAGATGAGAGNATTCAGTACTAAGGTATTGGCAGAGACAGATTTCTGT 904
Qy 121 GlyCysSerSerGluIleLeuArgMetGluArgIleIleLeuAspLysLeuAsnTrp 140
Db 905 GGATGTTCTCATCTGAAATTTTTCAGAAATGAGAGAAATTTCTGGATAAGTGAATTTGG 964
Qy 141 AspleuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 965 GATCTTCACAGCACACCATTCGATTTTCTTCATATTTTCCATGCAATTCGAGTGCA 1024
Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 1025 ACTAGGCTCAGTTACTCTTTTCAGTTTGCCTCCCAATTTGAGCCCATCTCAACATTTGGCAGTC 1084


```
Db 538 AGGCTCAGTTACTTTTTCAGTTTCCCAAAATGAGCCCATCTCAACATTTGGCAGTCCTT 597
Qy 182 ThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySerMet 201
Db 598 ACCAAGCACTACTTCTACTGTATGGCTGCAACCACTTCTGCATTCAGAGGATCCATG 657
Qy 202 LeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuLeuProAspTyrLeuSerLeu 221
Db 658 CTTGCTCTGGCCATGGTGTAGTCTGGAATGAGAAACTCATCTCGATTGGCTTCTCTT 717
Qy 222 ThrLeuGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuLeuHisCysArgGlu 241
Db 718 ACAATTGAATGCTTTCAGAAAGCAGATGATAGCTCCCACTGATTCATTCGCGGAG 777
Qy 242 LeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyrVal 261
Db 778 CTTGTGGCAGCATCACCCTTCTACTCTGAGTCTTCCCTGCTCTGATTCGGTTATGTC 837
Qy 262 TyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHisPro 281
Db 838 TACCGTCCCTCAAGCACACCCCTGGTACCTGTGACAAAGGAGTGTTCAGATTACATCCC 897
Qy 282 SerSerValProGlyProAspPheSerLysAspSerLysProGluValProValArg 301
Db 898 TCCTCTGTGCCAGCCAGACTTCTCCAAAGGACACAGCAGCAGAGTCCAGTCAGA 957
Qy 302 GlyThrAlaAlaPheTyrHisHisLeuProAlaSerGlyCysLysGlnThrSerThr 321
Db 958 GGTACAGCAGCCTTTTACCATCATCTCCAGCTGCCAGTGGGTGCAAGCAGCCTCTACT 1017
Qy 322 LysArgLysValGluGluMetGluValAspPheTyrAspGlyLeuLysArgLeuTyr 341
Db 1018 AAACGCAAGTAGAGGAAATGGAAGTGGATGACTTCTATGATGGAATCAAAACGGCTCTAT 1077
Qy 342 AsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArgGln 361
Db 1078 AATGAAGATAATGTCTCAGAAATGTGGGTCTGTGTGTGCACTGATTTATCAAGCAA 1137
Qy 362 GluGlyHisAlaSerProCysProLeuGlnProValSerValMet 377
Db 1138 GAGGACATGTTTCCCTTGTCCACCTTGGAGCCTGTTTCTGTCTCATG 1185
```

RESULT 12

ADL63374
ID ADL63374 standard; DNA; 2755 BP.

AC ADL63374;

XX 20-MAY-2004 (first entry)

XX Human ovarian cancer DNA marker #21586.

XX Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.

XX Homo sapiens.

XX WO200170979-A2.

XX 27-SEP-2001.

XX 21-MAR-2001; 2001WO-US009126.

XX 21-MAR-2000; 2000US-0191031P.

XX 25-MAY-2000; 2000US-0207124P.

XX 15-JUN-2000; 2000US-0211940P.

XX 07-JUL-2000; 2000US-0216820P.

XX 25-JUL-2000; 2000US-0220661P.

XX 21-DEC-2000; 2000US-0257672P.

XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX Lee J, Lillie J;

XX WPI; 2001-611502/70.

XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian cancer cells as compared to their normal non-cancerous ovarian cells are used to characterize stage, grade, histological type of ovarian cancer.

XX Disclosure; SEQ ID NO 21586; 106pp; English.

XX The invention relates to nucleic acid markers which are overexpressed in ovarian cancer cells as compared to their expression in normal (i.e. non-cancerous) ovarian cells. The invention also relates to polypeptides encoded by the markers, antibodies that selectively bind to the polypeptides, a method of inhibiting ovarian cancer in a patient at risk of developing ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a patient afflicted with ovarian cancer comprising providing to cells of the patient an antisense oligonucleotide complementary to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer, which involves comparing the level of expression of a marker in a patient sample and a normal level of expression of the marker in a control non-ovarian cancer sample. A difference between the expression levels indicates ovarian cancer. The level of expression of a marker corresponds to a secreted protein or to a transcribed polynucleotide or its portion. The level of expression of the marker is assessed by detecting the presence in the sample, a protein or protein fragment corresponding to the marker. The presence of protein or protein fragment is detected using an antibody that specifically binds with the protein or protein fragment. Alternatively, the level of expression of the marker is assessed by detecting the presence of a transcribed polynucleotide which anneals with the marker or anneals with a portion of the polynucleotide comprising the marker, under stringent conditions. The marker is also used for monitoring the progression of ovarian cancer in a patient which involves detecting expression of the marker in a patient sample at a first point in time, repeating the method at a subsequent time and comparing the level of expression. The method is carried out using an ovarian tissue sample. A composition comprising a marker, polypeptide or antibody of the invention is used to treat ovarian cancer. This sequence represents a human ovarian cancer DNA marker of the CC invention.

XX Sequence 2755 BP; 749 A; 673 C; 606 G; 727 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.55e-250 Length: 2755
Score: 266.00 Matches: 266
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 70.56% Indels: 0
DB: 5 Gaps: 0

US-09-736-250-1 (1-377) x ADL63374 (1-2755)

Qy 103 GluGluAspGluArgLysProValLeuLysValLeuAlaArgAspSerPheCysGlyCys 122
Db 1099 GAGGAAGATGAGAGAATTCAGACTACTAAAGGTATGGCAGAGACAGTTCCTGTGGATGT 1158
Qy 123 SerSerSerGluLeuLeuArgMetGluArgLysLeuAspLysLeuAsnTrpAspLeu 142
Db 1159 TCCTCATCTGAATTTTGAGATGGAGAGAATATTCTGGATAAGTTGAATGGATCTT 1218
Qy 143 HisThrAlaThrProLeuAspPheLeuHisLysPheHisAlaLysLysSerThrArg 162
Db 1219 CACACAGCCACACCATTTGATTTCTCATATTTTCCATTTCCCATTTGCAAGTCACTAGG 1278
Qy 163 ProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaValThr 182
Db 1279 CCTCAGTTACTTTTTCAGTTTGGCCCAATTCAGCCATCTCAACATTTGGCAGTCTTACC 1338
Qy 183 LysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuGlnPheArgGlySerMetLeu 202
Db 1339 AAGCACTACTTCTACTGTATGGCTGCAACCACTTCTGCAATTCAGAGGATCCATGCTT 1398


```

Db      422 GATCTTCACAGCCACACACCATGGATTCTTCATATT 460
|||||
RESULT 14
AAC01909
ID      AAC01909 standard; cDNA; 444 BP.
XX
AC      AAC01909;
XX
XX      06-OCT-2000 (first entry)
XX
DT      Human secreted protein 5' EST, SEQ ID NO: 1907.
XX
DE      Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW      gene therapy; chromosome mapping; ss.
XX
XX      Homo sapiens.
XX
XX      EP1033401-A2.
XX
XX      06-SEP-2000.
XX
XX      21-FEB-2000; 2000EP-00200610.
XX
XX      26-FEB-1999; 99US-0122487P.
XX
XX      (GSEST ) GENSET.
XX
XX      Dumas Milne Edwards J, Duclert A, Giordano J;
XX
XX      WPI; 2000-500381/45.
XX
XX      P-PSDB; AAG01903.
XX
XX      New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT      obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT      diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX
XX      Claim 1; SEQ ID NO 1907; 71pp + Sequence Listing; English.
XX
XX      The present sequence is one of a large number of 5' ESTs derived from
CC      mRNAs encoding secreted proteins. An ORF has been identified within the
CC      sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs
CC      derived from 30 different tissues. EST sequences usually correspond
CC      mainly to the 3' untranslated region (UTR) of the mRNA because they are
CC      often obtained from oligo-dT primed cDNA libraries. Such ESTs are not
CC      well suited for isolating cDNA sequences derived from the 5' ends of
CC      mRNAs and even in those cases where longer cDNA sequences have been
CC      obtained, the full 5' UTR is rarely included. 5' ESTs are derived from
CC      mRNAs with intact 5' ends and can therefore be used to obtain full length
CC      cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic,
CC      gene therapy and chromosome mapping procedures. They are used to obtain
CC      upstream regulatory sequences and to design expression and secretion
CC      vectors
XX
SQ      Sequence 444 BP; 106 A; 106 C; 87 G; 143 T; 0 U; 2 Other;

Alignment Scores:
Pred. No.:      1.44e-131      Length:      444
Score:          144.00      Matches:      144
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    38.20%      Indels:      0
DB:            3      Gaps:        0

US-09-736-250-1 (1-377) x AAC01909 (1-444)

Qy      117 AspSerPheCysGlyCysSerSerSerGluLeuLeuArgMetGluArgIleLeuAsp 136
|||||
Db      13 GACAGTTCTGTGGATGTTCTCTCATCTCGAAATTTTGAAGATGGAGAAATTTCTGGAT 72
|||||
Qy      137 LysLeuAanTrpAspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAla 156
|||||
Db      73 AAGTTGAATGGGATCTTCACACAGCCACACCATGGATTTTCTTCATATTTTCATGCC 132
|||||

```

```

Qy      157 IleAlaValSerThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGln 176
|||||
Db      133 ATTGCAGTGTCAACTAGGCCTCAGTTACTTTTCAGTTTGGCCAAATTGAGCCCATCTCAA 192
|||||
Qy      177 HisLeuAlaValLeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGln 196
|||||
Db      193 CATTTGGCAGTCTTACCAAGCAACTACTTACATGTATGGCTGCAACCAACTTCTGCAG 252
|||||
Qy      197 PheArgGlySerMetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIlePro 216
|||||
Db      253 TTCAGAGGATCCATGCTTGTCTGGCCATGGTTAGTCTGGAAATGGAGAAACTCATTCCT 312
|||||
Qy      217 AspTrpLeuSerLeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeu 236
|||||
Db      313 GATTGGCTTTCTCTTACAAATTGAACCTCTTCAGAAAGCAGACATGGATGGTCCAGTTG 372
|||||
Qy      237 IleHisCysArgGluLeuValAlaHisIleSerThrLeuGlnSerSerLeuProLeu 256
|||||
Db      373 ATCCATTGTCGGAGCTTGTGGCACATCACCTTTCTACTCTGCAGTCTTCCCTGCCTCTG 432
|||||
Qy      257 AsnSerValTyr 260
|||||
Db      433 AATTCCGTTTAT 444
|||||
RESULT 15
AAAX40003/C
ID      AAAX40003 standard; DNA; 804 BP.
XX
XX      AAAX40003;
XX
DT      02-JUL-1999 (first entry)
XX
DE      Prostate cancer associated gene.
XX
XX      Cancer associated antigen; diagnosis; research; treatment; human;
KW      breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer;
KW      prostate cancer; ss.
XX
XX      Homo sapiens.
XX
XX      WO9904265-A2.
XX
PD      28-JAN-1999.
XX
XX      15-JUL-1998; 98WO-US014679.
XX
XX      17-JUL-1997; 97US-00896164.
XX      10-OCT-1997; 97US-0061599P.
XX      10-OCT-1997; 97US-0061765P.
XX      10-OCT-1997; 97US-00948705.
XX      11-OCT-1997; 97GB-00021697.
XX      22-JUN-1998; 98US-00102322.
XX
XX      (LUDW-) LUDWIG INST CANCER RES.
XX
XX      Old LJ, Scanlan MJ, Stockert E, Gure A, Chen Y, Gout I;
PI      O'hare M, Obata Y, Pfreundschuh M, Tureci O, Sahin U;
XX
XX      WPI; 1999-112448/11.
XX
XX      New isolated cancer associated nucleic acids and polypeptides - isolated
PT      using sera from cancer patients, used to develop products for the
PT      diagnosis, monitoring or treatment of cancers.
XX
XX      Claim 67; Page 630; 787pp; English.
XX
XX      The invention relates to a method for diagnosing a disorder characterised
CC      by expression of a human cancer associated antigen precursor coded for by
CC      a nucleic acid molecule (NAM). The method comprises: (a) contacting a
CC      biological sample isolated from a subject with an agent that specifically
CC      binds to the NAM, an expression product or a fragment of an expression
CC      product complexed with an HLA molecule; and (b) determining the

```

CC interaction between the agent and the NAM or the expression product as a
CC determination of the disorder. The products and methods can be used in
CC the diagnosis, monitoring, research, or treatment of conditions
CC characterised by the expression of various cancer associated antigens.
CC The invention provides nucleic acid sequences and encoded polypeptides
CC which are cancer associated antigen precursors expressed in human breast
CC cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and
CC lung cancer
XX

SQ Sequence 804 BP; 208 A; 172 C; 188 G; 222 T; 0 U; 14 Other;

Alignment Scores:

Pred. No.:	1.34e-116	Length:	804
Score:	129.00	Matches:	129
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	34.22%	Indels:	0
DB:	2	Gaps:	0

US-09-736-250-1 (1-377) x AAX40003 (1-804)

Qy	249	ThrLeuGlnSerSerLeuProLeuAsnSerValTyrValTyrArgProLeuLysHisThr	268
Db	583	ACTCTGCAGTCTTCCCTGCCCTGAATTCGGTTTATGTCTACCGTCCCTCAAGCACACC	524
Qy	269	LeuValThrCysAspLysGlyValPheArgLeuHisProSerSerValProGlyProAsp	288
Db	523	CTGGTGACCTGTGACAAAGAGTGTTCAGATTACATCCCTCTCTGTCCAGGCCAGAC	464
Qy	289	PheSerLysAspAsnSerLysProGluValProValArgGlyThrAlaAlaPheTyrHis	308
Db	463	TTCTCCAAGGACAACAGCAGCCAGAGTGCAGGTACAGAGCTTTTACCAT	404
Qy	309	HisLeuProAlaAlaSerGlyCysLysGlnThrSerThrLysArgLysValGluGluMet	328
Db	403	CATCTCCAGCTGCCAGTGGGTGCAAGCAGACCTCTACTAAACGCAAGTAGAGGAATG	344
Qy	329	GluValAspAspPheTyrAspGlyIleLysArgLeuTyrAsnGluAspAsnValSerGlu	348
Db	343	GAAGTGGATGACTTCTATGATGGATCAACGGCTCTATATGAAGATATGTCTCAGAA	284
Qy	349	AsnValGlySerValCysGlyThrAspLeuSerArgGlnGluGlyHisAlaSerProCys	368
Db	283	AATGTGGGTCTGTGTGGCACTGATTATCAAGACAAGAGGACATGCTTCCCTTGT	224
Qy	369	ProProLeuGlnProValSerValMet	377
Db	223	CCACTTTGCAGCCTGTTCTGTGATG	197

Search completed: February 11, 2005, 10:38:39
Job time : 1046.8 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 11, 2005, 09:52:50 ; Search time 299.864 Seconds
(without alignments)
2057.184 Million cell updates/sec

Title: US-09-736-250-1

Perfect score: 377

Sequence: 1 MKPQPLENQLSLLEKAI.....LSRQEGHASPPLQPVSM 377

Scoring table:

OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Word size: 1

Total number of hits satisfying chosen parameters: 2400006

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/uspto.spool/US09736250/runat_07022005_154942_20670/app.query.fasta_1.718
-DB=Issued Patents NA -QWMT=fastap -SUFFIX=oligo.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=1000 -DOALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HAPSIZES=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09736250 @CEN 1.1 93 @runat_07022005_154942_20670 -NCPU=6 -ICPU=3
-NO_MMAP -LARGQUERY -NEG_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

Issued Patents NA:
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/FACTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query	Match	Length	ID	Description

1	377	100.0	1133	3	US-09-054-492B-2		Sequence 2, Appli
2	377	100.0	1260	2	US-08-969-106-5		Sequence 5, Appli
3	377	100.0	1260	4	US-09-338-125-5		Sequence 5, Appli
4	377	100.0	1260	4	US-09-023-655-899		Sequence 899, App
5	144	38.2	444	4	US-09-513-999C-1907		Sequence 1907, Ap
6	34	9.0	304	4	US-09-513-999C-29894		Sequence 29894, A
7	9	2.4	1643	3	US-09-129-112-1		Sequence 1, Appli
8	9	2.4	6265	3	US-09-129-112-3		Sequence 3, Appli
9	8	2.1	2775	4	US-09-313-294A-98		Sequence 98, Appli
10	8	2.1	279	4	US-09-513-999C-32630		Sequence 32630, A
11	8	2.1	382	4	US-09-270-767-26393		Sequence 26393, A
12	8	2.1	400	4	US-08-956-171E-1529		Sequence 1529, Ap

Sequence 1529, Ap
Sequence 8308, Ap
Sequence 23590, A
Sequence 88687, A
Sequence 103342,
Sequence 132642,
Sequence 155484,
Sequence 155485,
Sequence 156049,
Sequence 75, Appli
Sequence 5854, Ap
Sequence 649, App
Sequence 1908, A
Sequence 1664, Ap
Sequence 9318, Ap
Sequence 24600, A
Sequence 1677, Ap
Sequence 7, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 2315, Ap
Sequence 4, Appli
Sequence 864, App
Sequence 5, Appli
Sequence 4, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 632, App
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 16095, A
Sequence 14049, A
Sequence 12717, A
Sequence 14504, A
Sequence 15846, A
Sequence 16096, A
Sequence 15545, A
Sequence 12286, A
Sequence 13335, A
Sequence 12511, A
Sequence 13725, A
Sequence 40, Appli
Sequence 14202, A
Sequence 15127, A
Sequence 16151, A
Sequence 1368, A
Sequence 14259, A
Sequence 16509, A
Sequence 14184, A
Sequence 16101, A
Sequence 15473, A
Sequence 14577, A
Sequence 14578, A
Sequence 14, Appli
Sequence 57, Appli
Sequence 19, Appli
Sequence 19, Appli
Sequence 31, Appli
Sequence 31, Appli
Sequence 34, Appli
Sequence 16, Appli
Sequence 19, Appli
Sequence 19, Appli
Sequence 17622, A
Sequence 35806, A
Sequence 35807, A
Sequence 19, Appli
Sequence 17, Appli

86	7	1.9	33	3	US-09-054-492B-3	Sequence 3, Appli	c 159	7	1.9	601	4	US-09-949-016-23104	Sequence 23104, A
c 87	7	1.9	35	3	US-08-691-045-38	Sequence 38, Appli	c 160	7	1.9	601	4	US-09-949-016-24168	Sequence 24168, A
c 88	7	1.9	73	4	US-09-270-767-29784	Sequence 29784, A	c 161	7	1.9	601	4	US-09-949-016-24407	Sequence 24407, A
c 89	7	1.9	84	2	US-08-788-943A-14	Sequence 14, Appli	c 162	7	1.9	601	4	US-09-949-016-24408	Sequence 24408, A
c 90	7	1.9	84	5	PCT-US96-00952-15	Sequence 15, Appli	c 163	7	1.9	601	4	US-09-949-016-24409	Sequence 24409, A
c 91	7	1.9	87	2	US-08-788-943A-15	Sequence 15, Appli	c 164	7	1.9	601	4	US-09-949-016-24410	Sequence 24410, A
c 92	7	1.9	87	5	PCT-US96-00952-16	Sequence 16, Appli	c 165	7	1.9	601	4	US-09-949-016-24411	Sequence 24411, A
c 93	7	1.9	93	3	US-09-565-156A-17	Sequence 17, Appli	c 166	7	1.9	601	4	US-09-949-016-24412	Sequence 24412, A
c 94	7	1.9	97	4	US-09-270-767-27272	Sequence 27272, A	c 167	7	1.9	601	4	US-09-949-016-24746	Sequence 24746, A
c 95	7	1.9	109	4	US-09-513-999C-29336	Sequence 29336, A	c 168	7	1.9	601	4	US-09-949-016-27369	Sequence 27369, A
c 96	7	1.9	166	3	US-09-465-355-34	Sequence 34, Appli	c 169	7	1.9	601	4	US-09-949-016-27815	Sequence 27815, A
c 97	7	1.9	196	4	US-09-270-767-27040	Sequence 27040, A	c 170	7	1.9	601	4	US-09-949-016-28245	Sequence 28245, A
c 98	7	1.9	211	4	US-09-270-767-2975	Sequence 2975, Ap	c 171	7	1.9	601	4	US-09-949-016-29230	Sequence 29290, A
c 99	7	1.9	211	4	US-09-270-767-18257	Sequence 18257, Ap	c 172	7	1.9	601	4	US-09-949-016-29291	Sequence 29291, A
c 100	7	1.9	212	4	US-09-313-294A-7402	Sequence 7402, Ap	c 173	7	1.9	601	4	US-09-949-016-29292	Sequence 29292, A
c 101	7	1.9	219	4	US-09-583-110-1832	Sequence 1832, Ap	c 174	7	1.9	601	4	US-09-949-016-29293	Sequence 29293, A
c 102	7	1.9	221	4	US-09-513-999C-20246	Sequence 20246, A	c 175	7	1.9	601	4	US-09-949-016-29294	Sequence 29294, A
c 103	7	1.9	237	4	US-09-248-796A-11710	Sequence 11710, A	c 176	7	1.9	601	4	US-09-949-016-29295	Sequence 29295, A
c 104	7	1.9	251	4	US-09-513-999C-16329	Sequence 16329, A	c 177	7	1.9	601	4	US-09-949-016-29296	Sequence 29296, A
c 105	7	1.9	258	4	US-09-543-681A-4062	Sequence 4062, Ap	c 178	7	1.9	601	4	US-09-949-016-29297	Sequence 29297, A
c 106	7	1.9	281	4	US-09-313-294A-5735	Sequence 5735, Ap	c 179	7	1.9	601	4	US-09-949-016-29738	Sequence 29738, A
c 107	7	1.9	285	4	US-09-313-294A-6808	Sequence 6808, Ap	c 180	7	1.9	601	4	US-09-949-016-30563	Sequence 30563, A
c 108	7	1.9	333	4	US-09-543-681A-1302	Sequence 1302, Ap	c 181	7	1.9	601	4	US-09-949-016-30564	Sequence 30564, A
c 109	7	1.9	333	4	US-09-489-039A-1704	Sequence 1704, Ap	c 182	7	1.9	601	4	US-09-949-016-30565	Sequence 30565, A
c 110	7	1.9	334	4	US-09-270-767-28790	Sequence 28790, A	c 183	7	1.9	601	4	US-09-949-016-30567	Sequence 30567, A
c 111	7	1.9	338	4	US-09-513-999C-30716	Sequence 30716, A	c 184	7	1.9	601	4	US-09-949-016-30568	Sequence 30568, A
c 112	7	1.9	339	4	US-09-640-211A-420	Sequence 420, App	c 185	7	1.9	601	4	US-09-949-016-34213	Sequence 34213, A
c 113	7	1.9	347	4	US-09-513-999C-23861	Sequence 23861, A	c 186	7	1.9	601	4	US-09-949-016-34214	Sequence 34214, A
c 114	7	1.9	357	1	US-08-318-970B-31	Sequence 31, Appli	c 187	7	1.9	601	4	US-09-949-016-34737	Sequence 34737, A
c 115	7	1.9	367	4	US-09-621-976-10003	Sequence 10003, A	c 188	7	1.9	601	4	US-09-949-016-34738	Sequence 34738, A
c 116	7	1.9	384	4	US-09-603-777A-375	Sequence 375, App	c 189	7	1.9	601	4	US-09-949-016-35470	Sequence 35470, A
c 117	7	1.9	386	4	US-09-023-655-692	Sequence 692, App	c 190	7	1.9	601	4	US-09-949-016-37042	Sequence 37042, A
c 118	7	1.9	395	4	US-09-621-976-10223	Sequence 10223, A	c 191	7	1.9	601	4	US-09-949-016-37929	Sequence 37929, A
c 119	7	1.9	399	1	US-08-318-970B-40	Sequence 40, Appli	c 192	7	1.9	601	4	US-09-949-016-37930	Sequence 37930, A
c 120	7	1.9	400	4	US-08-956-171E-852	Sequence 852, App	c 193	7	1.9	601	4	US-09-949-016-39132	Sequence 39132, A
c 121	7	1.9	400	4	US-08-781-986A-852	Sequence 852, App	c 194	7	1.9	601	4	US-09-949-016-39454	Sequence 39454, A
c 122	7	1.9	402	1	US-08-318-970B-41	Sequence 41, Appli	c 195	7	1.9	601	4	US-09-949-016-39455	Sequence 39455, A
c 123	7	1.9	402	4	US-08-956-171E-1282	Sequence 1282, Ap	c 196	7	1.9	601	4	US-09-949-016-39913	Sequence 39913, A
c 124	7	1.9	402	4	US-08-781-986A-1282	Sequence 1282, Ap	c 197	7	1.9	601	4	US-09-949-016-39916	Sequence 39916, A
c 125	7	1.9	408	3	US-09-128-155-10	Sequence 10, Appli	c 198	7	1.9	601	4	US-09-949-016-39917	Sequence 39917, A
c 126	7	1.9	411	4	US-09-252-931A-13777	Sequence 13777, A	c 199	7	1.9	601	4	US-09-949-016-39919	Sequence 39919, A
c 127	7	1.9	411	4	US-09-401-084-180	Sequence 180, App	c 200	7	1.9	601	4	US-09-949-016-40395	Sequence 40395, A
c 128	7	1.9	452	4	US-09-621-976-493	Sequence 493, App	c 201	7	1.9	601	4	US-09-949-016-40396	Sequence 40396, A
c 129	7	1.9	452	4	US-09-640-211A-63	Sequence 63, Appli	c 202	7	1.9	601	4	US-09-949-016-40397	Sequence 40397, A
c 130	7	1.9	465	4	US-09-270-767-11456	Sequence 11456, A	c 203	7	1.9	601	4	US-09-949-016-40398	Sequence 40398, A
c 131	7	1.9	477	4	US-09-248-796A-2135	Sequence 2135, Ap	c 204	7	1.9	601	4	US-09-949-016-40399	Sequence 40399, A
c 132	7	1.9	482	4	US-09-270-767-1337	Sequence 1337, Ap	c 205	7	1.9	601	4	US-09-949-016-40400	Sequence 40400, A
c 133	7	1.9	482	4	US-09-270-767-16619	Sequence 16619, A	c 206	7	1.9	601	4	US-09-949-016-40401	Sequence 40401, A
c 134	7	1.9	490	2	US-08-967-101-76	Sequence 76, Appli	c 207	7	1.9	601	4	US-09-949-016-46815	Sequence 46815, A
c 135	7	1.9	490	2	US-08-592-541-76	Sequence 76, Appli	c 208	7	1.9	601	4	US-09-949-016-46816	Sequence 46816, A
c 136	7	1.9	490	3	US-09-124-698-76	Sequence 76, Appli	c 209	7	1.9	601	4	US-09-949-016-46817	Sequence 46817, A
c 137	7	1.9	490	3	US-09-127-480-76	Sequence 76, Appli	c 210	7	1.9	601	4	US-09-949-016-46818	Sequence 46818, A
c 138	7	1.9	490	3	US-08-496-841C-76	Sequence 76, Appli	c 211	7	1.9	601	4	US-09-949-016-46819	Sequence 46819, A
c 139	7	1.9	490	3	US-09-124-523-76	Sequence 76, Appli	c 212	7	1.9	601	4	US-09-949-016-46820	Sequence 46820, A
c 140	7	1.9	490	4	US-09-636-796A-76	Sequence 76, Appli	c 213	7	1.9	601	4	US-09-949-016-46821	Sequence 46821, A
c 141	7	1.9	490	4	US-08-431-048F-76	Sequence 76, Appli	c 214	7	1.9	601	4	US-09-949-016-46828	Sequence 46828, A
c 142	7	1.9	496	4	US-09-949-016-170229	Sequence 170229, A	c 215	7	1.9	601	4	US-09-949-016-46829	Sequence 46829, A
c 143	7	1.9	501	3	US-09-128-155-6	Sequence 6, Appli	c 216	7	1.9	601	4	US-09-949-016-46830	Sequence 46830, A
c 144	7	1.9	534	3	US-09-128-155-3	Sequence 3, Appli	c 217	7	1.9	601	4	US-09-949-016-46831	Sequence 46831, A
c 145	7	1.9	543	4	US-09-248-796A-9429	Sequence 9429, Ap	c 218	7	1.9	601	4	US-09-949-016-46832	Sequence 46832, A
c 146	7	1.9	563	4	US-09-949-016-170230	Sequence 170230, A	c 219	7	1.9	601	4	US-09-949-016-46833	Sequence 46833, A
c 147	7	1.9	564	4	US-09-327-138C-33	Sequence 33, Appli	c 220	7	1.9	601	4	US-09-949-016-46834	Sequence 46834, A
c 148	7	1.9	573	4	US-09-489-039A-3890	Sequence 3890, Ap	c 221	7	1.9	601	4	US-09-949-016-50242	Sequence 50242, A
c 149	7	1.9	584	4	US-09-187-999-26	Sequence 26, Appli	c 222	7	1.9	601	4	US-09-949-016-50861	Sequence 50861, A
c 150	7	1.9	594	4	US-09-868-352-7	Sequence 7, Appli	c 223	7	1.9	601	4	US-09-949-016-51256	Sequence 51256, A
c 151	7	1.9	598	3	US-09-073-237-25	Sequence 25, Appli	c 224	7	1.9	601	4	US-09-949-016-51477	Sequence 51477, A
c 152	7	1.9	599	4	US-09-513-999C-1512	Sequence 1512, Ap	c 225	7	1.9	601	4	US-09-949-016-51478	Sequence 51478, A
c 153	7	1.9	601	4	US-09-949-016-22064	Sequence 22064, A	c 226	7	1.9	601	4	US-09-949-016-51479	Sequence 51479, A
c 154	7	1.9	601	4	US-09-949-016-22696	Sequence 22696, A	c 227	7	1.9	601	4	US-09-949-016-53438	Sequence 53438, A
c 155	7	1.9	601	4	US-09-949-016-22697	Sequence 22697, A	c 228	7	1.9	601	4	US-09-949-016-53439	Sequence 53439, A
c 156	7	1.9	601	4	US-09-949-016-22698	Sequence 22698, A	c 229	7	1.9	601	4	US-09-949-016-53848	Sequence 53848, A
c 157	7	1.9	601	4	US-09-949-016-22699	Sequence 22699, A	c 230	7	1.9	601	4	US-09-949-016-53849	Sequence 53849, A
c 158	7	1.9	601	4	US-09-949-016-22777	Sequence 22777, A	c 231	7	1.9	601	4	US-09-949-016-57448	Sequence 57448, A

C 232	7	1.9	601	4	US-09-949-016-57743	Sequence 57743, A	C 305	7	1.9	601	4	US-09-949-016-102547	Sequence 102547,
C 233	7	1.9	601	4	US-09-949-016-57744	Sequence 57744, A	306	7	1.9	601	4	US-09-949-016-105061	Sequence 105061,
C 234	7	1.9	601	4	US-09-949-016-57745	Sequence 57745, A	307	7	1.9	601	4	US-09-949-016-105062	Sequence 105062,
C 235	7	1.9	601	4	US-09-949-016-58593	Sequence 58593, A	308	7	1.9	601	4	US-09-949-016-105063	Sequence 105063,
C 236	7	1.9	601	4	US-09-949-016-60285	Sequence 60285, A	309	7	1.9	601	4	US-09-949-016-105064	Sequence 105064,
C 237	7	1.9	601	4	US-09-949-016-60686	Sequence 60686, A	310	7	1.9	601	4	US-09-949-016-105065	Sequence 105065,
C 238	7	1.9	601	4	US-09-949-016-61280	Sequence 61280, A	311	7	1.9	601	4	US-09-949-016-105066	Sequence 105066,
C 239	7	1.9	601	4	US-09-949-016-63167	Sequence 63167, A	C 312	7	1.9	601	4	US-09-949-016-105227	Sequence 105227,
C 240	7	1.9	601	4	US-09-949-016-64844	Sequence 64844, A	313	7	1.9	601	4	US-09-949-016-105597	Sequence 105597,
C 241	7	1.9	601	4	US-09-949-016-64845	Sequence 64845, A	314	7	1.9	601	4	US-09-949-016-107759	Sequence 107759,
C 242	7	1.9	601	4	US-09-949-016-65234	Sequence 65234, A	315	7	1.9	601	4	US-09-949-016-107760	Sequence 107760,
C 243	7	1.9	601	4	US-09-949-016-66126	Sequence 66126, A	316	7	1.9	601	4	US-09-949-016-107761	Sequence 107761,
C 244	7	1.9	601	4	US-09-949-016-66127	Sequence 66127, A	C 317	7	1.9	601	4	US-09-949-016-108617	Sequence 108617,
C 245	7	1.9	601	4	US-09-949-016-66128	Sequence 66128, A	C 318	7	1.9	601	4	US-09-949-016-108618	Sequence 108618,
C 246	7	1.9	601	4	US-09-949-016-66698	Sequence 66698, A	319	7	1.9	601	4	US-09-949-016-109288	Sequence 109288,
C 247	7	1.9	601	4	US-09-949-016-70615	Sequence 70615, A	320	7	1.9	601	4	US-09-949-016-109289	Sequence 109289,
C 248	7	1.9	601	4	US-09-949-016-70616	Sequence 70616, A	321	7	1.9	601	4	US-09-949-016-109290	Sequence 109290,
C 249	7	1.9	601	4	US-09-949-016-70796	Sequence 70796, A	322	7	1.9	601	4	US-09-949-016-109291	Sequence 109291,
C 250	7	1.9	601	4	US-09-949-016-72369	Sequence 72369, A	323	7	1.9	601	4	US-09-949-016-109292	Sequence 109292,
C 251	7	1.9	601	4	US-09-949-016-72370	Sequence 72370, A	324	7	1.9	601	4	US-09-949-016-111466	Sequence 111466,
C 252	7	1.9	601	4	US-09-949-016-72371	Sequence 72371, A	325	7	1.9	601	4	US-09-949-016-111467	Sequence 111467,
C 253	7	1.9	601	4	US-09-949-016-72665	Sequence 72665, A	326	7	1.9	601	4	US-09-949-016-111468	Sequence 111468,
C 254	7	1.9	601	4	US-09-949-016-76511	Sequence 76511, A	327	7	1.9	601	4	US-09-949-016-111469	Sequence 111469,
C 255	7	1.9	601	4	US-09-949-016-76512	Sequence 76512, A	328	7	1.9	601	4	US-09-949-016-111470	Sequence 111470,
C 256	7	1.9	601	4	US-09-949-016-77659	Sequence 77659, A	329	7	1.9	601	4	US-09-949-016-111471	Sequence 111471,
C 257	7	1.9	601	4	US-09-949-016-79423	Sequence 79423, A	330	7	1.9	601	4	US-09-949-016-111472	Sequence 111472,
C 258	7	1.9	601	4	US-09-949-016-81228	Sequence 81228, A	331	7	1.9	601	4	US-09-949-016-111479	Sequence 111479,
C 259	7	1.9	601	4	US-09-949-016-83050	Sequence 83050, A	332	7	1.9	601	4	US-09-949-016-111480	Sequence 111480,
C 260	7	1.9	601	4	US-09-949-016-85110	Sequence 85110, A	333	7	1.9	601	4	US-09-949-016-111481	Sequence 111481,
C 261	7	1.9	601	4	US-09-949-016-85111	Sequence 85111, A	334	7	1.9	601	4	US-09-949-016-111482	Sequence 111482,
C 262	7	1.9	601	4	US-09-949-016-85112	Sequence 85112, A	335	7	1.9	601	4	US-09-949-016-111483	Sequence 111483,
C 263	7	1.9	601	4	US-09-949-016-85261	Sequence 85261, A	336	7	1.9	601	4	US-09-949-016-111484	Sequence 111484,
C 264	7	1.9	601	4	US-09-949-016-85262	Sequence 85262, A	337	7	1.9	601	4	US-09-949-016-111485	Sequence 111485,
C 265	7	1.9	601	4	US-09-949-016-85263	Sequence 85263, A	C 338	7	1.9	601	4	US-09-949-016-112183	Sequence 112183,
C 266	7	1.9	601	4	US-09-949-016-85762	Sequence 85762, A	C 339	7	1.9	601	4	US-09-949-016-112224	Sequence 112224,
C 267	7	1.9	601	4	US-09-949-016-85763	Sequence 85763, A	340	7	1.9	601	4	US-09-949-016-115539	Sequence 115539,
C 268	7	1.9	601	4	US-09-949-016-86783	Sequence 86783, A	341	7	1.9	601	4	US-09-949-016-115632	Sequence 115632,
C 269	7	1.9	601	4	US-09-949-016-86784	Sequence 86784, A	342	7	1.9	601	4	US-09-949-016-115725	Sequence 115725,
C 270	7	1.9	601	4	US-09-949-016-86785	Sequence 86785, A	343	7	1.9	601	4	US-09-949-016-115818	Sequence 115818,
C 271	7	1.9	601	4	US-09-949-016-87167	Sequence 87167, A	344	7	1.9	601	4	US-09-949-016-115911	Sequence 115911,
C 272	7	1.9	601	4	US-09-949-016-87400	Sequence 87400, A	345	7	1.9	601	4	US-09-949-016-116004	Sequence 116004,
C 273	7	1.9	601	4	US-09-949-016-87838	Sequence 87838, A	346	7	1.9	601	4	US-09-949-016-116097	Sequence 116097,
C 274	7	1.9	601	4	US-09-949-016-95218	Sequence 95218, A	347	7	1.9	601	4	US-09-949-016-116190	Sequence 116190,
C 275	7	1.9	601	4	US-09-949-016-95396	Sequence 95396, A	348	7	1.9	601	4	US-09-949-016-116283	Sequence 116283,
C 276	7	1.9	601	4	US-09-949-016-95574	Sequence 95574, A	349	7	1.9	601	4	US-09-949-016-116376	Sequence 116376,
C 277	7	1.9	601	4	US-09-949-016-95752	Sequence 95752, A	C 350	7	1.9	601	4	US-09-949-016-117633	Sequence 117633,
C 278	7	1.9	601	4	US-09-949-016-96629	Sequence 96629, A	351	7	1.9	601	4	US-09-949-016-117659	Sequence 117659,
C 279	7	1.9	601	4	US-09-949-016-96895	Sequence 96895, A	C 352	7	1.9	601	4	US-09-949-016-118193	Sequence 118193,
C 280	7	1.9	601	4	US-09-949-016-97161	Sequence 97161, A	C 353	7	1.9	601	4	US-09-949-016-120679	Sequence 120679,
C 281	7	1.9	601	4	US-09-949-016-97427	Sequence 97427, A	354	7	1.9	601	4	US-09-949-016-120698	Sequence 120698,
C 282	7	1.9	601	4	US-09-949-016-97693	Sequence 97693, A	C 355	7	1.9	601	4	US-09-949-016-125698	Sequence 125698,
C 283	7	1.9	601	4	US-09-949-016-97959	Sequence 97959, A	356	7	1.9	601	4	US-09-949-016-126044	Sequence 126044,
C 284	7	1.9	601	4	US-09-949-016-98225	Sequence 98225, A	C 357	7	1.9	601	4	US-09-949-016-128329	Sequence 128329,
C 285	7	1.9	601	4	US-09-949-016-98491	Sequence 98491, A	358	7	1.9	601	4	US-09-949-016-128330	Sequence 128330,
C 286	7	1.9	601	4	US-09-949-016-98507	Sequence 98507, A	C 359	7	1.9	601	4	US-09-949-016-129016	Sequence 129016,
C 287	7	1.9	601	4	US-09-949-016-99023	Sequence 99023, A	360	7	1.9	601	4	US-09-949-016-134208	Sequence 134208,
C 288	7	1.9	601	4	US-09-949-016-99289	Sequence 99289, A	C 361	7	1.9	601	4	US-09-949-016-134209	Sequence 134209,
C 289	7	1.9	601	4	US-09-949-016-99555	Sequence 99555, A	362	7	1.9	601	4	US-09-949-016-134210	Sequence 134210,
C 290	7	1.9	601	4	US-09-949-016-99821	Sequence 99821, A	363	7	1.9	601	4	US-09-949-016-134945	Sequence 134945,
C 291	7	1.9	601	4	US-09-949-016-100087	Sequence 100087, A	364	7	1.9	601	4	US-09-949-016-135021	Sequence 135021,
C 292	7	1.9	601	4	US-09-949-016-100353	Sequence 100353, A	365	7	1.9	601	4	US-09-949-016-135022	Sequence 135022,
C 293	7	1.9	601	4	US-09-949-016-100619	Sequence 100619, A	366	7	1.9	601	4	US-09-949-016-136283	Sequence 136283,
C 294	7	1.9	601	4	US-09-949-016-100885	Sequence 100885, A	C 367	7	1.9	601	4	US-09-949-016-137806	Sequence 137806,
C 295	7	1.9	601	4	US-09-949-016-101189	Sequence 101189, A	368	7	1.9	601	4	US-09-949-016-139786	Sequence 139786,
C 296	7	1.9	601	4	US-09-949-016-101455	Sequence 101455, A	C 369	7	1.9	601	4	US-09-949-016-139786	Sequence 139786,
C 297	7	1.9	601	4	US-09-949-016-101721	Sequence 101721, A	370	7	1.9	601	4	US-09-949-016-140403	Sequence 140403,
C 298	7	1.9	601	4	US-09-949-016-101987	Sequence 101987, A	371	7	1.9	601	4	US-09-949-016-142722	Sequence 142722,
C 299	7	1.9	601	4	US-09-949-016-102043	Sequence 102043, A	372	7	1.9	601	4	US-09-949-016-142723	Sequence 142723,
C 300	7	1.9	601	4	US-09-949-016-102099	Sequence 102099, A	C 373	7	1.9	601	4	US-09-949-016-149820	Sequence 149820,
C 301	7	1.9	601	4	US-09-949-016-102155	Sequence 102155, A	C 374	7	1.9	601	4	US-09-949-016-153218	Sequence 153218,
C 302	7	1.9	601	4	US-09-949-016-102211	Sequence 102211, A	C 375	7	1.9	601	4	US-09-949-016-153219	Sequence 153219,
C 303	7	1.9	601	4	US-09-949-016-102267	Sequence 102267, A	C 376	7	1.9	601	4	US-09-949-016-153220	Sequence 153220,
C 304	7	1.9	601	4	US-09-949-016-102407	Sequence 102407, A	C 377	7	1.9	601	4	US-09-949-016-153222	Sequence 153222,
						Sequence 102407, A	C 377	7	1.9	601	4	US-09-949-016-157645	Sequence 157645,

C 378	7	1.9	601	4	US-09-949-016-157646	Sequence 157646,	451	7	1.9	621	3	US-09-221-017B-608	Sequence 608, App
C 379	7	1.9	601	4	US-09-949-016-161716	Sequence 161716,	452	7	1.9	634	4	US-09-917-254-33	Sequence 33, Appl
C 380	7	1.9	601	4	US-09-949-016-164878	Sequence 164878,	453	7	1.9	636	4	US-09-134-000C-929	Sequence 929, App
C 381	7	1.9	601	4	US-09-949-016-165765	Sequence 165765,	454	7	1.9	648	4	US-09-949-016-5717	Sequence 5717, Ap
C 382	7	1.9	601	4	US-09-949-016-165766	Sequence 165766,	455	7	1.9	657	4	US-09-398-412B-3	Sequence 3, Appli
C 383	7	1.9	601	4	US-09-949-016-166744	Sequence 166744,	c 456	7	1.9	663	4	US-09-328-352-1833	Sequence 1833, Ap
C 384	7	1.9	601	4	US-09-949-016-168466	Sequence 168466,	c 457	7	1.9	690	4	US-09-270-767-11657	Sequence 11657, A
C 385	7	1.9	601	4	US-09-949-016-168467	Sequence 168467,	458	7	1.9	696	4	US-09-248-796A-969	Sequence 969, App
C 386	7	1.9	601	4	US-09-949-016-168689	Sequence 168689,	459	7	1.9	696	4	US-09-902-540-8542	Sequence 8542, Ap
C 387	7	1.9	601	4	US-09-949-016-169606	Sequence 169606,	460	7	1.9	708	4	US-09-248-796A-1181	Sequence 1181, Ap
C 388	7	1.9	601	4	US-09-949-016-170085	Sequence 170085,	461	7	1.9	750	3	US-09-446-504-2	Sequence 2, Appli
C 389	7	1.9	601	4	US-09-949-016-170086	Sequence 170086,	462	7	1.9	750	3	US-09-712-266-2	Sequence 2, Appli
C 390	7	1.9	601	4	US-09-949-016-170231	Sequence 170231,	c 463	7	1.9	756	4	US-09-506-286B-3	Sequence 3, Appli
C 391	7	1.9	601	4	US-09-949-016-170231	Sequence 170231,	c 464	7	1.9	756	4	US-09-506-286B-6	Sequence 6, Appli
C 392	7	1.9	601	4	US-09-949-016-172693	Sequence 172693,	c 465	7	1.9	756	4	US-09-762-861B-3	Sequence 3, Appli
C 393	7	1.9	601	4	US-09-949-016-172694	Sequence 172694,	c 466	7	1.9	756	4	US-09-762-861B-6	Sequence 6, Appli
C 394	7	1.9	601	4	US-09-949-016-172695	Sequence 172695,	c 467	7	1.9	756	4	US-10-065-133A-3	Sequence 3, Appli
C 395	7	1.9	601	4	US-09-949-016-172696	Sequence 172696,	c 468	7	1.9	756	4	US-10-065-133A-6	Sequence 6, Appli
C 396	7	1.9	601	4	US-09-949-016-172755	Sequence 172755,	c 469	7	1.9	756	4	US-10-434-811A-3	Sequence 3, Appli
C 397	7	1.9	601	4	US-09-949-016-175310	Sequence 175310,	c 470	7	1.9	756	4	US-10-434-811A-6	Sequence 6, Appli
C 398	7	1.9	601	4	US-09-949-016-175311	Sequence 175311,	471	7	1.9	759	4	US-09-107-532A-2865	Sequence 2865, Ap
C 399	7	1.9	601	4	US-09-949-016-175868	Sequence 175868,	472	7	1.9	762	4	US-09-270-767-11453	Sequence 11453, A
C 400	7	1.9	601	4	US-09-949-016-176849	Sequence 176849,	c 473	7	1.9	765	4	US-09-248-796A-3490	Sequence 3490, Ap
C 401	7	1.9	601	4	US-09-949-016-179379	Sequence 179379,	c 474	7	1.9	768	4	US-09-583-110-906	Sequence 906, App
C 402	7	1.9	601	4	US-09-949-016-179380	Sequence 179380,	475	7	1.9	800	4	US-09-252-991A-13462	Sequence 13462, A
C 403	7	1.9	601	4	US-09-949-016-181018	Sequence 181018,	c 476	7	1.9	771	4	US-09-107-433-1732	Sequence 1732, Ap
C 404	7	1.9	601	4	US-09-949-016-181071	Sequence 181071,	c 477	7	1.9	774	4	US-09-148-545-13	Sequence 13, Appl
C 405	7	1.9	601	4	US-09-949-016-181137	Sequence 181137,	c 478	7	1.9	792	4	US-09-248-796A-933	Sequence 933, App
C 406	7	1.9	601	4	US-09-949-016-182519	Sequence 182519,	479	7	1.9	800	4	US-09-270-767-6262	Sequence 6262, Ap
C 407	7	1.9	601	4	US-09-949-016-182520	Sequence 182520,	480	7	1.9	800	4	US-09-270-767-21544	Sequence 21544, A
C 408	7	1.9	601	4	US-09-949-016-182639	Sequence 182639,	481	7	1.9	802	3	US-09-293-625-1	Sequence 1, Appli
C 409	7	1.9	601	4	US-09-949-016-182640	Sequence 182640,	c 482	7	1.9	816	4	US-09-311-784A-13	Sequence 13, Appl
C 410	7	1.9	601	4	US-09-949-016-185239	Sequence 185239,	c 483	7	1.9	816	4	US-09-328-352-133	Sequence 133, App
C 411	7	1.9	601	4	US-09-949-016-185240	Sequence 185240,	c 484	7	1.9	816	4	US-09-902-540-7095	Sequence 7095, Ap
C 412	7	1.9	601	4	US-09-949-016-185242	Sequence 185242,	c 485	7	1.9	825	4	US-09-328-352-1318	Sequence 1318, Ap
C 413	7	1.9	601	4	US-09-949-016-185372	Sequence 185372,	c 486	7	1.9	826	4	US-09-270-767-2213	Sequence 2213, A
C 414	7	1.9	601	4	US-09-949-016-185373	Sequence 185373,	c 487	7	1.9	826	4	US-09-270-767-17495	Sequence 17495, A
C 415	7	1.9	601	4	US-09-949-016-186441	Sequence 186441,	c 488	7	1.9	831	4	US-09-107-532A-1114	Sequence 1114, Ap
C 416	7	1.9	601	4	US-09-949-016-186442	Sequence 186442,	c 489	7	1.9	831	4	US-09-902-540-4228	Sequence 4228, Ap
C 417	7	1.9	601	4	US-09-949-016-186443	Sequence 186443,	c 490	7	1.9	842	3	US-09-154-750A-72	Sequence 72, Appl
C 418	7	1.9	601	4	US-09-949-016-186854	Sequence 186854,	c 491	7	1.9	857	4	US-09-500-495A-9	Sequence 9, Appli
C 419	7	1.9	601	4	US-09-949-016-187337	Sequence 187337,	c 492	7	1.9	864	4	US-09-489-039A-3716	Sequence 3716, Ap
C 420	7	1.9	601	4	US-09-949-016-187338	Sequence 187338,	c 493	7	1.9	864	4	US-09-270-767-12924	Sequence 12924, A
C 421	7	1.9	601	4	US-09-949-016-187339	Sequence 187339,	c 494	7	1.9	885	4	US-09-714-948-2	Sequence 2, Appli
C 422	7	1.9	601	4	US-09-949-016-187340	Sequence 187340,	c 495	7	1.9	908	3	US-09-457-046B-7	Sequence 7, Appli
C 423	7	1.9	601	4	US-09-949-016-187729	Sequence 187729,	c 496	7	1.9	908	3	US-09-457-046B-23	Sequence 23, Appli
C 424	7	1.9	601	4	US-09-949-016-187770	Sequence 187770,	c 497	7	1.9	908	4	US-09-866-570B-7	Sequence 7, Appli
C 425	7	1.9	601	4	US-09-949-016-189658	Sequence 189658,	c 498	7	1.9	908	4	US-09-866-570B-23	Sequence 23, Appli
C 426	7	1.9	601	4	US-09-949-016-190362	Sequence 190362,	c 499	7	1.9	915	4	US-09-107-532A-354	Sequence 354, App
C 427	7	1.9	601	4	US-09-949-016-191511	Sequence 191511,	500	7	1.9	920	3	US-09-457-046B-1	Sequence 1, Appli
C 428	7	1.9	601	4	US-09-949-016-191689	Sequence 191689,	501	7	1.9	920	4	US-09-866-570B-1	Sequence 2, Appli
C 429	7	1.9	601	4	US-09-949-016-191867	Sequence 191867,	c 502	7	1.9	960	2	US-08-683-908-2	Sequence 2, Appli
C 430	7	1.9	601	4	US-09-949-016-192045	Sequence 192045,	c 503	7	1.9	960	4	US-10-000-489-45	Sequence 45, Appl
C 431	7	1.9	601	4	US-09-949-016-192297	Sequence 192297,	c 504	7	1.9	969	4	US-09-328-352-1363	Sequence 1363, Ap
C 432	7	1.9	601	4	US-09-949-016-192549	Sequence 192549,	c 505	7	1.9	969	4	US-09-543-681A-2774	Sequence 2774, Ap
C 433	7	1.9	601	4	US-09-949-016-194183	Sequence 194183,	c 506	7	1.9	987	4	US-09-252-991A-15392	Sequence 15392, A
C 434	7	1.9	601	4	US-09-949-016-195681	Sequence 195681,	507	7	1.9	989	3	US-09-128-155-1	Sequence 1, Appli
C 435	7	1.9	601	4	US-09-949-016-195967	Sequence 195967,	c 508	7	1.9	989	3	US-09-446-504-41	Sequence 41, Appl
C 436	7	1.9	601	4	US-09-949-016-196975	Sequence 196975,	c 509	7	1.9	989	3	US-09-712-266-41	Sequence 41, Appl
C 437	7	1.9	601	4	US-09-949-016-199578	Sequence 199578,	c 510	7	1.9	990	4	US-09-327-138C-6	Sequence 6, Appli
C 438	7	1.9	601	4	US-09-949-016-199579	Sequence 199579,	c 511	7	1.9	996	4	US-09-328-352-1213	Sequence 1213, Ap
C 439	7	1.9	601	4	US-09-949-016-199580	Sequence 199580,	c 512	7	1.9	999	3	US-08-870-511-7	Sequence 7, Appli
C 440	7	1.9	601	4	US-09-949-016-199581	Sequence 199581,	c 513	7	1.9	1012	4	US-09-270-767-12677	Sequence 12677, A
C 441	7	1.9	601	4	US-09-949-016-199582	Sequence 199582,	c 514	7	1.9	1014	4	US-09-327-138C-9	Sequence 9, Appli
C 442	7	1.9	601	4	US-09-949-016-199583	Sequence 199583,	c 515	7	1.9	1023	4	US-09-506-286B-1	Sequence 1, Appli
C 443	7	1.9	601	4	US-09-949-016-199687	Sequence 199687,	c 516	7	1.9	1023	4	US-09-762-861B-1	Sequence 4, Appli
C 444	7	1.9	601	4	US-09-949-016-200040	Sequence 200040,	c 517	7	1.9	1023	4	US-09-506-286B-4	Sequence 4, Appli
C 445	7	1.9	601	4	US-09-949-016-200074	Sequence 200074,	c 518	7	1.9	1023	4	US-09-762-861B-1	Sequence 1, Appli
C 446	7	1.9	601	4	US-09-949-016-200182	Sequence 200182,	c 519	7	1.9	1023	4	US-10-065-133A-1	Sequence 1, Appli
C 447	7	1.9	601	4	US-09-949-016-202141	Sequence 202141,	c 520	7	1.9	1023	4	US-10-065-133A-4	Sequence 4, Appli
C 448	7	1.9	601	4	US-09-949-016-203231	Sequence 203231,	c 521	7	1.9	1023	4	US-10-065-133A-1	Sequence 1, Appli
C 449	7	1.9	601	4	US-09-949-016-203232	Sequence 203232,	c 522	7	1.9	1023	4	US-10-434-811A-1	Sequence 1, Appli
C 450	7	1.9	601	4	US-09-949-016-204463	Sequence 204463,	c 523	7	1.9	1024	4	US-10-434-811A-4	Sequence 4, Appli
					Sequence 204533,							US-09-327-138C-7	Sequence 7, Appli

c 524	7	1.9	1027	5	PCT-US95-12357A-3	Sequence 3, Appli	c 597	7	1.9	1457	4	US-09-949-016-3988	Sequence 3988, Ap
525	7	1.9	1046	4	US-09-949-016-2992	Sequence 2992, Ap	c 598	7	1.9	1473	4	US-09-248-796A-5807	Sequence 5807, Ap
526	7	1.9	1062	4	US-09-016-434-1286	Sequence 1286, Ap	c 599	7	1.9	1479	4	US-09-902-540-6689	Sequence 6689, Ap
527	7	1.9	1062	4	US-08-134-231C-33	Sequence 33, Appli	600	7	1.9	1504	3	US-09-010-998-3	Sequence 3, Appli
528	7	1.9	1062	4	US-09-023-655-1327	Sequence 1327, Ap	601	7	1.9	1529	3	US-08-477-451-17	Sequence 17, Appli
529	7	1.9	1062	4	US-08-728-160-33	Sequence 33, Appli	c 602	7	1.9	1529	2	US-08-477-451-21	Sequence 21, Appli
530	7	1.9	1065	4	US-09-348-352-3136	Sequence 3136, Ap	c 603	7	1.9	1529	4	US-09-523-263B-7	Sequence 7, Appli
531	7	1.9	1070	4	US-09-976-594-1062	Sequence 1062, Ap	604	7	1.9	1540	4	US-09-560-761B-3	Sequence 3, Appli
532	7	1.9	1075	4	US-09-660-107-10	Sequence 12, Appli	c 605	7	1.9	1554	4	US-09-252-991A-13880	Sequence 2279, A
c 533	7	1.9	1086	4	US-09-479-040-10	Sequence 10, Appli	c 606	7	1.9	1569	4	US-09-252-991A-13880	Sequence 13880, A
c 534	7	1.9	1088	4	US-09-327-138C-12	Sequence 12, Appli	607	7	1.9	1593	4	US-09-023-655-1498	Sequence 1498, Ap
535	7	1.9	1113	4	US-09-252-991A-8037	Sequence 8037, Ap	608	7	1.9	1593	4	US-08-248-628A-1	Sequence 1, Appli
536	7	1.9	1113	4	US-09-620-312D-406	Sequence 406, App	c 609	7	1.9	1596	4	US-09-023-655-1476	Sequence 1476, Ap
c 537	7	1.9	1113	4	US-09-583-110-744	Sequence 744, App	610	7	1.9	1600	1	US-08-073-384C-12	Sequence 12, Appli
c 538	7	1.9	1113	4	US-09-107-433-1099	Sequence 1099, Ap	611	7	1.9	1600	1	US-08-254-359A-12	Sequence 12, Appli
c 539	7	1.9	1125	3	US-09-436-983-2	Sequence 2, Appli	612	7	1.9	1600	1	US-08-483-043-12	Sequence 12, Appli
c 540	7	1.9	1173	4	US-09-252-991A-9438	Sequence 9438, Ap	613	7	1.9	1600	1	US-08-481-238-12	Sequence 12, Appli
c 541	7	1.9	1182	3	US-09-469-242-1	Sequence 1, Appli	614	7	1.9	1600	2	US-08-471-066B-12	Sequence 12, Appli
c 542	7	1.9	1194	4	US-09-506-286B-21	Sequence 21, Appli	615	7	1.9	1600	2	US-08-484-356-12	Sequence 12, Appli
c 543	7	1.9	1194	4	US-09-506-286B-25	Sequence 25, Appli	616	7	1.9	1600	2	US-08-757-653-12	Sequence 12, Appli
c 544	7	1.9	1194	4	US-09-762-861B-21	Sequence 21, Appli	617	7	1.9	1600	2	US-08-599-491-12	Sequence 12, Appli
c 545	7	1.9	1194	4	US-09-762-861B-25	Sequence 25, Appli	618	7	1.9	1600	2	US-08-756-386-12	Sequence 12, Appli
c 546	7	1.9	1194	4	US-10-065-133A-21	Sequence 21, Appli	619	7	1.9	1600	2	US-08-823-516-12	Sequence 12, Appli
c 547	7	1.9	1194	4	US-10-065-133A-25	Sequence 25, Appli	620	7	1.9	1600	3	US-08-682-853A-12	Sequence 12, Appli
c 548	7	1.9	1194	4	US-10-434-811A-21	Sequence 21, Appli	621	7	1.9	1600	3	US-08-759-038-12	Sequence 12, Appli
c 549	7	1.9	1203	4	US-10-434-811A-25	Sequence 25, Appli	622	7	1.9	1600	3	US-08-758-314-12	Sequence 12, Appli
550	7	1.9	1209	4	US-09-252-991A-9395	Sequence 9395, Ap	623	7	1.9	1600	3	US-09-350-109-12	Sequence 12, Appli
551	7	1.9	1225	4	US-09-489-039A-6373	Sequence 6373, Ap	624	7	1.9	1600	3	US-08-520-946-12	Sequence 12, Appli
552	7	1.9	1225	4	US-09-398-412B-1	Sequence 1, Appli	625	7	1.9	1600	4	US-09-684-938-12	Sequence 12, Appli
553	7	1.9	1226	4	US-09-976-594-1110	Sequence 1110, Ap	626	7	1.9	1600	4	US-09-308-825A-12	Sequence 12, Appli
c 554	7	1.9	1232	4	US-09-506-286B-22	Sequence 22, Appli	627	7	1.9	1600	4	US-09-655-378A-12	Sequence 12, Appli
c 555	7	1.9	1232	4	US-09-506-286B-23	Sequence 23, Appli	628	7	1.9	1600	4	US-09-940-244-12	Sequence 12, Appli
c 556	7	1.9	1232	4	US-09-762-861B-22	Sequence 22, Appli	629	7	1.9	1600	4	US-09-333-145-12	Sequence 12, Appli
c 557	7	1.9	1232	4	US-09-762-861B-25	Sequence 25, Appli	c 630	7	1.9	1614	4	US-09-252-991A-9387	Sequence 9387, Ap
c 558	7	1.9	1232	4	US-10-065-133A-22	Sequence 22, Appli	c 631	7	1.9	1618	2	US-08-533-669A-9	Sequence 9, Appli
c 559	7	1.9	1232	4	US-10-065-133A-23	Sequence 23, Appli	c 632	7	1.9	1618	2	US-08-607-509-1	Sequence 1, Appli
c 560	7	1.9	1232	4	US-10-434-811A-22	Sequence 22, Appli	c 633	7	1.9	1618	2	US-08-454-036-1	Sequence 1, Appli
c 561	7	1.9	1232	4	US-10-434-811A-23	Sequence 23, Appli	c 634	7	1.9	1618	3	US-08-634-642-1	Sequence 1, Appli
c 562	7	1.9	1233	4	US-09-506-286B-19	Sequence 19, Appli	c 635	7	1.9	1618	3	US-08-989-370-1	Sequence 1, Appli
c 563	7	1.9	1233	4	US-09-762-861B-19	Sequence 19, Appli	c 636	7	1.9	1618	3	US-09-183-861-9	Sequence 9, Appli
c 564	7	1.9	1233	4	US-10-065-133A-19	Sequence 19, Appli	c 637	7	1.9	1618	3	US-09-022-765-9	Sequence 9, Appli
c 565	7	1.9	1233	4	US-10-434-811A-19	Sequence 19, Appli	c 638	7	1.9	1618	4	US-09-551-974A-9	Sequence 9, Appli
c 566	7	1.9	1242	4	US-09-252-991A-12428	Sequence 12428, A	c 639	7	1.9	1618	4	US-09-565-501A-9	Sequence 9, Appli
c 567	7	1.9	1251	4	US-09-205-258-156	Sequence 156, App	c 640	7	1.9	1618	4	US-09-639-206A-9	Sequence 9, Appli
c 568	7	1.9	1251	4	US-09-248-796A-2693	Sequence 2693, Ap	c 641	7	1.9	1618	4	US-09-874-923-9	Sequence 9, Appli
c 569	7	1.9	1253	2	US-08-786-606-6	Sequence 6, Appli	c 642	7	1.9	1618	4	US-09-398-169-1	Sequence 1, Appli
c 570	7	1.9	1253	4	US-09-016-434-5	Sequence 5, Appli	c 643	7	1.9	1618	4	US-08-798-841-9	Sequence 9, Appli
c 571	7	1.9	1254	4	US-09-489-039A-4384	Sequence 4384, Ap	c 644	7	1.9	1618	5	PCT-US95-05064-1	Sequence 1, Appli
c 572	7	1.9	1260	1	US-08-029-404-1	Sequence 1, Appli	c 645	7	1.9	1629	4	US-09-799-451-699	Sequence 699, App
c 573	7	1.9	1260	3	US-08-459-953A-1	Sequence 1, Appli	646	7	1.9	1638	3	US-09-351-224E-2	Sequence 2, Appli
c 574	7	1.9	1260	4	US-09-393-212-1	Sequence 1, Appli	647	7	1.9	1638	4	US-09-677-488A-2	Sequence 2, Appli
c 575	7	1.9	1272	4	US-09-248-796A-1740	Sequence 1740, Ap	648	7	1.9	1638	4	US-09-677-682B-2	Sequence 2, Appli
c 576	7	1.9	1317	3	US-09-457-046B-27	Sequence 27, Appli	649	7	1.9	1638	4	US-09-882-694B-2	Sequence 2, Appli
c 577	7	1.9	1317	4	US-09-023-655-051	Sequence 851, App	650	7	1.9	1660	4	US-09-142-108C-16	Sequence 16, Appli
578	7	1.9	1317	4	US-09-866-570B-27	Sequence 27, Appli	651	7	1.9	1662	1	US-08-565-386-2	Sequence 2, Appli
579	7	1.9	1329	4	US-09-252-991A-12162	Sequence 12162, A	652	7	1.9	1683	4	US-09-912-559-1	Sequence 1, Appli
580	7	1.9	1347	3	US-09-457-046B-55	Sequence 55, Appli	653	7	1.9	1683	3	US-09-912-559-2	Sequence 2, Appli
581	7	1.9	1347	4	US-09-866-570B-55	Sequence 55, Appli	654	7	1.9	1691	3	US-09-351-324E-1	Sequence 1, Appli
582	7	1.9	1367	4	US-09-023-655-971	Sequence 971, App	655	7	1.9	1691	4	US-09-677-488A-1	Sequence 1, Appli
c 583	7	1.9	1368	4	US-09-902-540-4506	Sequence 4506, App	656	7	1.9	1691	4	US-09-677-682B-1	Sequence 1, Appli
584	7	1.9	1381	3	US-08-936-165A-225	Sequence 225, App	657	7	1.9	1691	4	US-09-882-694B-1	Sequence 1, Appli
585	7	1.9	1390	2	US-08-683-908-3	Sequence 3, Appli	c 658	7	1.9	1703	3	US-09-135-021-77	Sequence 77, Appli
586	7	1.9	1406	3	US-09-287-097-1	Sequence 1, Appli	c 659	7	1.9	1703	3	US-09-135-020-3	Sequence 3, Appli
c 587	7	1.9	1419	4	US-09-252-991A-15908	Sequence 15908, A	c 660	7	1.9	1703	3	US-09-135-010A-3	Sequence 3, Appli
c 588	7	1.9	1425	4	US-09-252-991A-15878	Sequence 15878, A	c 661	7	1.9	1703	3	US-09-444-871-3	Sequence 3, Appli
c 589	7	1.9	1425	4	US-09-543-681A-2701	Sequence 2701, Ap	c 662	7	1.9	1703	3	US-09-597-735-3	Sequence 3, Appli
c 590	7	1.9	1428	4	US-09-489-039A-3243	Sequence 3243, Ap	c 663	7	1.9	1703	3	US-09-444-295-3	Sequence 3, Appli
c 591	7	1.9	1433	1	US-07-968-971A-11	Sequence 11, Appli	c 664	7	1.9	1703	3	US-09-597-732-3	Sequence 3, Appli
c 592	7	1.9	1433	1	US-08-383-756-5	Sequence 5, Appli	c 665	7	1.9	1703	4	US-09-597-731-3	Sequence 3, Appli
c 593	7	1.9	1433	1	US-08-424-406-2	Sequence 2, Appli	666	7	1.9	1704	4	US-09-023-655-263	Sequence 263, App
c 594	7	1.9	1433	1	US-08-464-523B-8	Sequence 8, Appli	667	7	1.9	1715	3	US-09-023-655-230A-1	Sequence 1, Appli
c 595	7	1.9	1433	2	US-08-460-898-5	Sequence 5, Appli	668	7	1.9	1715	4	US-08-757-230A-1	Sequence 1, Appli
c 596	7	1.9	1439	4	US-09-640-211A-332	Sequence 332, App	669	7	1.9	1715	5	PCT-US95-02315-1	Sequence 1, Appli

670	7	1.9	1737	4	US-09-142-108C-3	Sequence 3, Appl	743	7	1.9	2502	4	US-09-684-938-21	Sequence 21, Appl
c 671	7	1.9	1774	3	US-09-215-252-16	Sequence 16, Appl	744	7	1.9	2502	4	US-09-308-825A-21	Sequence 21, Appl
c 672	7	1.9	1774	4	US-09-970-989A-16	Sequence 16, Appl	745	7	1.9	2502	4	US-09-758-282B-39	Sequence 39, Appl
c 673	7	1.9	1798	3	US-09-797-906-1	Sequence 1, Appl	746	7	1.9	2502	4	US-09-655-378A-21	Sequence 21, Appl
c 674	7	1.9	1803	4	US-09-327-138C-5	Sequence 5, Appl	747	7	1.9	2502	4	US-09-940-244-21	Sequence 21, Appl
c 675	7	1.9	1815	4	US-09-328-352-341	Sequence 341, App	748	7	1.9	2502	4	US-09-333-145-21	Sequence 21, Appl
c 676	7	1.9	1831	4	US-09-799-451-646	Sequence 646, App	749	7	1.9	2502	4	US-09-577-304A-39	Sequence 39, Appl
c 677	7	1.9	1839	4	US-09-774-528-214	Sequence 214, App	750	7	1.9	2508	2	US-08-850-993-1	Sequence 1, Appl
c 678	7	1.9	1855	4	US-09-023-655-856	Sequence 856, App	751	7	1.9	2520	1	US-08-405-254-9	Sequence 9, Appl
c 679	7	1.9	1866	4	US-09-252-931A-2554	Sequence 2554, App	c 752	7	1.9	2520	4	US-09-023-655-917	Sequence 917, App
c 680	7	1.9	1866	4	US-09-902-540-2398	Sequence 2398, App	753	7	1.9	2540	4	US-09-799-451-463	Sequence 463, App
c 681	7	1.9	1881	4	US-09-248-796A-752	Sequence 752, App	754	7	1.9	2574	4	US-09-902-540-1961	Sequence 1961, App
c 682	7	1.9	1926	4	US-09-328-352-2865	Sequence 2865, App	755	7	1.9	2588	3	US-09-087-465-7	Sequence 7, Appl
c 683	7	1.9	1930	5	PCT-US95-07874-1	Sequence 1, Appl	756	7	1.9	2588	4	US-09-016-434-1145	Sequence 1145, App
c 684	7	1.9	1930	4	US-09-544-900-1	Sequence 1, Appl	757	7	1.9	2588	4	US-09-972-800A-7	Sequence 7, Appl
c 685	7	1.9	1950	4	US-09-640-419C-1	Sequence 1, Appl	c 758	7	1.9	2588	4	US-09-023-655-958	Sequence 958, App
c 686	7	1.9	1974	4	US-09-540-236-1239	Sequence 1239, App	759	7	1.9	2606	1	US-08-408-318-1	Sequence 1, Appl
c 687	7	1.9	1991	4	US-09-270-767-14329	Sequence 14329, App	c 760	7	1.9	2606	1	US-08-839-164-1	Sequence 1, Appl
c 688	7	1.9	2017	3	US-09-436-983-1	Sequence 1, Appl	c 761	7	1.9	2628	4	US-09-919-831-1	Sequence 1, Appl
c 689	7	1.9	2028	4	US-10-162-012-28	Sequence 28, Appl	762	7	1.9	2658	3	US-08-727-308-2	Sequence 2, Appl
c 690	7	1.9	2099	4	US-09-800-729-56	Sequence 56, Appl	763	7	1.9	2658	3	US-08-727-308-3	Sequence 3, Appl
c 691	7	1.9	2108	4	US-09-800-729-20	Sequence 20, Appl	764	7	1.9	2730	4	US-09-789-599A-1	Sequence 1, Appl
c 692	7	1.9	2116	3	US-09-000-041A-1	Sequence 1, Appl	c 765	7	1.9	2787	4	US-09-252-991A-9331	Sequence 9331, App
c 693	7	1.9	2116	4	US-09-734-002-1	Sequence 1, Appl	766	7	1.9	2790	4	US-09-252-991A-2632	Sequence 2632, App
c 694	7	1.9	2145	3	US-09-059-584-48	Sequence 48, Appl	c 767	7	1.9	2791	4	US-09-327-138C-4	Sequence 4, Appl
c 695	7	1.9	2147	4	US-09-949-016-3887	Sequence 3887, App	c 768	7	1.9	2899	4	US-09-270-767-13753	Sequence 13753, A
c 696	7	1.9	2195	1	US-08-915-003-1	Sequence 1, Appl	769	7	1.9	2907	4	US-09-417-197-48	Sequence 48, Appl
c 697	7	1.9	2195	2	US-08-642-247-1	Sequence 1, Appl	770	7	1.9	2913	4	US-09-417-197-66	Sequence 66, Appl
c 698	7	1.9	2196	4	US-09-540-236-124	Sequence 124, App	c 771	7	1.9	2917	2	US-08-624-581-3	Sequence 3, Appl
c 699	7	1.9	2220	4	US-09-489-039A-4703	Sequence 4703, App	c 772	7	1.9	2923	1	US-08-480-449-1	Sequence 1, Appl
c 700	7	1.9	2220	6	5171850-1	Patent No. 5171850	c 773	7	1.9	2923	3	US-08-660-542-1	Sequence 1, Appl
c 701	7	1.9	2220	6	5171850-1	Patent No. 5171850	c 774	7	1.9	2923	3	US-08-479-603-1	Sequence 1, Appl
c 702	7	1.9	2259	4	US-09-252-991A-13556	Sequence 13556, A	c 775	7	1.9	2923	4	US-08-939-107-1	Sequence 1, Appl
c 703	7	1.9	2277	4	US-09-506-286B-46	Sequence 46, Appl	c 776	7	1.9	2923	4	US-08-931-764-1	Sequence 1, Appl
c 704	7	1.9	2277	4	US-09-506-286B-49	Sequence 49, Appl	c 777	7	1.9	2923	4	US-09-591-992-1	Sequence 1, Appl
c 705	7	1.9	2277	4	US-10-065-133A-46	Sequence 46, Appl	c 778	7	1.9	2923	4	US-09-067-447B-1	Sequence 1, Appl
c 706	7	1.9	2277	4	US-10-065-133A-49	Sequence 49, Appl	c 779	7	1.9	2923	4	US-08-479-620-1	Sequence 1, Appl
c 707	7	1.9	2281	4	US-09-023-655-26	Sequence 26, Appl	c 780	7	1.9	2927	3	US-09-232-878-5	Sequence 5, Appl
c 708	7	1.9	2283	4	US-09-107-532A-1836	Sequence 1836, App	781	7	1.9	2931	3	US-09-151-189-1	Sequence 1, Appl
c 709	7	1.9	2287	3	US-09-059-584-47	Sequence 47, Appl	782	7	1.9	2931	4	US-09-596-794-1	Sequence 1, Appl
c 710	7	1.9	2326	4	US-10-162-012-26	Sequence 26, Appl	783	7	1.9	2931	4	US-09-840-762A-1	Sequence 1, Appl
c 711	7	1.9	2329	1	US-08-455-559-9	Sequence 9, Appl	c 784	7	1.9	2967	4	US-09-902-540-7756	Sequence 7756, App
c 712	7	1.9	2329	3	US-09-145-060-9	Sequence 9, Appl	785	7	1.9	3008	4	US-09-949-016-587	Sequence 587, App
c 713	7	1.9	2329	5	PCT-US94-00657-9	Sequence 9, Appl	786	7	1.9	3013	4	US-09-949-016-4921	Sequence 4921, App
c 714	7	1.9	2341	4	US-09-506-286B-44	Sequence 44, Appl	c 787	7	1.9	3064	4	US-09-620-312D-378	Sequence 378, App
c 715	7	1.9	2341	4	US-09-506-286B-47	Sequence 47, Appl	c 788	7	1.9	3150	4	US-09-489-039A-5843	Sequence 5843, App
c 716	7	1.9	2341	4	US-10-065-133A-44	Sequence 44, Appl	c 789	7	1.9	3236	3	US-08-961-527-222	Sequence 222, App
c 717	7	1.9	2341	4	US-10-065-133A-47	Sequence 47, Appl	c 790	7	1.9	3301	2	US-08-447-430A-42	Sequence 42, Appl
c 718	7	1.9	2372	4	US-09-774-528-362	Sequence 362, App	c 791	7	1.9	3301	4	US-09-342-673-42	Sequence 42, Appl
c 719	7	1.9	2379	4	US-09-134-000C-2490	Sequence 2490, App	c 792	7	1.9	3340	4	US-09-714-948-1	Sequence 1, Appl
c 720	7	1.9	2394	4	US-09-799-451-931	Sequence 931, App	c 793	7	1.9	3372	1	US-07-906-349A-1	Sequence 1, Appl
c 721	7	1.9	2403	4	US-09-949-016-4376	Sequence 4376, App	c 794	7	1.9	3372	1	US-08-167-035-1	Sequence 1, Appl
c 722	7	1.9	2403	4	US-09-949-016-4377	Sequence 4377, App	c 795	7	1.9	3372	1	US-08-167-035-48	Sequence 48, Appl
c 723	7	1.9	2415	4	US-10-029-180-137	Sequence 137, App	796	7	1.9	3372	1	US-08-208-887A-1	Sequence 1, Appl
c 724	7	1.9	2475	4	US-09-799-451-932	Sequence 932, App	797	7	1.9	3372	2	US-08-539-005-1	Sequence 1, Appl
c 725	7	1.9	2484	3	US-08-961-527-234	Sequence 234, App	c 798	7	1.9	3372	2	US-08-539-005-48	Sequence 48, Appl
c 726	7	1.9	2492	4	US-09-902-540-421	Sequence 421, App	799	7	1.9	3372	3	US-09-344-521-1	Sequence 1, Appl
c 727	7	1.9	2495	4	US-09-949-016-5571	Sequence 5571, App	800	7	1.9	3372	3	US-09-280-598-1	Sequence 1, Appl
c 728	7	1.9	2502	1	US-08-073-384C-21	Sequence 21, Appl	801	7	1.9	3372	4	US-09-963-137-180	Sequence 180, App
c 729	7	1.9	2502	1	US-08-254-359A-21	Sequence 21, Appl	c 802	7	1.9	3423	2	US-08-447-430A-40	Sequence 40, Appl
c 730	7	1.9	2502	1	US-08-483-043-21	Sequence 21, Appl	c 803	7	1.9	3423	3	US-09-485-737B-86	Sequence 86, Appl
c 731	7	1.9	2502	1	US-08-481-238-21	Sequence 21, Appl	c 804	7	1.9	3423	4	US-09-342-673-40	Sequence 40, Appl
c 732	7	1.9	2502	2	US-08-471-066B-21	Sequence 21, Appl	c 805	7	1.9	3423	4	US-10-071-485-86	Sequence 86, Appl
c 733	7	1.9	2502	2	US-08-484-956-21	Sequence 21, Appl	c 806	7	1.9	3474	2	US-08-447-430A-41	Sequence 41, Appl
c 734	7	1.9	2502	2	US-08-757-653-21	Sequence 21, Appl	c 807	7	1.9	3474	2	US-08-318-837-10	Sequence 10, Appl
c 735	7	1.9	2502	2	US-08-599-431-21	Sequence 21, Appl	c 808	7	1.9	3474	3	US-08-122-458D-8	Sequence 8, Appl
c 736	7	1.9	2502	2	US-08-756-386-21	Sequence 21, Appl	c 809	7	1.9	3474	4	US-09-342-673-41	Sequence 41, Appl
c 737	7	1.9	2502	2	US-08-823-516-21	Sequence 21, Appl	c 810	7	1.9	3519	2	US-08-380-403A-1	Sequence 1, Appl
c 738	7	1.9	2502	3	US-08-682-853A-21	Sequence 21, Appl	c 811	7	1.9	3519	2	US-08-895-628-1	Sequence 1, Appl
c 739	7	1.9	2502	3	US-08-759-038-21	Sequence 21, Appl	c 812	7	1.9	3519	3	US-08-895-628-1	Sequence 1, Appl
c 740	7	1.9	2502	3	US-08-758-314-21	Sequence 21, Appl	c 813	7	1.9	3538	4	US-09-902-540-528	Sequence 528, App
c 741	7	1.9	2502	3	US-09-350-309-21	Sequence 21, Appl	814	7	1.9	3545	3	US-09-221-017B-468	Sequence 468, App
c 742	7	1.9	2502	3	US-08-520-946-21	Sequence 21, Appl	815	7	1.9	3635	2	US-08-553-436A-5	Sequence 5, Appl

C 816	7	1.9	3646	4	US-09-327-138C-36	Sequence 36, Appl	889	7	1.9	4986	3	US-09-338-907-121	Sequence 121, App
C 817	7	1.9	3651	4	US-09-134-000C-1725	Sequence 1725, Ap	890	7	1.9	4986	3	US-09-218-207-121	Sequence 121, App
C 818	7	1.9	3651	4	US-09-583-110-1163	Sequence 1163, Ap	891	7	1.9	4990	3	US-08-776-511-1	Sequence 1, Appl
C 819	7	1.9	3665	4	US-09-327-138C-35	Sequence 35, Appl	C 892	7	1.9	5005	4	US-09-695-437A-60	Sequence 60, Appl
C 820	7	1.9	3675	4	US-09-107-433-1744	Sequence 1744, Ap	893	7	1.9	5009	4	US-09-221-013A-4	Sequence 4, Appl
C 821	7	1.9	3686	4	US-09-327-138C-3	Sequence 3, Appl	894	7	1.9	5020	3	US-09-338-907-120	Sequence 120, App
C 822	7	1.9	3686	4	US-09-327-138C-37	Sequence 37, Appl	895	7	1.9	5020	3	US-09-218-207-120	Sequence 120, App
C 823	7	1.9	3801	4	US-09-640-882-1	Sequence 1, Appl	896	7	1.9	5044	3	US-09-338-907-115	Sequence 115, App
C 824	7	1.9	3937	4	US-09-620-312D-280	Sequence 280, App	897	7	1.9	5044	3	US-09-218-207-115	Sequence 115, App
C 825	7	1.9	3940	4	US-09-327-138C-1	Sequence 1, Appl	898	7	1.9	5057	3	US-09-338-907-123	Sequence 123, App
C 826	7	1.9	3966	3	US-09-215-131-1	Sequence 1, Appl	899	7	1.9	5057	3	US-09-218-207-123	Sequence 123, App
C 827	7	1.9	3966	3	US-09-222-734-1	Sequence 1, Appl	900	7	1.9	5076	4	US-09-991-258-8	Sequence 8, Appl
C 828	7	1.9	4009	2	US-08-500-860A-2	Sequence 2, Appl	C 901	7	1.9	5098	1	US-08-450-257-10	Sequence 10, Appl
C 829	7	1.9	4023	4	US-08-809-513A-8	Sequence 8, Appl	C 902	7	1.9	5098	1	US-08-450-246-10	Sequence 10, Appl
C 830	7	1.9	4108	3	US-08-981-729-8	Sequence 8, Appl	C 903	7	1.9	5098	1	US-08-450-098-10	Sequence 10, Appl
C 831	7	1.9	4108	3	US-08-981-446B-1	Sequence 1, Appl	C 904	7	1.9	5098	1	US-08-451-233-10	Sequence 10, Appl
C 832	7	1.9	4108	3	US-09-613-811-8	Sequence 8, Appl	C 905	7	1.9	5098	1	US-08-450-236-10	Sequence 10, Appl
C 833	7	1.9	4196	4	US-09-453-313-1	Sequence 1, Appl	C 906	7	1.9	5098	3	US-08-235-403-10	Sequence 10, Appl
C 834	7	1.9	4198	4	US-09-949-016-934	Sequence 934, App	C 907	7	1.9	5100	3	US-09-338-907-122	Sequence 122, App
C 835	7	1.9	4199	3	US-09-204-117B-1	Sequence 1, Appl	908	7	1.9	5100	3	US-09-218-207-122	Sequence 122, App
C 836	7	1.9	4245	2	US-08-929-967-4	Sequence 4, Appl	909	7	1.9	5115	3	US-08-825-852-19	Sequence 19, Appl
C 837	7	1.9	4309	5	PCT-US91-02954-11	Sequence 11, Appl	910	7	1.9	5115	3	US-09-052-888-19	Sequence 19, Appl
C 838	7	1.9	4342	3	US-09-338-907-107	Sequence 107, App	911	7	1.9	5115	4	US-09-723-890-19	Sequence 19, Appl
C 839	7	1.9	4342	3	US-09-218-207-107	Sequence 107, App	912	7	1.9	5115	4	US-09-723-901-19	Sequence 19, Appl
C 840	7	1.9	4352	4	US-09-601-326-77	Sequence 77, Appl	913	7	1.9	5115	4	US-09-723-547-19	Sequence 19, Appl
C 841	7	1.9	4451	3	US-09-303-064-45	Sequence 45, Appl	914	7	1.9	5115	4	US-08-724-127-19	Sequence 19, Appl
C 842	7	1.9	4451	3	US-09-086-503-45	Sequence 45, Appl	915	7	1.9	5115	4	US-09-723-931-19	Sequence 19, Appl
C 843	7	1.9	4481	3	US-08-867-611-1	Sequence 1, Appl	916	7	1.9	5115	4	US-09-723-873-19	Sequence 19, Appl
C 844	7	1.9	4481	4	US-09-690-359-1	Sequence 1, Appl	917	7	1.9	5115	4	US-09-724-114-19	Sequence 19, Appl
C 845	7	1.9	4481	5	PCT-US92-06965A-6	Sequence 6, Appl	918	7	1.9	5115	4	US-09-723-913-19	Sequence 19, Appl
C 846	7	1.9	4529	1	US-08-565-386-1	Sequence 1, Appl	919	7	1.9	5115	4	US-09-723-912-19	Sequence 19, Appl
C 847	7	1.9	4529	3	US-09-338-907-118	Sequence 118, App	920	7	1.9	5148	3	US-09-338-907-112	Sequence 112, App
C 848	7	1.9	4582	3	US-09-218-207-118	Sequence 118, App	921	7	1.9	5148	3	US-09-218-207-112	Sequence 112, App
C 849	7	1.9	4593	3	US-08-801-344-1	Sequence 1, Appl	C 922	7	1.9	5197	3	US-09-293-170-6	Sequence 6, Appl
C 850	7	1.9	4593	3	US-09-498-599-1	Sequence 1, Appl	C 923	7	1.9	5201	4	US-09-640-882-2	Sequence 2, Appl
C 851	7	1.9	4612	4	US-09-626-301-1	Sequence 1, Appl	C 924	7	1.9	5201	4	US-09-640-882-3	Sequence 3, Appl
C 852	7	1.9	4642	4	US-09-626-301-3	Sequence 3, Appl	C 925	7	1.9	5227	2	US-08-996-306-3	Sequence 3, Appl
C 853	7	1.9	4686	3	US-09-338-907-117	Sequence 117, App	C 926	7	1.9	5227	2	US-09-338-907-113	Sequence 113, App
C 854	7	1.9	4686	3	US-09-218-207-117	Sequence 117, App	C 927	7	1.9	5234	3	US-09-218-207-113	Sequence 113, App
C 855	7	1.9	4775	3	US-09-303-064-37	Sequence 37, Appl	C 928	7	1.9	5234	3	US-09-218-207-113	Sequence 113, App
C 856	7	1.9	4775	3	US-09-086-503-37	Sequence 37, Appl	C 929	7	1.9	5234	3	US-09-338-907-113	Sequence 113, App
C 857	7	1.9	4819	1	US-08-450-257-20	Sequence 20, Appl	C 930	7	1.9	5234	3	US-09-338-907-113	Sequence 113, App
C 858	7	1.9	4819	1	US-08-450-257-20	Sequence 20, Appl	C 931	7	1.9	5234	3	US-09-338-907-113	Sequence 113, App
C 859	7	1.9	4819	1	US-08-450-098-20	Sequence 20, Appl	C 932	7	1.9	5238	6	5453363-1	Patent No. 5453363
C 860	7	1.9	4819	1	US-08-451-233-20	Sequence 20, Appl	C 933	7	1.9	5238	6	5453363-1	Patent No. 5453363
C 861	7	1.9	4819	1	US-08-450-236-20	Sequence 20, Appl	C 934	7	1.9	5241	4	US-08-809-513A-1	Sequence 1, Appl
C 862	7	1.9	4819	3	US-08-235-403-20	Sequence 20, Appl	C 935	7	1.9	5241	4	US-08-809-513A-2	Sequence 2, Appl
C 863	7	1.9	4875	3	US-09-338-907-114	Sequence 114, App	C 936	7	1.9	5241	4	US-09-338-907-3	Sequence 3, Appl
C 864	7	1.9	4875	3	US-09-218-207-114	Sequence 114, App	C 937	7	1.9	5245	3	US-09-218-207-3	Sequence 3, Appl
C 865	7	1.9	4910	1	US-08-450-257-11	Sequence 11, Appl	C 938	7	1.9	5245	4	US-09-949-016-4210	Sequence 4210, Ap
C 866	7	1.9	4910	1	US-08-450-246-11	Sequence 11, Appl	C 939	7	1.9	5245	4	US-09-688-649-3	Sequence 3, Appl
C 867	7	1.9	4910	1	US-08-450-098-11	Sequence 11, Appl	C 940	7	1.9	5249	1	US-08-688-649-3	Sequence 3, Appl
C 868	7	1.9	4910	1	US-08-451-233-11	Sequence 11, Appl	C 941	7	1.9	5249	1	US-08-688-649-4	Sequence 4, Appl
C 869	7	1.9	4910	1	US-08-450-236-11	Sequence 11, Appl	C 942	7	1.9	5250	3	US-09-338-907-69	Sequence 69, Appl
C 870	7	1.9	4910	3	US-09-303-064-40	Sequence 40, Appl	C 943	7	1.9	5250	3	US-09-218-207-69	Sequence 69, Appl
C 871	7	1.9	4910	3	US-08-235-403-11	Sequence 11, Appl	C 944	7	1.9	5252	3	US-09-949-016-338	Sequence 338, App
C 872	7	1.9	4936	4	US-09-086-503-40	Sequence 40, Appl	C 945	7	1.9	5252	3	US-09-303-064-48	Sequence 48, Appl
C 873	7	1.9	4954	4	US-09-573-080A-329	Sequence 329, App	C 946	7	1.9	5258	3	US-09-086-503-48	Sequence 48, Appl
C 874	7	1.9	4954	4	US-09-949-016-4527	Sequence 4527, Ap	C 947	7	1.9	5290	3	US-09-338-907-119	Sequence 119, App
C 875	7	1.9	4958	3	US-09-338-907-116	Sequence 116, App	C 948	7	1.9	5290	3	US-09-218-207-119	Sequence 119, App
C 876	7	1.9	4958	3	US-09-218-207-116	Sequence 116, App	C 949	7	1.9	5290	3	US-09-338-907-124	Sequence 124, App
C 877	7	1.9	4977	1	US-08-450-257-17	Sequence 17, Appl	C 950	7	1.9	5326	3	US-09-218-207-124	Sequence 124, App
C 878	7	1.9	4977	1	US-08-450-257-17	Sequence 17, Appl	C 951	7	1.9	5326	3	US-09-218-207-124	Sequence 124, App
C 879	7	1.9	4977	1	US-08-450-246-14	Sequence 14, Appl	C 952	7	1.9	5418	3	US-09-949-016-14328	Sequence 14328, A
C 880	7	1.9	4977	1	US-08-450-246-17	Sequence 17, Appl	C 953	7	1.9	5438	3	US-08-809-326A-25	Sequence 25, Appl
C 881	7	1.9	4977	1	US-08-450-098-14	Sequence 14, Appl	C 954	7	1.9	5438	4	US-09-689-914A-25	Sequence 25, Appl
C 882	7	1.9	4977	1	US-08-450-098-17	Sequence 17, Appl	C 955	7	1.9	5438	4	US-09-689-913A-25	Sequence 25, Appl
C 883	7	1.9	4977	1	US-08-451-233-14	Sequence 14, Appl	C 956	7	1.9	5438	4	US-09-689-916A-25	Sequence 25, Appl
C 884	7	1.9	4977	1	US-08-451-233-17	Sequence 17, Appl	C 957	7	1.9	5446	4	US-09-338-907-124	Sequence 124, App
C 885	7	1.9	4977	1	US-08-450-236-17	Sequence 17, Appl	C 958	7	1.9	5552	3	US-08-155-888-1	Sequence 1, Appl
C 886	7	1.9	4977	1	US-08-450-236-17	Sequence 17, Appl	C 959	7	1.9	5574	1	US-08-450-257-22	Sequence 22, Appl
C 887	7	1.9	4977	3	US-08-235-403-14	Sequence 14, Appl	C 960	7	1.9	5574	1	US-08-450-098-22	Sequence 22, Appl
C 888	7	1.9	4977	3	US-08-235-403-17	Sequence 17, Appl	C 961	7	1.9	5574	1	US-08-451-233-22	Sequence 22, Appl

QY 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db 781 GTCTACCGTCCCTCCCAAGCACACCTGGTACCTGTGTGACAAAGGAGTGTTCAGATTACAT 840
QY 281 ProSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
Db 841 CCTCTCTGTCCAGGCCAGACTTCTCCAGGACACACAGCCAGAGTCCAGTC 900
QY 301 ArgGlyThrAlaAlaPheTyrHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
Db 901 AGAGTACAGCAGCGCTTTTACCATCATCTCCAGCTGCCAGTGGGTGCAAGCAGACCTCT 960
QY 321 ThrLysArgLysValGluGluMetGluValAspPheTyrAspGlyLysArgLeu 340
Db 961 ACTAAACCAAGTAGAGGAAATGGAGTGGATGACTTCTATGATGGGAATCAAAACGGCTC 1020
QY 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
Db 1021 TATATGAGATATATGTCAGAAATGTGGTCTGTGTGGCACTGATTTATCAGA 1080
QY 361 GlnGluGlyHisAlaSerProCysProProLeuGlnProValSerValMet 377
Db 1081 CAAGGAGCATGCTTCCCTTGTCCACTTTCAGCGCTGTTCTGTCTATG 1131

RESULT 2

US-08-969-106-5
; Sequence 5, Application US/08969106
; Patent No. 5986055
; GENERAL INFORMATION:
; APPLICANT: Yang, M.
; APPLICANT: Nandabalan, K.
; APPLICANT: Schulz, V.
; TITLE OF INVENTION: CDK2 INTERACTIONS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/969,106
; FILING DATE: 13-NOV-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7934-057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1260 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...1131
; OTHER INFORMATION:
US-08-969-106-5

Alignment Scores:

Pred. No.: 0 Length: 1260

Score: 377.00 Matches: 377
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0
US-09-736-250-1 (1-377) x US-08-969-106-5 (1-1260)
QY 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle 20
Db 1 ATGAAGTTTCAGGGCCTTTGGAAACACAGAGATTGTCTTCTCTGTGTGAAAGGCAATC 60
QY 21 ThrArgGluAlaGlnMetTyrLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 61 ACTAGGGAAGCACAGATGTGGAAAGTGAATGTGCGGAAATGCGCTTCAAAATCAGATGTT 120
QY 41 SerProSerGlnArgAspGluValIleGlnTyrLeuAlaLysLeuLysTyrGlnPheAsn 60
Db 121 TCTCCATCCAGAGAGATGAAGTAATTCATGGCTGGCCAACTCAAGTACCAATTCAC 180
QY 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 181 CTTTACCAGAAACATTTGCTGTGGCTAGCAGTCTTTTGGATAGGTTTATAGCTACCGTA 240
QY 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaLys 100
Db 241 AAGGCTCATCCAAATACTTTGAGTGTATTGCAATCAGCTGTTTTTCTAGCTGCCAAG 300
QY 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 301 ACTGTTGAGGAGATGAGAGAAATTCAGTACTAAGGTATTTGGCAAGAGACAGTTCTGT 360
QY 121 GlyCysSerSerGluIleLeuArgMetGluArgIleLeuLeuAspLysLeuAsnTrp 140
Db 361 GGATGTTCTCATCTGAAATTTTGGAGAAATGAGAGAAATTTCTGGATAAGTGAATGG 420
QY 141 AspleuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 421 GATCTTCACACAGCCACACCATTTGATTTCTTCATATTTTCCATGTCATTTGAGTGTCA 480
QY 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 481 ACTAGGCTCAGTTACTTTTTCAGTTGCCAAATTTGAGCCCATCTCAACATTTGGCAGTC 540
QY 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
Db 541 CTTACCAAGCAACTTACTTCTACTGTATGCGCTGCAACCAACTTCTGCAATTCAGAGGATCC 600
QY 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
Db 601 ATGCTTGTCTGGCCATGGTTAGTCTGGAATGAGAAACTCATTTCTGATTTGCTTTCT 660
QY 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
Db 661 CTTACAAATTGAATGCTTTCAGAAAGCACAGATGATAGTCTCCAGATTTGATCCATTTGCG 720
QY 241 GluLeuValAlaHisHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
Db 721 GAGCTTGTGGCACATCACCTTTTCTACTCTGAGTCTTCCCTGCTCTGAAATTCGGTTAT 780
QY 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db 781 GTCTACCGTCCCTCCAAAGCACACCTGTTGACAAAGGAGTGTTCAGATTACAT 840
QY 281 ProSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
Db 841 CCTCTCTGTCCAGGCCAGACTTCTCCAGGACACACAGCCAGAGTCCAGTCCAGTC 900
QY 301 ArgGlyThrAlaAlaPheTyrHisHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
Db 901 AGAGTACAGCAGCGCTTTTACCATCATCTCCAGCTGCCAGTGGGTGCAAGCAGACCTCT 960
QY 321 ThrLysArgLysValGluGluMetGluValAspAspPheTyrAspGlyLysArgLeu 340

Db 961 ACTAAACGCAAGTAGAGGAAATGGAAGTGGATGACTTCTATGATGGAATCAAAACGGCTC 1020
Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
Db 1021 TATAATGAAGATAAATGTCTCAGAAAATGGGGTCTCTGTGTGGCACTGATTTATCAAGA 1080
Qy 361 GlnGluGlyHisAlaSerProCysProCysProLeuGlnProValSerValMet 377
Db 1081 CAAGAGGACATGCTTCCCTTGTCCACTTGGACCTTGTTCGTCTATG 1131

RESULT 3

US-09-338-125-5
; Sequence 5, Application US/09338125
; Patent No. 6521412
; GENERAL INFORMATION:
; APPLICANT: Yang, M.
; APPLICANT: Nandabalan, K.
; APPLICANT: Schulz, V.
; TITLE OF INVENTION: CDK2 INTERACTIONS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/338,125
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/969,106
; FILING DATE: 13-NOV-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7934-057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1260 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...1131
; OTHER INFORMATION:
US-09-338-125-5

Alignment Scores:
Pred. No.: 0 Length: 1260
Score: 377.00 Matches: 377
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-736-250-1 (1-377) x US-09-338-125-5 (1-1260)

Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuGluLysAla 20
|||||

Db 1 ATGAAGTTTCCAGGGCCTTTTGGAAAACACAGAGATTGTCTTTCTGTGTTGAAAAGGCAATC 60
Qy 21 ThrArgGluAlaGlnMetTyrLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 61 ACTAGGAAGCAGATGTGGAAAGTGAATGTGGGAAAATGCCCTTCAAATCAGAATGTT 120
Qy 41 SerProSerGlnArgAspGluValIleGlnTyrLeuAlaLysLeuLysTyrGlnPheAsn 60
Db 121 TCTCCATCCAGAGAGATGAAGTAATTCATGGCTGGCCAACTCAAGATCAATTCAC 180
Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 181 CTTTACCACAGAAACATTTGCTCTGGCTAGCAGTCTTTTGGATAGGTTTTTAGCTACCGTA 240
Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaLys 100
Db 241 AAGGCTCATCCAAAATACCTTGAGTTGTATTGCAATCAGCTGTTTTTCTAGCTGCCAAG 300
Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 301 ACTGTTGAGGAGATGAGAAATTCAGTACTAAAGGTATTGGCAGAGACAGTTTCTGT 360
Qy 121 GlyCysSerSerGluIleLeuArgMetGluArgIleLeuAspLysLeuAsnTyr 140
Db 361 GGATGTTCTTCATCTGAAATTTTGAGAAATGGAGAAATTTCTGGATAAAGTTGAATTGG 420
Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 421 GATCTTCACAGCAGCCACCATTTGGATTTCTTCATATTTTCCATGTCATTTGAGTGTCA 480
Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 481 ACTAGGCTCAGTTACTTTTCAGTTTGGCCCAATTTGAGCCCATCTCAACATTTGGCAGTC 540
Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
Db 541 CTTACCAAGCAACTACTTCACTGTATGGCCTGCAACCAACTTCTGCAATTCAGAGGATCC 600
Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTyrLeuSer 220
Db 601 ATGCTTGTCTGGCCATGGTTAGTCTGGAAATGGAGAAATCAATCTCTGATTTGGCTTCT 660
Qy 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
Db 661 CTTACAATTCGAATGCTTTCAGAAAGCAGACAGATGATAGTCTCCAGATTCATTTGTCGG 720
Qy 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
Db 721 GAGCTTTGTGGCAGATCACCTTTCTACTCTGCACTTCTCCCTGCTCTGAAATTCGGTTAT 780
Qy 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db 781 GTCTACCGTCCCTCAAGCACACCTTGGTGAATCTGTGACAAAGAGTGTTCAGATTACAT 840
Qy 281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
Db 841 CCCTCTCTGTCCAGGCCAGACTTCTCCAGGACAAACAGCAAGCCAGAAAGTCCAGTC 900
Qy 301 ArgGlyThrAlaAlaPheTyrHisHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
Db 901 AGAGGTACAGCAGCCTTTTACCATCATCTCCAGCTGCCAGTGGGTGCAAGCAGACCTCT 960
Qy 321 ThrLysArgLysValGluGluMetGluValAspAspPheTyrAspGlyIleLysArgLeu 340
Db 961 ACTAAACGCAAGTAGAGGAAATGGAAAGTGGATGACTTCTATGATGGAATCAAAACGGCTC 1020
Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
Db 1021 TATAATGAAGATAAATGTCTCAGAAAATGGGGTCTGTGTGGCACTGATTTATCAAGA 1080
Qy 361 GlnGluGlyHisAlaSerProCysProCysProLeuGlnProValSerValMet 377
Db 1081 CAAGAGGACATGCTTCCCTTGTCCACCTTTGACGCTGTTTCTGTGTCAG 1131

RESULT 4

US-09-023-655-899
; Sequence 899, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 899:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1260 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g1183161
; US-09-023-655-899

Alignment Scores:
Pred. No.: 0 Length: 1260
Score: 377.00 Matches: 377
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-736-250-1 (1-377) x US-09-023-655-899 (1-1260)

Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaLys 20
Db 1 ATGAAGTTTCAGGGCCCTTGGAACCAAGAGATGCTCTTCTGTTGGAAAAGGCAATC 60
Qy 21 ThrArgGluAlaGlnMetTplysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 61 ACTAGGGAAGCACACATGTGGAAAGTGAATGTCGGGAAATGCCCTTCAATCAGAAATGTT 120
Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTrpGlnPheAsn 60
Db 121 TCTCCATCCAGAGAGATGAAGTAATTCATGGCTGGCCAACTCAAGTACCAATTCAC 180
Qy 61 LeuTyProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80

Db 181 CTTTACCAGAAACATTTGCTCTGGCTAGACGCTCTTTGGATAGGTTTGTAGTACCCTA 240
Qy 81 LysAlaHisProLysTrpLeuSerCysIleAlaIleSerCysPhePheLeuAlaLys 100
Db 241 AAGGCTCATCCAAATACCTTGAAGTGTATGCAATCAGCTGTTTCTTCTAGTCCCAAG 300
Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 301 ACTGTTGAGAAAGATGAGAAATCCAGTACTAAAGTATTGGCAAGACAGATTTCTGT 360
Qy 121 GlyCysSerSerGluIleLeuArgMetGluArgIleIleLeuAspLysLeuAsnTrp 140
Db 361 GGAATGTCCTCATCTGAAATTTGAGATGGAGAAATATTCTGGATGAATGGATTGG 420
Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 421 GATCTTCACACAGCCACCATTTGATTTCTTCATATTTTCCATGCAATTCAGAGTGTCA 480
Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 481 ACTAGGCTCAGTTACTTTTTCAGTTTGGCCAAATTTGAGCCCATCTCAACATTTGGCAGTC 540
Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
Db 541 CTTTACCAGCAACTTCTGATGGCTGCAACCACTTTCGCAATTCAGAGGATCC 600
Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
Db 601 ATGCTTGTCTGGCCATGTTAGTCTGGAATGAGAAACTCATTTCTGATGGCTTTCT 660
Qy 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
Db 661 CTTTACAAATGAACTGCTTCAGAAAGCACAGATGATGATGATGATGATGATGATGATG 720
Qy 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuLeuAsnSerValTyr 260
Db 721 GAGCTTGTGGCACAATCCTTTCTTACTCTGAGTCTTCCCTGCTCTGAAATTCGTTAT 780
Qy 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db 781 GTCTACCGTCCCTCAAGCACACCTGCTGTCACCAAGAGAGGATGTTTTCAGATTACAT 840
Qy 281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
Db 841 CCTCTCTCTGTCAGGCTCCAGCTTCTTCCAAAGACACAGAGCCAGAGTCCAGTCC 900
Qy 301 ArgGlyThrAlaAlaPheTyrHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
Db 901 AGAGGTACAGAGCCTTTTACCATCATCTCCAGCTGCCAGTGGGTGCAAGACACCTCT 960
Qy 321 ThrLysArgLysValGluGluMetGluValAspPheTyrAspGlyIleLysArgLeu 340
Db 961 ACTAAACGCAAGTAGAGGAAATGGAAGTGAATGATCTTCTATGATGAAATCAAGGCTC 1020
Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
Db 1021 TATAATGAAGATAATGTCTCAGAAATGTGGTCTCTGTGTGGCACTGATTTATCAAGA 1080
Qy 361 GlnGluGlyHisAlaSerProCysProLeuGlnProValSerValMet 377
Db 1081 CAAGAGGAGCATGCTTCCCTTGTCCACCTTTGAGCCTGTTCTGTGCTATG 1131

RESULT 5

US-09-513-999C-1907
; Sequence 1907, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.V.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961

```
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 1907
; LENGTH: 444
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 52..444
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 10
; OTHER INFORMATION: k=g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 11
; OTHER INFORMATION: n=a, g, c or t
US-09-513-999C-1907

Alignment Scores:
Pred. No.: 3,47e-138 Length: 444
Score: 144.00 Matches: 144
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 38.20% Indels: 0
DB: 4 Gaps: 0

US-09-736-250-1 (1-377) x US-09-513-999C-1907 (1-444)

Qy 117 AspSerPheCysGlyCysSerSerSerGluLeuLeuArgMetGluArgIleLeuLeuAsp 136
Db 13 GACAGTTCCTGGGATGTTCTCTCATCTGAAATTTTGAGATGGAGAAATTTATCTGGAT 72

Qy 137 LysLeuAsnTrpAspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAla 156
Db 73 AAGTTGAATTGGGATCTTCACAGCCACACCATGGATTTCTTCATATTTTCCATGCC 132

Qy 157 IleAlaValSerThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGln 176
Db 133 ATTGCAGTGTCACACTAGGCCTCAGTTACTTTTCAGTTTGCCCAATTTGAGCCCATCTCAA 192

Qy 177 HisLeuAlaValLeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGln 196
Db 193 CATTTGGCAGTCCCTTACCAGCAACTACTTCCACTGTATGGCTGCAACCAACTTCTGCAA 252

Qy 197 PheArgGlySerMetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIlePro 216
Db 253 TTCAGAGATCCATGCTTGCTCTGGCCATGTTAGTCTGGAAATGGAGAACTCATTCCT 312

Qy 217 AspTrpLeuSerLeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeu 236
Db 313 GATTGGCTTCTCTTACAAATTAAGTCTCTCAGAAAGCACAGATGATGCTCCAGTTG 372

Qy 237 IleHisCysArgGluLeuValAlaHisIleSerThrLeuGlnSerSerLeuProLeu 256
Db 373 ATCCATTCTGGGAGCTTGTGGACATCACCTTTCTACTCTGCAGTCTTCCCTGCCTCTG 432

Qy 257 AsnSerValTyr 260
Db 433 AATTCGGTTTAT 444

RESULT 6
US-09-513-999C-29894
; Sequence 1, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
```

```
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 29894
; LENGTH: 304
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 230
; OTHER INFORMATION: m=a or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 231
; OTHER INFORMATION: n=a, g, c or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 268
; OTHER INFORMATION: w=a or t
US-09-513-999C-29894

Alignment Scores:
Pred. No.: 1.23e-25 Length: 304
Score: 34.00 Matches: 34
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 9.02% Indels: 0
DB: 4 Gaps: 0

US-09-736-250-1 (1-377) x US-09-513-999C-29894 (1-304)

Qy 344 AspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArgGlnGluGly 363
Db 2 GATAATCTCTCAGAAATGTTGGTCTGTGTGGCACTGATTATCAACAGACAGAGGA 61

Qy 364 HisAlaSerProCysProProLeuGlnProValSerValMet 377
Db 62 CATGCTTCCCTTGTCACCTTTGCAGCCGTTTCTGTCATG 103

RESULT 7
US-09-129-112-1
; Sequence 1, Application US/09129112
; Patent No. 6465716
; GENERAL INFORMATION:
; APPLICANT: Etzler, Marilyn B.
; APPLICANT: Murphy, Judith B.
; TITLE OF INVENTION: The Regents of the University of California
; FILE REFERENCE: 023070-079810US
; CURRENT APPLICATION NUMBER: US/09/129,112
; CURRENT FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: US 08/907,226
; PRIOR FILING DATE: 1997-08-06
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1643
; TYPE: DNA
; ORGANISM: Dolichos biflorus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (51)..(1439)
; OTHER INFORMATION: NEP46 (DB46) No. 6465716 factor binding lectin
; NAME/KEY: mat_peptide
; LOCATION: (195)..(1436)
US-09-129-112-1
```

Alignment Scores:
 Pred. No.: 26.8 Length: 1643
 Score: 9.00 Matches: 9
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.39% Indels: 0
 DB: 3 Gaps: 0

US-09-736-250-1 (1-377) x US-09-129-112-1 (1-1643)

Qy 165 LeuLeuPheSerLeuProLysLeuSer 173
 Db 108 CTACTCTTCTCATTCGCCAAACTTCT 134

RESULT 8
 US-09-129-112-3
 ; Sequence 3, Application US/09129112
 ; Patent No. 6465716
 ; GENERAL INFORMATION:
 ; APPLICANT: Etzler, Marilyn E.
 ; APPLICANT: Murphy, Judith B.
 ; TITLE OF INVENTION: The Regents of the University of California
 ; FILE REFERENCE: 023070-079810US
 ; CURRENT APPLICATION NUMBER: US/09/129,112
 ; CURRENT FILING DATE: 1998-08-04
 ; PRIOR FILING DATE: 1997-08-06
 ; NUMBER OF SEQ ID NOS: 19
 ; SOFTWARE: Patent In Ver. 2.1
 ; SEQ ID NO 3
 ; LENGTH: 6265
 ; TYPE: DNA
 ; ORGANISM: Dolichos biflorus
 ; FEATURE:
 ; NAME/KEY: exon
 ; LOCATION: (633)..(944)
 ; NAME/KEY: intron
 ; LOCATION: (945)..(1022)
 ; NAME/KEY: exon
 ; LOCATION: (1023)..(1151)
 ; NAME/KEY: intron
 ; LOCATION: (1152)..(1559)
 ; NAME/KEY: exon
 ; LOCATION: (1560)..(1616)
 ; NAME/KEY: intron
 ; LOCATION: (1617)..(1697)
 ; NAME/KEY: exon
 ; LOCATION: (1698)..(1790)
 US-09-129-112-3

Alignment Scores:
 Pred. No.: 99.8 Length: 6265
 Score: 9.00 Matches: 9
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.39% Indels: 0
 DB: 3 Gaps: 0

US-09-736-250-1 (1-377) x US-09-129-112-3 (1-6265)

Qy 165 LeuLeuPheSerLeuProLysLeuSer 173
 Db 732 CTACTCTTCTCATTCGCCAAACTTCT 758

RESULT 9
 US-09-313-294A-98
 ; Sequence 98, Application US/09313294A
 ; Patent No. 6476212
 ; GENERAL INFORMATION:
 ; APPLICANT: Lalgudi, Raghunath V.

; APPLICANT: Ito, Laura Y.
 ; APPLICANT: Sherman, Bradley K.
 ; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
 ; FILE REFERENCE: PL-0017 US
 ; CURRENT APPLICATION NUMBER: US/09/313,294A
 ; CURRENT FILING DATE: 1999-05-14
 ; NUMBER OF SEQ ID NOS: 7600
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 98
 ; LENGTH: 277
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; OTHER INFORMATION: incyte ID No. 6476212 700548521H1
 ; NAME/KEY: unsure
 ; LOCATION: 57, 79, 106, 202, 275
 ; OTHER INFORMATION: a, t, c, g, or other
 US-09-313-294A-98

Alignment Scores:
 Pred. No.: 49.2 Length: 277
 Score: 8.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.12% Indels: 0
 DB: 4 Gaps: 0

US-09-736-250-1 (1-377) x US-09-313-294A-98 (1-277)

Qy 172 LeuSerProSerGlnHisLeuAla 179
 Db 2 CTATCCCATCGCAGCATCTGCC 25

RESULT 10
 US-09-513-999C-32630/c
 ; Sequence 32630, Application US/09513999C
 ; Patent No. 6783961
 ; GENERAL INFORMATION:
 ; APPLICANT: Dumas Milne Edwards, J.B.
 ; APPLICANT: Duclert, A.
 ; APPLICANT: Giordano, J.Y.
 ; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
 ; Patent No. 6783961
 ; FILE REFERENCE: 59.US2.REG
 ; CURRENT APPLICATION NUMBER: US/09/513,999C
 ; CURRENT FILING DATE: 2000-02-24
 ; PRIOR APPLICATION NUMBER: US 60/122,487
 ; PRIOR FILING DATE: 1999-02-26
 ; NUMBER OF SEQ ID NOS: 36681
 ; SOFTWARE: Patent.pm
 ; SEQ ID NO 32630
 ; LENGTH: 279
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: 139
 ; OTHER INFORMATION: n=a, g, c or t
 ; NAME/KEY: misc_feature
 ; LOCATION: 221
 ; OTHER INFORMATION: k=g or t
 ; NAME/KEY: misc_feature
 ; LOCATION: 252
 ; OTHER INFORMATION: m=a or c
 US-09-513-999C-32630

Alignment Scores:
 Pred. No.: 49.6 Length: 279
 Score: 8.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0

US-08-781-986A-1529

Alignment Scores:
Pred. No.: 70.7 Length: 400
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.12% Indels: 0
DB: 4 Gaps: 0

US-09-736-250-1 (1-377) x US-08-781-986A-1529 (1-400)

Qy 165 LeuLeuPheSerLeuProLysLeu 172
Db 130 CTACTTTTCTCTTCCAAATTA 153

RESULT 14

US-09-767-8308
; Sequence 8308, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8308
; LENGTH: 512
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-8308

Alignment Scores:
Pred. No.: 90.1 Length: 512
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.12% Indels: 0
DB: 4 Gaps: 0

US-09-736-250-1 (1-377) x US-09-270-767-8308 (1-512)

Qy 219 LeuSerLeuThrIleGluLeuLeu 226
Db 215 CTCTCACTTACTATAGAGCTGCTA 238

RESULT 15

US-09-270-767-23590
; Sequence 23590, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23590
; LENGTH: 512
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-23590

Alignment Scores:
Pred. No.: 90.1 Length: 512
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.12% Indels: 0
DB: 4 Gaps: 0

US-09-736-250-1 (1-377) x US-09-270-767-23590 (1-512)

Qy 219 LeuSerLeuThrIleGluLeuLeu 226
Db 215 CTCTCACTTACTATAGAGCTGCTA 238

Search completed: February 11, 2005, 14:37:22
Job time : 320.864 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model
Run on: February 11, 2005, 12:22:06 ; Search time 987.335 Seconds
(without alignments)
2253.008 Million cell updates/sec

Title: US-09-736-250-1
Perfect score: 377
Sequence: 1 MKFPGPLENORLSFLEKAI.....LSRQGHASCPPLQPVSM 377

Scoring table:
OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5378673 seqs, 295022984 residues

Word size: 1

Total number of hits satisfying chosen parameters: 10747261

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Command line parameters:
-MODEL=frame+p2n.model -DEV=xlh
-O=/cgn2_1/USPTO_spool/US09736250/runat_07022005_154944_20748/app_query_fasta_1.718
-DB=Published_applications NA -QFMT=fastap -SUFFIX=oligo.rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo
-TRANS=human40.cdi -LIST=1000 -DOCLIGN=200 -THR SCORE=quality -THR MIN=1
-ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USAR=US09736250 @CGN 1.1.582 @runat_07022005_154944_20748
-NCPU=6 -ICPU=3 -NO_WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DRV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60
-FPGAPOP=6 -FPGAEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : Published Applications NA:*

- 1: /cgn2_6/ptodata/1/pubna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/1/pubna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/1/pubna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/1/pubna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/1/pubna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/1/pubna/PCTUS_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/1/pubna/US08_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/1/pubna/US08_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/1/pubna/US09A_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/1/pubna/US09B_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/1/pubna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/1/pubna/US09_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/1/pubna/US10A_PUBCOMB.seq.*
- 14: /cgn2_6/ptodata/1/pubna/US10B_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/1/pubna/US10C_PUBCOMB.seq.*
- 16: /cgn2_6/ptodata/1/pubna/US10D_PUBCOMB.seq.*
- 17: /cgn2_6/ptodata/1/pubna/US10E_PUBCOMB.seq.*
- 18: /cgn2_6/ptodata/1/pubna/US10F_PUBCOMB.seq.*
- 19: /cgn2_6/ptodata/1/pubna/US11_NEW_PUB.seq.*
- 20: /cgn2_6/ptodata/1/pubna/US11_NEW_PUB.seq.*
- 21: /cgn2_6/ptodata/1/pubna/US60_NEW_PUB.seq.*
- 22: /cgn2_6/ptodata/1/pubna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	377	100.0	1134	12	US-09-736-250-2	Sequence 2, Appl1
2	377	100.0	1260	17	US-10-172-118-1326	Sequence 1326, Ap
3	377	100.0	1260	17	US-10-342-887-1326	Sequence 1326, Ap
4	377	100.0	1260	17	US-10-641-643-899	Sequence 899, App
5	377	100.0	1889	9	US-09-867-701-10907	Sequence 10907, A
6	266	70.6	2755	10	US-09-814-353-21586	Sequence 21586, A
7	139	36.9	444	17	US-10-242-535A-16032	Sequence 16032, A
8	139	36.9	444	17	US-10-085-783A-16032	Sequence 16032, A
9	133	35.3	490	17	US-10-242-535A-30212	Sequence 30212, A
10	133	35.3	490	17	US-10-085-783A-30212	Sequence 30212, A
11	123	32.6	2146	10	US-09-814-353-21294	Sequence 21294, A
12	118	31.3	389	17	US-10-242-535A-6834	Sequence 6834, Ap
13	118	31.3	389	17	US-10-085-783A-6834	Sequence 6834, Ap
14	112	29.7	369	17	US-10-242-535A-33391	Sequence 33391, A
15	112	29.7	369	17	US-10-085-783A-33391	Sequence 33391, A
16	77	20.4	350	17	US-10-242-535A-20816	Sequence 20816, A
17	77	20.4	350	17	US-10-085-783A-20816	Sequence 20816, A
C 18	75	19.9	486	10	US-09-814-353-17297	Sequence 17297, A
19	70	18.6	387	9	US-09-796-692-3935	Sequence 3935, Ap
20	70	18.6	387	14	US-10-040-862-3935	Sequence 3935, Ap
21	70	18.6	387	17	US-10-057-475B-3935	Sequence 3935, Ap
22	70	18.6	387	17	US-10-154-884B-3935	Sequence 3935, Ap
23	70	18.6	387	18	US-10-764-324-3935	Sequence 3935, Ap
24	65	17.2	447	9	US-09-777-564-1252	Sequence 1252, Ap
25	65	17.2	447	14	US-10-015-219-1252	Sequence 1252, Ap
26	62	16.4	889	9	US-09-867-701-10906	Sequence 10906, A
C 27	49	13.0	426	10	US-09-814-353-4614	Sequence 4614, Ap
C 28	49	13.0	426	10	US-09-814-353-10913	Sequence 10913, A
29	41	10.9	288	17	US-10-242-535A-57578	Sequence 57578, A
30	41	10.9	288	17	US-10-085-783A-57578	Sequence 57578, A
C 31	40	10.6	477	10	US-09-814-353-5374	Sequence 5374, Ap
C 32	40	10.6	477	10	US-09-814-353-11661	Sequence 11661, A
C 33	40	10.6	516	10	US-09-814-353-18045	Sequence 18045, A
C 34	37	9.8	444	9	US-09-920-300A-1413	Sequence 1413, Ap
C 35	37	9.8	444	13	US-10-033-528-1413	Sequence 1413, Ap
C 36	37	9.8	444	16	US-10-099-926-1413	Sequence 1413, Ap
37	34	9.0	308	17	US-10-242-535A-41781	Sequence 41781, A
38	34	9.0	308	17	US-10-085-783A-41781	Sequence 41781, A
39	30	8.0	247	9	US-09-998-598-2340	Sequence 2340, Ap
C 40	25	6.6	469	10	US-09-918-995-13873	Sequence 13873, A
41	24	6.4	244	17	US-10-242-535A-58868	Sequence 58868, A
42	24	6.4	244	17	US-10-085-783A-58868	Sequence 58868, A
43	24	6.4	420	9	US-09-960-352-9810	Sequence 9810, Ap
44	20	5.3	200	17	US-10-242-535A-5568	Sequence 5568, Ap
45	20	5.3	200	17	US-10-085-783A-5568	Sequence 5568, Ap
46	19	5.0	60	10	US-09-908-975-12858	Sequence 12858, A
47	18	4.8	348	9	US-09-728-445-666	Sequence 666, App
48	18	4.8	666	17	US-10-240-425-64	Sequence 64, Appl
49	15	4.0	251	17	US-10-242-535A-34894	Sequence 34894, A
50	15	4.0	251	17	US-10-085-783A-34894	Sequence 34894, A
51	14	3.7	65	10	US-09-908-975-28496	Sequence 28496, A
52	12	3.2	183	17	US-10-242-535A-48968	Sequence 48968, A
53	12	3.2	183	17	US-10-085-783A-48968	Sequence 48968, A
54	10	2.7	50	17	US-10-131-827-740	Sequence 740, App
C 55	9	2.4	431	13	US-10-027-632-21884	Sequence 21884, A
C 56	9	2.4	431	17	US-10-027-632-21884	Sequence 21884, A
57	9	2.4	1643	9	US-09-129-112-1	Sequence 1, Appli
58	9	2.4	6265	9	US-09-129-112-3	Sequence 3, Appli
59	8	2.1	25	19	US-10-367-094-179	Sequence 179, App
60	8	2.1	25	19	US-10-719-900-297656	Sequence 297656, A
61	8	2.1	25	19	US-10-719-900-297657	Sequence 297657, A
62	8	2.1	25	19	US-10-719-900-570691	Sequence 570691, A
63	8	2.1	25	19	US-10-719-900-712383	Sequence 712383, A
64	8	2.1	25	19	US-10-719-900-765056	Sequence 765056, A
C 65	8	2.1	156	18	US-10-437-963-31670	Sequence 31670, A
66	8	2.1	201	18	US-10-741-601-18231	Sequence 18231, A
67	8	2.1	201	18	US-10-741-601-18232	Sequence 18232, A
68	8	2.1	201	19	US-10-741-600-49334	Sequence 49334, A
69	8	2.1	201	19	US-10-741-600-49335	Sequence 49335, A

c 70	8	2.1	267	9	US-09-923-876-331	Sequence 331, App	c 143	8	2.1	825	13	US-10-027-632-156599	Sequence 156599,
c 71	8	2.1	267	10	US-09-923-876-331	Sequence 331, App	c 144	8	2.1	825	13	US-10-027-632-156600	Sequence 156600,
c 72	8	2.1	311	18	US-10-425-115-138356	Sequence 138356	c 145	8	2.1	825	17	US-10-027-632-156598	Sequence 156598,
c 73	8	2.1	342	18	US-10-425-115-175287	Sequence 175287,	c 146	8	2.1	825	17	US-10-027-632-156599	Sequence 156599,
c 74	8	2.1	400	8	US-08-781-986A-1529	Sequence 1529, Ap	c 147	8	2.1	825	17	US-10-027-632-156600	Sequence 156600,
c 75	8	2.1	400	17	US-10-329-624-1529	Sequence 1529, Ap	c 148	8	2.1	846	18	US-10-425-115-164850	Sequence 164850,
c 76	8	2.1	433	18	US-10-425-115-72890	Sequence 72890, A	c 149	8	2.1	855	13	US-10-027-632-157373	Sequence 157373,
c 77	8	2.1	437	17	US-10-424-599-95269	Sequence 95269, A	c 150	8	2.1	855	17	US-10-027-632-157373	Sequence 157373,
c 78	8	2.1	454	18	US-10-425-115-2103	Sequence 2103, Ap	c 151	8	2.1	865	13	US-10-027-632-157329	Sequence 157329,
c 79	8	2.1	465	17	US-10-424-599-102869	Sequence 102869,	c 152	8	2.1	865	17	US-10-027-632-157329	Sequence 157329,
c 80	8	2.1	487	17	US-10-424-599-68700	Sequence 68700, A	c 153	8	2.1	871	18	US-10-767-795-4424	Sequence 4424, Ap
c 81	8	2.1	494	18	US-10-021-323-10833	Sequence 10833, A	c 154	8	2.1	901	17	US-10-425-114-29891	Sequence 29891, A
c 82	8	2.1	496	18	US-10-425-115-163797	Sequence 163797,	c 155	8	2.1	903	17	US-10-424-599-54004	Sequence 54004, A
c 83	8	2.1	501	18	US-10-425-115-5892	Sequence 5892, Ap	c 156	8	2.1	907	17	US-10-425-114-19888	Sequence 19888, A
c 84	8	2.1	508	18	US-10-425-115-68144	Sequence 68144, A	c 157	8	2.1	912	9	US-09-891-641-75	Sequence 75, Appl
c 85	8	2.1	527	17	US-10-425-114-7572	Sequence 7572, Ap	c 158	8	2.1	912	17	US-10-602-747A-75	Sequence 75, Appl
c 86	8	2.1	547	13	US-10-027-632-246125	Sequence 246125,	c 159	8	2.1	912	17	US-10-275-191-75	Sequence 75, Appl
c 87	8	2.1	547	17	US-10-027-632-246125	Sequence 246125,	c 160	8	2.1	999	17	US-10-424-599-85830	Sequence 85830, A
c 88	8	2.1	551	17	US-10-264-049-1871	Sequence 1871, Ap	c 161	8	2.1	1088	13	US-10-027-632-101341	Sequence 101341,
c 89	8	2.1	568	13	US-10-027-632-298827	Sequence 298827,	c 162	8	2.1	1088	13	US-10-027-632-101342	Sequence 101342,
c 90	8	2.1	568	17	US-10-027-632-298827	Sequence 298827,	c 163	8	2.1	1088	17	US-10-027-632-101341	Sequence 101341,
c 91	8	2.1	573	18	US-10-425-115-175290	Sequence 175290,	c 164	8	2.1	1088	17	US-10-027-632-101342	Sequence 101342,
c 92	8	2.1	585	13	US-10-027-632-225673	Sequence 225673,	c 165	8	2.1	1089	9	US-09-866-562-60	Sequence 60, Appl
c 93	8	2.1	585	13	US-10-027-632-225674	Sequence 225674,	c 166	8	2.1	1106	17	US-10-425-114-29284	Sequence 29284, A
c 94	8	2.1	585	17	US-10-027-632-225673	Sequence 225673,	c 167	8	2.1	1110	17	US-10-282-122A-32544	Sequence 32544, A
c 95	8	2.1	585	17	US-10-027-632-225674	Sequence 225674,	c 168	8	2.1	1119	17	US-10-240-425-1330	Sequence 1330, Ap
c 96	8	2.1	610	13	US-10-027-632-197848	Sequence 197848,	c 169	8	2.1	1140	18	US-10-437-963-43099	Sequence 43099, A
c 97	8	2.1	610	17	US-10-027-632-197848	Sequence 197848,	c 170	8	2.1	1176	9	US-09-866-562-59	Sequence 59, Appl
c 98	8	2.1	611	13	US-10-027-632-190099	Sequence 190099,	c 171	8	2.1	1309	18	US-10-425-115-150303	Sequence 150303,
c 99	8	2.1	611	13	US-10-027-632-190100	Sequence 190100,	c 172	8	2.1	1345	18	US-10-739-930-1384	Sequence 1384, Ap
c 100	8	2.1	611	13	US-10-027-632-190101	Sequence 190101,	c 173	8	2.1	1353	13	US-10-027-632-250414	Sequence 250414,
c 101	8	2.1	611	13	US-10-027-632-190102	Sequence 190102,	c 174	8	2.1	1353	17	US-10-027-632-250414	Sequence 250414,
c 102	8	2.1	611	17	US-10-027-632-190099	Sequence 190099,	c 175	8	2.1	1356	17	US-10-236-392-91	Sequence 91, Appl
c 103	8	2.1	611	17	US-10-027-632-190100	Sequence 190100,	c 176	8	2.1	1374	10	US-09-934-455-429	Sequence 429, App
c 104	8	2.1	611	17	US-10-027-632-190101	Sequence 190101,	c 177	8	2.1	1401	17	US-10-369-493-43536	Sequence 43536, A
c 105	8	2.1	611	17	US-10-027-632-190102	Sequence 190102,	c 178	8	2.1	1421	18	US-10-425-114-1192	Sequence 1192, Ap
c 106	8	2.1	612	13	US-10-027-632-193498	Sequence 193498,	c 179	8	2.1	1510	18	US-10-425-115-47751	Sequence 47751, A
c 107	8	2.1	612	17	US-10-027-632-193498	Sequence 193498,	c 180	8	2.1	1550	18	US-09-814-353-20781	Sequence 20781, A
c 108	8	2.1	623	18	US-10-425-115-122212	Sequence 122212,	c 181	8	2.1	1557	18	US-10-491-733-59	Sequence 59, Appl
c 109	8	2.1	637	17	US-10-425-114-15520	Sequence 15520, A	c 182	8	2.1	1559	17	US-10-425-114-30121	Sequence 30121, A
c 110	8	2.1	649	13	US-10-027-632-221754	Sequence 221754,	c 183	8	2.1	1638	17	US-10-424-599-53838	Sequence 53838, A
c 111	8	2.1	649	13	US-10-027-632-221755	Sequence 221755,	c 184	8	2.1	1703	17	US-10-264-237-952	Sequence 952, App
c 112	8	2.1	649	13	US-10-027-632-221756	Sequence 221756,	c 185	8	2.1	1715	10	US-09-397-945-87	Sequence 87, Appl
c 113	8	2.1	649	13	US-10-027-632-221757	Sequence 221757,	c 186	8	2.1	1715	17	US-10-653-595-87	Sequence 595, A
c 114	8	2.1	649	13	US-10-027-632-221758	Sequence 221758,	c 187	8	2.1	1722	18	US-10-424-599-11538	Sequence 11538, A
c 115	8	2.1	649	13	US-10-027-632-221759	Sequence 221759,	c 188	8	2.1	1722	18	US-10-437-963-515	Sequence 515, App
c 116	8	2.1	649	13	US-10-027-632-221760	Sequence 221760,	c 189	8	2.1	1781	17	US-10-424-599-13029	Sequence 13029, A
c 117	8	2.1	649	13	US-10-027-632-221761	Sequence 221761,	c 190	8	2.1	1790	18	US-10-723-860-359	Sequence 359, App
c 118	8	2.1	649	17	US-10-027-632-221754	Sequence 221754,	c 191	8	2.1	1848	18	US-10-767-701-12892	Sequence 12892, A
c 119	8	2.1	649	17	US-10-027-632-221755	Sequence 221755,	c 192	8	2.1	1907	18	US-10-437-963-24686	Sequence 24686, A
c 120	8	2.1	649	17	US-10-027-632-221756	Sequence 221756,	c 193	8	2.1	1936	17	US-10-425-114-33720	Sequence 33720, A
c 121	8	2.1	649	17	US-10-027-632-221757	Sequence 221757,	c 194	8	2.1	1957	18	US-10-437-963-9811	Sequence 9811, A
c 122	8	2.1	649	17	US-10-027-632-221758	Sequence 221758,	c 195	8	2.1	1962	17	US-10-369-493-31804	Sequence 31804, A
c 123	8	2.1	649	17	US-10-027-632-221759	Sequence 221759,	c 196	8	2.1	1986	17	US-10-282-122A-8409	Sequence 8409, Ap
c 124	8	2.1	649	17	US-10-027-632-221760	Sequence 221760,	c 197	8	2.1	1993	13	US-10-027-632-98093	Sequence 98093, A
c 125	8	2.1	649	17	US-10-027-632-221761	Sequence 221761,	c 198	8	2.1	1993	17	US-10-027-632-98093	Sequence 98093, A
c 126	8	2.1	650	17	US-10-424-599-53835	Sequence 53835, A	c 199	8	2.1	2004	18	US-10-437-963-24687	Sequence 24687, A
c 127	8	2.1	657	13	US-10-027-632-49333	Sequence 49333, A	c 200	8	2.1	2007	9	US-09-815-242-4207	Sequence 4207, Ap
c 128	8	2.1	657	17	US-10-027-632-49333	Sequence 49333, A	c 201	8	2.1	2010	9	US-09-815-242-8236	Sequence 8236, Ap
c 129	8	2.1	674	18	US-10-767-701-25591	Sequence 25591, A	c 202	8	2.1	2010	17	US-10-282-122A-8189	Sequence 8189, Ap
c 130	8	2.1	708	13	US-10-027-632-268871	Sequence 268871,	c 203	8	2.1	2021	17	US-09-974-300-1157	Sequence 1157, Ap
c 131	8	2.1	708	17	US-10-027-632-268871	Sequence 268871,	c 204	8	2.1	2041	18	US-10-425-115-26537	Sequence 26537, A
c 132	8	2.1	738	17	US-10-172-118-2378	Sequence 2378, Ap	c 205	8	2.1	2114	17	US-10-264-049-714	Sequence 714, App
c 133	8	2.1	738	17	US-10-342-887-2378	Sequence 2378, Ap	c 206	8	2.1	2161	11	US-09-997-722-101	Sequence 101, App
c 134	8	2.1	747	17	US-10-027-632-12227	Sequence 12227, A	c 207	8	2.1	2165	9	US-09-866-562-58	Sequence 58, Appl
c 135	8	2.1	747	17	US-10-027-632-12227	Sequence 12227, A	c 208	8	2.1	2165	18	US-10-643-795A-60	Sequence 60, Appl
c 136	8	2.1	779	17	US-10-425-115-134444	Sequence 134444,	c 209	8	2.1	2235	18	US-10-767-701-14511	Sequence 14511, A
c 137	8	2.1	779	17	US-10-424-599-115803	Sequence 115803,	c 210	8	2.1	2304	17	US-10-276-774-746	Sequence 746, App
c 138	8	2.1	791	18	US-10-363-345A-23639	Sequence 23639, A	c 211	8	2.1	2393	17	US-10-425-115-85772	Sequence 85772, A
c 139	8	2.1	791	18	US-10-363-345A-23640	Sequence 23640, A	c 212	8	2.1	2464	17	US-10-276-774-467	Sequence 467, App
c 140	8	2.1	796	18	US-10-363-345A-20749	Sequence 20749, A	c 213	8	2.1	2490	18	US-10-425-115-174924	Sequence 174924, A
c 141	8	2.1	796	18	US-10-363-345A-20750	Sequence 20750, A	c 214	8	2.1	2497	18	US-10-739-930-5364	Sequence 5364, Ap
c 142	8	2.1	825	13	US-10-027-632-156598	Sequence 156598,	c 215	8	2.1	2508	18	US-10-425-115-174920	Sequence 174920,

C 216	8	2.1	2532	18	US-10-437-963-14825	Sequence 14825, A	289	7	1.9	25	18	US-10-765-672-34	Sequence 34, Appl
C 217	8	2.1	2790	14	US-10-300-834-5	Sequence 5, Appl	290	7	1.9	25	19	US-10-719-900-204432	Sequence 204432, A
C 218	8	2.1	2800	17	US-10-108-260A-23	Sequence 23, Appl	291	7	1.9	25	19	US-10-719-900-275167	Sequence 275167, A
C 219	8	2.1	3275	18	US-10-357-930-23833	Sequence 23833, A	292	7	1.9	25	19	US-10-719-900-307773	Sequence 307773, A
C 220	8	2.1	3381	18	US-10-425-115-101082	Sequence 101082, A	293	7	1.9	25	19	US-10-719-900-379090	Sequence 379090, A
C 221	8	2.1	3387	18	US-10-661-809-14	Sequence 14, Appl	294	7	1.9	25	19	US-10-719-900-479965	Sequence 479965, A
C 222	8	2.1	3416	18	US-10-425-115-69463	Sequence 69463, A	295	7	1.9	25	19	US-10-719-900-492311	Sequence 492311, A
C 223	8	2.1	3432	14	US-10-300-834-4	Sequence 4, Appl	296	7	1.9	25	19	US-10-719-900-827583	Sequence 827583, A
C 224	8	2.1	3486	18	US-10-473-126-20	Sequence 20, Appl	297	7	1.9	25	19	US-10-719-900-938778	Sequence 938778, A
C 225	8	2.1	4003	18	US-10-723-860-5060	Sequence 5060, A	298	7	1.9	25	19	US-10-719-900-956705	Sequence 956705, A
C 226	8	2.1	4434	17	US-10-282-122A-10150	Sequence 10150, A	299	7	1.9	25	19	US-10-719-900-956706	Sequence 956706, A
C 227	8	2.1	4938	11	US-09-958-007A-686	Sequence 686, App	300	7	1.9	25	19	US-10-719-900-973233	Sequence 973233, A
C 228	8	2.1	4938	18	US-10-425-115-79300	Sequence 79300, A	301	7	1.9	25	19	US-10-719-900-973234	Sequence 973234, A
C 229	8	2.1	5793	18	US-10-437-963-35838	Sequence 35838, A	302	7	1.9	33	12	US-09-736-250-3	Sequence 3, Appl
C 230	8	2.1	6657	17	US-10-062-674-1937	Sequence 1937, App	303	7	1.9	35	9	US-09-484-704-38	Sequence 38, Appl
C 231	8	2.1	6669	15	US-10-311-455-166	Sequence 166, App	304	7	1.9	35	18	US-10-765-672-38	Sequence 38, Appl
C 232	8	2.1	6669	17	US-10-240-589C-6	Sequence 6, Appl	305	7	1.9	41	17	US-10-035-833A-1348	Sequence 1348, App
C 233	8	2.1	8285	9	US-09-732-025-3	Sequence 3, Appl	306	7	1.9	41	17	US-10-035-833A-4136	Sequence 4136, App
C 234	8	2.1	8285	16	US-10-153-317-3	Sequence 3, Appl	307	7	1.9	65	10	US-09-908-975-26809	Sequence 26809, A
C 235	8	2.1	8522	9	US-09-817-181-3	Sequence 3, Appl	308	7	1.9	65	10	US-10-741-849-3212	Sequence 3212, App
C 236	8	2.1	8522	14	US-10-300-828-3	Sequence 3, Appl	309	7	1.9	82	13	US-10-027-632-177870	Sequence 177870, A
C 237	8	2.1	9224	13	US-10-108-605-254	Sequence 254, App	310	7	1.9	82	17	US-10-027-632-177870	Sequence 177870, A
C 238	8	2.1	9299	15	US-10-311-455-1697	Sequence 1697, App	311	7	1.9	110	9	US-09-969-373-149	Sequence 149, App
C 239	8	2.1	9352	15	US-10-311-455-76	Sequence 76, Appl	312	7	1.9	117	18	US-10-437-963-3743	Sequence 3743, App
C 240	8	2.1	11827	9	US-09-733-455-3	Sequence 3, Appl	313	7	1.9	129	18	US-10-425-115-43161	Sequence 43161, A
C 241	8	2.1	11827	16	US-10-153-919-3	Sequence 3, Appl	314	7	1.9	135	9	US-09-864-761-24101	Sequence 24101, A
C 242	8	2.1	17000	18	US-10-837-624-3	Sequence 3, Appl	315	7	1.9	138	18	US-10-466-894-18	Sequence 18, Appl
C 243	8	2.1	17934	15	US-10-311-455-1691	Sequence 1691, App	316	7	1.9	149	17	US-10-424-599-48325	Sequence 48325, A
C 244	8	2.1	21840	13	US-10-087-192-313	Sequence 310, App	317	7	1.9	154	10	US-09-754-853A-234	Sequence 234, App
C 245	8	2.1	24617	18	US-10-741-601-5765	Sequence 5765, App	318	7	1.9	156	9	US-09-864-761-23900	Sequence 23900, A
C 246	8	2.1	24617	18	US-10-741-601-5767	Sequence 5767, A	319	7	1.9	159	17	US-10-424-599-71839	Sequence 71839, A
C 247	8	2.1	26071	19	US-10-322-281-575	Sequence 575, App	320	7	1.9	167	17	US-10-424-599-19075	Sequence 19075, A
C 248	8	2.1	27310	13	US-10-087-192-1162	Sequence 1162, App	321	7	1.9	186	15	US-10-425-115-164623	Sequence 164623, A
C 249	8	2.1	32220	9	US-09-764-877-3933	Sequence 3933, App	322	7	1.9	187	18	US-10-156-761-5741	Sequence 5741, App
C 250	8	2.1	32220	17	US-10-242-515-3933	Sequence 3933, App	323	7	1.9	187	18	US-10-425-115-17741	Sequence 17741, A
C 251	8	2.1	34176	13	US-10-087-192-1918	Sequence 1918, App	324	7	1.9	189	17	US-10-425-115-17741	Sequence 46879, A
C 252	8	2.1	39443	17	US-10-085-117-313	Sequence 313, App	325	7	1.9	189	17	US-10-085-783A-46879	Sequence 46879, A
C 253	8	2.1	39827	17	US-10-041-018-399	Sequence 399, App	326	7	1.9	193	17	US-10-342-535A-30452	Sequence 30452, A
C 254	8	2.1	40394	18	US-10-741-601-5774	Sequence 5774, App	327	7	1.9	193	17	US-10-085-783A-30452	Sequence 30452, A
C 255	8	2.1	40394	13	US-10-741-600-17987	Sequence 17987, A	328	7	1.9	195	18	US-10-425-115-109444	Sequence 109444, A
C 256	8	2.1	48680	19	US-10-087-192-2044	Sequence 2044, App	329	7	1.9	198	18	US-10-674-124A-6137	Sequence 6137, App
C 257	8	2.1	50781	13	US-10-087-192-769	Sequence 769, App	330	7	1.9	201	18	US-10-741-601-11909	Sequence 11909, A
C 258	8	2.1	55996	11	US-09-937-722-7	Sequence 7, Appl	331	7	1.9	201	18	US-10-741-601-19718	Sequence 19718, A
C 259	8	2.1	56339	17	US-10-085-117-280	Sequence 280, App	332	7	1.9	201	18	US-10-719-993-5389	Sequence 5389, App
C 260	8	2.1	63718	19	US-10-741-600-17743	Sequence 17743, A	333	7	1.9	201	18	US-10-719-993-5395	Sequence 5395, App
C 261	8	2.1	67097	17	US-10-085-117-88	Sequence 88, Appl	334	7	1.9	201	18	US-10-719-993-5396	Sequence 5396, App
C 262	8	2.1	67126	18	US-10-741-601-5691	Sequence 5691, App	335	7	1.9	201	18	US-10-719-993-5402	Sequence 5402, App
C 263	8	2.1	67126	19	US-10-741-600-17762	Sequence 17762, A	336	7	1.9	201	18	US-10-719-993-5403	Sequence 5403, App
C 264	8	2.1	70768	13	US-10-135-322-13	Sequence 13, Appl	337	7	1.9	201	18	US-10-719-993-5409	Sequence 5409, App
C 265	8	2.1	96592	11	US-09-997-722-88	Sequence 88, Appl	338	7	1.9	201	18	US-10-719-993-6654	Sequence 6654, App
C 266	8	2.1	115780	18	US-10-367-094-96	Sequence 96, Appl	339	7	1.9	201	18	US-10-719-993-6655	Sequence 6655, App
C 267	8	2.1	119211	17	US-10-672-787-40	Sequence 40, Appl	340	7	1.9	201	18	US-10-719-993-6654	Sequence 22664, A
C 268	8	2.1	119472	19	US-10-741-600-17865	Sequence 17865, A	341	7	1.9	201	18	US-10-719-993-22664	Sequence 22664, A
C 269	8	2.1	129710	13	US-10-027-632-178902	Sequence 178902, A	342	7	1.9	201	18	US-10-719-993-28333	Sequence 28333, A
C 270	8	2.1	129710	17	US-10-027-632-178902	Sequence 178902, A	343	7	1.9	201	18	US-10-719-993-28428	Sequence 28428, A
C 271	8	2.1	130207	13	US-10-087-192-1372	Sequence 1372, App	344	7	1.9	201	18	US-10-719-993-28430	Sequence 28430, A
C 272	8	2.1	133632	13	US-10-087-192-1810	Sequence 1810, App	345	7	1.9	201	18	US-10-719-993-29217	Sequence 29217, A
C 273	8	2.1	166910	17	US-10-292-337-11	Sequence 11, Appl	346	7	1.9	201	18	US-10-719-993-31264	Sequence 31264, A
C 274	8	2.1	176930	18	US-10-741-601-5679	Sequence 5679, App	347	7	1.9	201	18	US-10-719-993-33571	Sequence 33571, A
C 275	8	2.1	176930	19	US-10-741-600-17725	Sequence 17725, A	348	7	1.9	201	18	US-10-719-993-36604	Sequence 36604, A
C 276	8	2.1	203127	19	US-10-741-601-5654	Sequence 5654, App	349	7	1.9	201	18	US-10-719-993-36629	Sequence 36629, A
C 277	8	2.1	203127	19	US-10-741-600-17666	Sequence 17666, A	350	7	1.9	201	18	US-10-719-993-38502	Sequence 38502, A
C 278	8	2.1	312477	18	US-10-317-883A-12	Sequence 12, Appl	351	7	1.9	201	18	US-10-719-993-39622	Sequence 39622, A
C 279	8	2.1	339234	18	US-10-322-696-73	Sequence 73, Appl	352	7	1.9	201	18	US-10-719-993-39623	Sequence 39623, A
C 280	8	2.1	2140405	13	US-10-027-632-76212	Sequence 76212, A	353	7	1.9	201	18	US-10-719-993-39674	Sequence 39674, A
C 281	8	2.1	2140405	17	US-10-027-632-76212	Sequence 76212, A	354	7	1.9	201	18	US-10-719-993-41624	Sequence 41624, A
C 282	8	2.1	2256646	18	US-10-470-565-1	Sequence 1, Appl	355	7	1.9	201	18	US-10-719-993-41626	Sequence 41626, A
C 283	7	1.9	22	14	US-10-175-225-14	Sequence 14, Appl	356	7	1.9	201	18	US-10-719-993-43908	Sequence 43908, A
C 284	7	1.9	25	9	US-09-484-704-31	Sequence 31, Appl	357	7	1.9	201	18	US-10-719-993-43909	Sequence 43909, A
C 285	7	1.9	25	9	US-09-484-704-31	Sequence 31, Appl	358	7	1.9	201	18	US-10-719-993-49159	Sequence 49159, A
C 286	7	1.9	25	15	US-10-098-263B-29901	Sequence 29901, A	359	7	1.9	201	18	US-10-719-993-49167	Sequence 49167, A
C 287	7	1.9	25	18	US-10-775-169-4005	Sequence 4005, App	360	7	1.9	201	18	US-10-719-993-49168	Sequence 49168, A
C 288	7	1.9	25	18	US-10-765-672-31	Sequence 31, Appl	361	7	1.9	201	18	US-10-719-993-49983	Sequence 49983, A

C 362	7	1.9	201	18	US-10-719-993-49989	Sequence 49989, A	435	7	1.9	283	10	US-09-237-183A-1543	Sequence 1543, Ap
C 363	7	1.9	201	18	US-10-719-993-50004	Sequence 50004, A	436	7	1.9	283	11	US-09-987-899-3752	Sequence 3752, Ap
C 364	7	1.9	201	18	US-10-719-993-53130	Sequence 53130, A	437	7	1.9	283	17	US-10-424-599-66605	Sequence 66605, A
C 365	7	1.9	201	18	US-10-719-993-53132	Sequence 53132, A	438	7	1.9	283	18	US-10-674-124A-21549	Sequence 21549, A
C 366	7	1.9	201	18	US-10-719-993-54108	Sequence 54108, A	439	7	1.9	287	18	US-10-357-930-59715	Sequence 59715, A
C 367	7	1.9	201	19	US-10-741-600-22208	Sequence 22208, A	440	7	1.9	290	17	US-10-242-535A-1743	Sequence 1743, Ap
C 368	7	1.9	201	19	US-10-741-600-22217	Sequence 22217, A	441	7	1.9	290	17	US-10-425-114-12429	Sequence 12429, A
C 369	7	1.9	201	19	US-10-741-600-42497	Sequence 42497, A	442	7	1.9	290	17	US-10-085-783A-1743	Sequence 1743, Ap
C 370	7	1.9	201	19	US-10-741-600-48813	Sequence 48813, A	443	7	1.9	291	9	US-09-294-093B-1050	Sequence 1050, Ap
C 371	7	1.9	201	19	US-10-741-600-49418	Sequence 49418, A	444	7	1.9	291	17	US-10-282-122A-3720	Sequence 3720, A
C 372	7	1.9	201	19	US-10-741-600-52817	Sequence 52817, A	445	7	1.9	291	18	US-10-425-115-112494	Sequence 112494, A
C 373	7	1.9	201	19	US-10-741-600-54662	Sequence 54662, A	446	7	1.9	292	13	US-10-001-843-84	Sequence 84, Appl
C 374	7	1.9	201	19	US-10-741-600-56642	Sequence 56642, A	447	7	1.9	292	17	US-10-242-535A-3803	Sequence 3803, Ap
C 375	7	1.9	201	19	US-10-741-600-62224	Sequence 62224, A	448	7	1.9	292	17	US-10-085-783A-3803	Sequence 3803, Ap
C 376	7	1.9	201	19	US-10-741-600-66878	Sequence 66878, A	449	7	1.9	293	9	US-09-294-093B-295	Sequence 295, App
C 377	7	1.9	201	19	US-10-741-600-69849	Sequence 69849, A	450	7	1.9	293	9	US-09-294-093B-2025	Sequence 2025, Ap
C 378	7	1.9	201	19	US-10-741-600-69882	Sequence 69882, A	451	7	1.9	293	9	US-09-764-860-115	Sequence 115, App
C 379	7	1.9	201	19	US-10-741-600-69856	Sequence 69856, A	452	7	1.9	293	14	US-10-074-095-115	Sequence 115, App
C 380	7	1.9	201	19	US-10-741-600-71518	Sequence 71518, A	453	7	1.9	293	17	US-10-212-872-115	Sequence 115, App
C 381	7	1.9	203	17	US-10-424-599-61988	Sequence 61988, A	454	7	1.9	293	18	US-10-723-860-2410	Sequence 2410, Ap
C 382	7	1.9	206	18	US-09-510-332-104	Sequence 104, App	455	7	1.9	294	18	US-10-425-115-970	Sequence 970, App
C 383	7	1.9	206	18	US-10-770-127-104	Sequence 104, App	456	7	1.9	299	17	US-10-369-493-29158	Sequence 29158, A
C 384	7	1.9	210	17	US-10-335-977-2450	Sequence 2450, App	457	7	1.9	299	17	US-10-424-599-99283	Sequence 99283, A
C 385	7	1.9	213	17	US-10-335-977-2451	Sequence 2451, App	458	7	1.9	300	9	US-09-294-093B-1644	Sequence 1644, Ap
C 386	7	1.9	213	18	US-10-425-115-111306	Sequence 111306, A	459	7	1.9	300	18	US-10-425-115-33626	Sequence 33626, A
C 387	7	1.9	216	19	US-10-472-928-2619	Sequence 2619, Ap	460	7	1.9	300	18	US-10-357-930-59696	Sequence 59696, A
C 388	7	1.9	225	18	US-10-674-124A-10379	Sequence 10379, A	461	7	1.9	303	18	US-10-425-115-43372	Sequence 43372, A
C 389	7	1.9	231	9	US-09-878-178-1620	Sequence 1620, Ap	462	7	1.9	304	18	US-10-437-963-83772	Sequence 83772, A
C 390	7	1.9	231	13	US-10-046-935-1620	Sequence 1620, Ap	463	7	1.9	306	18	US-10-425-115-156390	Sequence 156390, A
C 391	7	1.9	231	14	US-10-146-502-1620	Sequence 1620, Ap	464	7	1.9	307	9	US-09-983-965-4120	Sequence 4120, Ap
C 392	7	1.9	232	18	US-10-357-930-59891	Sequence 59891, A	465	7	1.9	310	11	US-09-864-408A-991	Sequence 991, App
C 393	7	1.9	232	18	US-10-674-124A-20391	Sequence 20391, A	466	7	1.9	313	11	US-10-425-115-19000	Sequence 19000, A
C 394	7	1.9	235	17	US-10-424-599-115635	Sequence 115635, A	467	7	1.9	313	18	US-10-425-115-59582	Sequence 59582, A
C 395	7	1.9	240	11	US-09-864-408A-1789	Sequence 1789, Ap	468	7	1.9	314	18	US-10-357-930-1573	Sequence 1573, Ap
C 396	7	1.9	242	17	US-10-424-599-81355	Sequence 81355, A	469	7	1.9	315	9	US-09-867-550-1573	Sequence 4071, Ap
C 397	7	1.9	245	10	US-09-237-183A-1542	Sequence 1542, Ap	470	7	1.9	317	10	US-09-814-353-4071	Sequence 10378, A
C 398	7	1.9	245	11	US-09-987-899-3751	Sequence 3751, Ap	471	7	1.9	317	10	US-09-814-353-10378	Sequence 15, Appl
C 399	7	1.9	246	10	US-09-918-995-31236	Sequence 31236, A	472	7	1.9	324	14	US-10-091-572-15	Sequence 20982, A
C 400	7	1.9	246	17	US-10-424-599-469	Sequence 469, App	473	7	1.9	324	17	US-10-424-599-20982	Sequence 100969, A
C 401	7	1.9	248	9	US-09-867-701-5528	Sequence 5528, Ap	474	7	1.9	324	18	US-10-437-963-100969	Sequence 21858, A
C 402	7	1.9	249	18	US-10-425-115-106663	Sequence 106663, A	475	7	1.9	325	17	US-10-242-535A-21858	Sequence 21858, A
C 403	7	1.9	250	18	US-10-425-115-137000	Sequence 137000, A	476	7	1.9	325	17	US-10-085-783A-21858	Sequence 102926, A
C 404	7	1.9	252	18	US-10-425-115-134187	Sequence 134187, A	477	7	1.9	327	18	US-10-425-115-102926	Sequence 4168, Ap
C 405	7	1.9	253	18	US-10-425-115-78037	Sequence 78037, A	478	7	1.9	330	10	US-09-814-353-4168	Sequence 10474, A
C 406	7	1.9	255	10	US-09-930-213-344	Sequence 344, App	479	7	1.9	330	17	US-09-814-353-10474	Sequence 48625, A
C 407	7	1.9	255	17	US-10-424-599-40897	Sequence 40897, A	480	7	1.9	330	17	US-10-424-599-48625	Sequence 818, App
C 408	7	1.9	256	11	US-09-922-293-3289	Sequence 3289, Ap	481	7	1.9	330	17	US-10-152-318A-818	Sequence 560, App
C 409	7	1.9	257	18	US-10-437-963-8593	Sequence 8593, Ap	482	7	1.9	332	18	US-10-914-037-560	Sequence 5826, Ap
C 410	7	1.9	260	18	US-10-437-963-8590	Sequence 8590, Ap	483	7	1.9	333	9	US-09-796-692-5826	Sequence 5826, Ap
C 411	7	1.9	260	18	US-10-674-124A-10353	Sequence 10353, A	484	7	1.9	333	14	US-10-040-862-5826	Sequence 5826, Ap
C 412	7	1.9	261	9	US-09-864-761-23833	Sequence 23833, A	485	7	1.9	333	17	US-10-057-475B-5826	Sequence 5826, Ap
C 413	7	1.9	261	17	US-10-424-599-16138	Sequence 16138, A	486	7	1.9	333	17	US-10-154-884B-5826	Sequence 5826, Ap
C 414	7	1.9	261	18	US-10-437-963-67368	Sequence 67368, A	487	7	1.9	333	18	US-10-764-324-5826	Sequence 5826, Ap
C 415	7	1.9	262	18	US-10-425-115-19440	Sequence 19440, A	488	7	1.9	335	17	US-10-242-535A-12432	Sequence 12432, A
C 416	7	1.9	262	18	US-10-357-930-56952	Sequence 56952, A	489	7	1.9	335	17	US-10-085-783A-12432	Sequence 379, App
C 417	7	1.9	262	18	US-10-425-115-184183	Sequence 184183, A	490	7	1.9	336	9	US-09-969-373-379	Sequence 89865, A
C 418	7	1.9	266	14	US-10-082-830-11	Sequence 11, Appl	491	7	1.9	339	18	US-10-425-115-89865	Sequence 420, App
C 419	7	1.9	266	18	US-10-425-115-39917	Sequence 39917, A	492	7	1.9	339	18	US-10-856-499-420	Sequence 20460, A
C 420	7	1.9	268	10	US-09-237-183A-1546	Sequence 1546, Ap	493	7	1.9	340	17	US-10-242-535A-20460	Sequence 20460, A
C 421	7	1.9	268	11	US-09-987-899-3755	Sequence 3755, Ap	494	7	1.9	340	17	US-10-085-783A-20460	Sequence 20460, A
C 422	7	1.9	269	17	US-10-424-599-39933	Sequence 39933, A	495	7	1.9	342	17	US-10-243-552-20	Sequence 20, Appl
C 423	7	1.9	269	18	US-10-674-124A-10378	Sequence 10378, A	496	7	1.9	342	17	US-10-335-977-4117	Sequence 4117, Ap
C 424	7	1.9	271	18	US-10-425-115-22091	Sequence 22091, A	497	7	1.9	343	17	US-10-381-813-118	Sequence 118, App
C 425	7	1.9	272	8	US-10-425-115-15307	Sequence 15307, A	498	7	1.9	343	17	US-10-381-813-119	Sequence 119, App
C 426	7	1.9	273	9	US-09-933-797-230	Sequence 230, App	499	7	1.9	345	17	US-10-335-977-4116	Sequence 4116, Ap
C 427	7	1.9	273	18	US-10-425-115-5786	Sequence 5786, Ap	500	7	1.9	345	17	US-10-381-813-111	Sequence 111, App
C 428	7	1.9	273	18	US-10-357-930-60047	Sequence 60047, A	501	7	1.9	347	9	US-09-880-107-2217	Sequence 2217, Ap
C 429	7	1.9	274	9	US-09-969-708-528	Sequence 528, App	502	7	1.9	348	9	US-09-960-352-5894	Sequence 5894, Ap
C 430	7	1.9	274	9	US-09-880-107-313	Sequence 313, App	503	7	1.9	348	10	US-09-814-353-667	Sequence 667, App
C 431	7	1.9	274	17	US-10-424-599-21697	Sequence 21697, A	504	7	1.9	351	10	US-09-814-353-7043	Sequence 7043, Ap
C 432	7	1.9	276	18	US-10-437-963-38765	Sequence 38765, A	505	7	1.9	351	11	US-09-864-408A-667	Sequence 667, App
C 433	7	1.9	281	13	US-10-027-632-77053	Sequence 77053, A	506	7	1.9	352	17	US-10-170-385-194	Sequence 194, App
C 434	7	1.9	281	17	US-10-027-632-77053	Sequence 77053, A	507	7	1.9	353	17	US-10-424-599-76487	Sequence 76487, A

508	7	1.9	355	9	US-09-960-352-5460	Sequence 5460, Ap	c 581	7	1.9	417	17	US-10-282-122A-13640	Sequence 13640, A
509	7	1.9	356	18	US-10-425-115-57347	Sequence 57347, A	582	7	1.9	418	18	US-10-425-115-183688	Sequence 183688, A
510	7	1.9	357	17	US-10-424-599-38756	Sequence 38756, A	583	7	1.9	419	13	US-10-027-632-48577	Sequence 48577, A
511	7	1.9	357	18	US-10-437-963-87453	Sequence 87453, A	584	7	1.9	421	17	US-10-027-632-48577	Sequence 48577, A
512	7	1.9	363	17	US-10-335-977-4118	Sequence 4118, Ap	585	7	1.9	421	17	US-10-027-632-48577	Sequence 48577, A
513	7	1.9	364	18	US-10-357-930-6775	Sequence 6775, Ap	586	7	1.9	421	18	US-10-425-115-167481	Sequence 167481, A
514	7	1.9	365	17	US-10-424-599-130146	Sequence 130146, A	587	7	1.9	423	9	US-09-983-965-2637	Sequence 2637, Ap
515	7	1.9	366	17	US-10-260-238-1403	Sequence 1403, Ap	c 588	7	1.9	423	18	US-10-357-930-607	Sequence 607, App
516	7	1.9	366	18	US-10-425-115-182292	Sequence 182292, A	589	7	1.9	424	13	US-10-027-632-96967	Sequence 96967, A
517	7	1.9	367	18	US-10-357-930-3376	Sequence 3376, Ap	590	7	1.9	424	13	US-10-027-632-306400	Sequence 306400, A
518	7	1.9	369	17	US-10-369-493-23853	Sequence 23853, A	591	7	1.9	424	17	US-10-027-632-96967	Sequence 96967, A
519	7	1.9	372	9	US-09-960-352-3227	Sequence 3227, Ap	592	7	1.9	424	17	US-10-027-632-306400	Sequence 306400, A
520	7	1.9	373	9	US-09-962-832-16	Sequence 16, Appl	593	7	1.9	424	17	US-10-424-599-4396	Sequence 4396, Ap
521	7	1.9	373	9	US-09-954-456-177	Sequence 177, App	594	7	1.9	424	18	US-10-767-701-5537	Sequence 5537, Ap
522	7	1.9	374	17	US-10-424-599-17137	Sequence 17137, A	c 595	7	1.9	424	18	US-10-424-599-68649	Sequence 68649, A
523	7	1.9	374	17	US-10-425-114-18037	Sequence 18037, A	596	7	1.9	425	18	US-10-357-930-9776	Sequence 9776, Ap
524	7	1.9	378	18	US-10-674-124A-21328	Sequence 21328, A	597	7	1.9	427	9	US-09-864-761-3626	Sequence 3626, Ap
525	7	1.9	379	18	US-10-425-115-184122	Sequence 184122, A	c 598	7	1.9	429	9	US-09-983-965-4102	Sequence 4102, Ap
526	7	1.9	380	18	US-10-425-115-89414	Sequence 89414, A	599	7	1.9	429	10	US-09-764-891-9485	Sequence 9485, Ap
527	7	1.9	381	9	US-09-960-352-12211	Sequence 12211, A	600	7	1.9	429	10	US-09-764-891-9486	Sequence 9486, Ap
528	7	1.9	383	10	US-09-918-995-18831	Sequence 18831, A	601	7	1.9	429	10	US-09-764-891-9487	Sequence 9487, Ap
529	7	1.9	383	18	US-10-425-115-166430	Sequence 166430, A	602	7	1.9	429	13	US-10-001-887-73	Sequence 73, Appl
530	7	1.9	384	18	US-10-357-930-15267	Sequence 15267, A	603	7	1.9	429	13	US-10-027-632-180838	Sequence 180838, A
531	7	1.9	385	17	US-10-242-535A-6746	Sequence 6746, Ap	604	7	1.9	429	15	US-10-205-428-866	Sequence 866, App
532	7	1.9	385	17	US-10-085-783A-6746	Sequence 6746, Ap	605	7	1.9	429	15	US-10-205-428-867	Sequence 867, App
533	7	1.9	386	9	US-09-770-791-75	Sequence 75, Appl	606	7	1.9	429	15	US-10-205-428-868	Sequence 868, App
534	7	1.9	386	17	US-10-641-643-692	Sequence 692, App	607	7	1.9	429	17	US-10-027-632-180838	Sequence 180838, A
535	7	1.9	388	17	US-10-191-803-820	Sequence 820, App	c 608	7	1.9	432	10	US-09-918-995-34514	Sequence 34514, A
536	7	1.9	390	14	US-10-066-543-1320	Sequence 1320, Ap	609	7	1.9	432	13	US-10-027-632-43681	Sequence 43681, A
537	7	1.9	390	17	US-10-260-238-5295	Sequence 5295, Ap	610	7	1.9	433	13	US-10-027-632-72860	Sequence 72860, A
538	7	1.9	390	18	US-10-425-115-132416	Sequence 132416, A	611	7	1.9	433	13	US-10-027-632-312826	Sequence 312826, A
539	7	1.9	394	17	US-10-424-599-50246	Sequence 50246, A	612	7	1.9	433	17	US-10-027-632-43681	Sequence 43681, A
540	7	1.9	395	9	US-09-783-590-6434	Sequence 6434, Ap	613	7	1.9	433	17	US-10-027-632-72860	Sequence 72860, A
541	7	1.9	395	17	US-10-424-599-98673	Sequence 98673, A	614	7	1.9	433	17	US-10-027-632-312826	Sequence 312826, A
542	7	1.9	398	18	US-10-425-115-79190	Sequence 79190, A	615	7	1.9	433	18	US-10-574-124A-16331	Sequence 16331, A
543	7	1.9	399	9	US-09-960-352-6868	Sequence 6868, Ap	616	7	1.9	433	18	US-10-357-930-32584	Sequence 32584, A
544	7	1.9	399	10	US-09-814-353-16858	Sequence 16858, A	617	7	1.9	433	18	US-10-357-930-41510	Sequence 41510, A
545	7	1.9	400	8	US-08-781-986A-852	Sequence 852, App	c 618	7	1.9	434	18	US-10-767-701-22247	Sequence 22247, A
546	7	1.9	400	10	US-09-814-353-16762	Sequence 16762, A	c 619	7	1.9	435	18	US-10-437-963-63636	Sequence 63636, A
547	7	1.9	400	17	US-10-424-599-130022	Sequence 130022, A	c 620	7	1.9	436	18	US-10-674-124A-5265	Sequence 5265, Ap
548	7	1.9	400	17	US-10-329-624-852	Sequence 852, App	621	7	1.9	437	15	US-09-764-891-2251	Sequence 2251, Ap
549	7	1.9	400	18	US-10-425-115-121967	Sequence 121967, A	c 622	7	1.9	437	15	US-10-205-428-179	Sequence 179, App
550	7	1.9	401	13	US-10-027-632-75873	Sequence 75873, A	c 623	7	1.9	437	17	US-10-424-599-127046	Sequence 127046, A
551	7	1.9	401	17	US-10-027-632-75873	Sequence 75873, A	624	7	1.9	439	9	US-09-924-035A-382	Sequence 382, App
552	7	1.9	402	11	US-08-781-986A-1282	Sequence 1282, Ap	c 625	7	1.9	439	18	US-10-767-701-2816	Sequence 2816, Ap
553	7	1.9	402	18	US-08-781-986A-1282	Sequence 1282, Ap	c 626	7	1.9	441	10	US-09-918-995-36870	Sequence 36870, A
554	7	1.9	402	17	US-10-329-624-1282	Sequence 1282, Ap	c 627	7	1.9	441	17	US-10-424-599-85815	Sequence 85815, A
555	7	1.9	403	17	US-10-424-599-70666	Sequence 70666, A	c 628	7	1.9	443	10	US-09-918-995-37067	Sequence 37067, A
556	7	1.9	404	9	US-09-867-701-4500	Sequence 4500, Ap	c 629	7	1.9	443	13	US-10-027-632-183309	Sequence 183309, A
557	7	1.9	404	10	US-09-918-995-18751	Sequence 18751, A	c 630	7	1.9	443	13	US-10-027-632-183310	Sequence 183310, A
558	7	1.9	406	13	US-10-027-632-301592	Sequence 301592, A	c 631	7	1.9	443	17	US-10-027-632-183309	Sequence 183309, A
559	7	1.9	406	16	US-10-181-447A-31	Sequence 31, Appl	c 632	7	1.9	448	9	US-10-425-114-20465	Sequence 20465, A
560	7	1.9	406	17	US-10-027-632-301592	Sequence 301592, A	c 633	7	1.9	449	17	US-09-864-761-2168	Sequence 2168, Ap
561	7	1.9	407	9	US-09-864-761-17101	Sequence 17101, A	c 634	7	1.9	450	17	US-10-131-827-8406	Sequence 8406, Ap
562	7	1.9	407	18	US-10-425-115-177335	Sequence 177335, A	c 635	7	1.9	451	10	US-09-918-995-15375	Sequence 15375, A
563	7	1.9	408	13	US-10-095-407-10	Sequence 10, Appl	c 640	7	1.9	451	9	US-09-864-761-11355	Sequence 11355, A
564	7	1.9	408	18	US-10-437-963-13286	Sequence 13286, A	c 642	7	1.9	452	17	US-10-424-599-84528	Sequence 84528, A
565	7	1.9	408	18	US-10-674-124A-768	Sequence 768, App	c 643	7	1.9	452	18	US-10-856-499-63	Sequence 63, Appl
566	7	1.9	408	18	US-10-425-115-105713	Sequence 105713, A	644	7	1.9	453	11	US-09-969-034-1832	Sequence 1832, Ap
567	7	1.9	410	18	US-10-425-115-44036	Sequence 44036, A	645	7	1.9	453	18	US-10-425-115-71694	Sequence 71694, A
568	7	1.9	411	9	US-09-922-217-180	Sequence 180, App	646	7	1.9	454	13	US-10-027-632-89646	Sequence 89646, A
569	7	1.9	411	9	US-09-833-263-180	Sequence 180, App	c 647	7	1.9	454	17	US-10-027-632-89646	Sequence 89646, A
570	7	1.9	411	13	US-10-025-380-180	Sequence 180, App	c 648	7	1.9	455	10	US-09-918-995-21800	Sequence 21800, A
571	7	1.9	411	17	US-10-242-535A-44077	Sequence 44077, A	649	7	1.9	455	18	US-10-674-124A-6999	Sequence 6999, Ap
572	7	1.9	411	17	US-10-424-599-117379	Sequence 117379, A	c 550	7	1.9	456	10	US-09-918-995-26925	Sequence 26925, A
573	7	1.9	411	17	US-10-085-783A-44077	Sequence 44077, A	651	7	1.9	456	18	US-10-425-115-34555	Sequence 34555, A
574	7	1.9	411	18	US-10-437-963-41061	Sequence 41061, A	c 552	7	1.9	459	10	US-09-918-995-27189	Sequence 27189, A
575	7	1.9	412	13	US-09-918-995-3007	Sequence 3007, Ap	c 553	7	1.9	459	10	US-09-918-995-27189	Sequence 27189, A
576	7	1.9	412	13	US-10-027-632-309030	Sequence 309030, A	c 554	7	1.9	459	10	US-09-918-995-27189	Sequence 27189, A
577	7	1.9	412	13	US-10-027-632-309030	Sequence 309030, A	c 555	7	1.9	459	10	US-09-918-995-27189	Sequence 27189, A
578	7	1.9	413	9	US-09-983-965-407	Sequence 407, App	c 556	7	1.9	459	10	US-09-918-995-27189	Sequence 27189, A
579	7	1.9	413	14	US-10-198-846-7400	Sequence 7400, Ap	c 557	7	1.9	459	10	US-09-918-995-27189	Sequence 27189, A
580	7	1.9	416	10	US-09-918-995-33390	Sequence 33390, A	c 558	7	1.9	459	10	US-09-918-995-27189	Sequence 27189, A

c 654	7	1.9	460	9	US-09-770-444-432	Sequence 432, App	727	7	1.9	495	13	US-10-027-632-193912	Sequence 193912, A
c 655	7	1.9	460	18	US-10-283-975A-598	Sequence 598, App	728	7	1.9	495	17	US-10-027-632-193912	Sequence 193912, A
c 656	7	1.9	460	18	US-10-357-930-9628	Sequence 9628, App	729	7	1.9	496	18	US-10-357-930-9628	Sequence 9628, App
c 657	7	1.9	460	18	US-10-357-930-36089	Sequence 36089, A	730	7	1.9	496	18	US-10-027-632-193912	Sequence 193912, A
c 658	7	1.9	461	9	US-09-770-444-432	Sequence 432, App	731	7	1.9	497	13	US-10-027-632-193912	Sequence 193912, A
c 659	7	1.9	461	18	US-10-357-930-30830	Sequence 30830, A	732	7	1.9	497	13	US-10-027-632-193912	Sequence 193912, A
c 660	7	1.9	461	18	US-10-357-930-39799	Sequence 39799, A	733	7	1.9	497	17	US-10-027-632-193912	Sequence 193912, A
c 661	7	1.9	462	15	US-10-156-761-7438	Sequence 7438, App	734	7	1.9	497	17	US-10-027-632-193912	Sequence 193912, A
c 662	7	1.9	462	17	US-10-425-114-18774	Sequence 18774, A	c 735	7	1.9	498	18	US-10-357-930-59631	Sequence 59631, A
c 663	7	1.9	464	9	US-09-864-761-5412	Sequence 5412, App	c 736	7	1.9	498	18	US-09-318-995-2826	Sequence 2826, App
c 664	7	1.9	464	17	US-10-242-535A-55966	Sequence 55966, A	c 737	7	1.9	500	10	US-09-991-936-662	Sequence 662, App
c 665	7	1.9	464	17	US-10-085-783A-55966	Sequence 55966, A	c 738	7	1.9	501	9	US-09-867-701-2998	Sequence 2998, App
c 666	7	1.9	464	18	US-10-437-963-55501	Sequence 55501, A	c 739	7	1.9	501	13	US-09-814-353-14349	Sequence 14349, A
c 667	7	1.9	466	13	US-10-027-632-95025	Sequence 95025, A	740	7	1.9	501	18	US-10-095-407-6	Sequence 6, Appli
c 668	7	1.9	466	13	US-10-027-632-305639	Sequence 305639, A	741	7	1.9	502	17	US-10-767-701-29192	Sequence 29192, A
c 669	7	1.9	466	17	US-10-027-632-95025	Sequence 95025, A	c 742	7	1.9	503	17	US-10-424-599-64863	Sequence 64863, A
c 670	7	1.9	466	17	US-10-027-632-305639	Sequence 305639, A	743	7	1.9	503	17	US-09-770-961-376	Sequence 376, App
c 671	7	1.9	467	18	US-10-357-930-30977	Sequence 30977, A	744	7	1.9	504	9	US-10-424-599-58265	Sequence 58265, A
c 672	7	1.9	468	9	US-09-864-761-6081	Sequence 6081, App	c 745	7	1.9	504	13	US-09-878-178-1058	Sequence 1058, App
c 673	7	1.9	468	9	US-09-864-761-6081	Sequence 29297, A	c 746	7	1.9	504	13	US-10-046-935-1058	Sequence 1058, App
c 674	7	1.9	469	17	US-10-242-535A-39422	Sequence 39422, A	747	7	1.9	504	13	US-10-027-632-47671	Sequence 47671, A
c 675	7	1.9	469	17	US-10-085-783A-39422	Sequence 39422, A	748	7	1.9	504	13	US-10-027-632-214204	Sequence 214204, A
c 676	7	1.9	469	18	US-10-425-115-120294	Sequence 120294, A	c 749	7	1.9	504	14	US-10-027-632-214205	Sequence 214205, A
c 677	7	1.9	470	11	US-09-732-627A-3406	Sequence 3406, App	c 750	7	1.9	504	17	US-10-146-502-1058	Sequence 1058, App
c 678	7	1.9	471	18	US-10-674-124A-3252	Sequence 3252, App	c 751	7	1.9	504	17	US-10-027-632-47671	Sequence 47671, A
c 679	7	1.9	471	18	US-10-425-115-15821	Sequence 15821, A	752	7	1.9	504	17	US-10-027-632-214204	Sequence 214204, A
c 680	7	1.9	472	17	US-10-424-599-24967	Sequence 24967, A	c 753	7	1.9	505	9	US-10-027-632-214205	Sequence 214205, A
c 681	7	1.9	473	13	US-10-027-632-34455	Sequence 34455, A	754	7	1.9	505	13	US-09-998-598-1092	Sequence 1092, App
c 682	7	1.9	473	13	US-10-027-632-34455	Sequence 34455, A	c 755	7	1.9	505	13	US-10-027-632-86655	Sequence 86655, A
c 683	7	1.9	473	17	US-10-027-632-34455	Sequence 34455, A	756	7	1.9	505	13	US-10-027-632-317058	Sequence 317058, A
c 684	7	1.9	473	17	US-10-027-632-34455	Sequence 34455, A	c 757	7	1.9	505	17	US-10-027-632-86655	Sequence 86655, A
c 685	7	1.9	474	10	US-09-918-995-443	Sequence 443, App	758	7	1.9	505	17	US-10-027-632-317058	Sequence 317058, A
c 686	7	1.9	474	10	US-09-918-995-21887	Sequence 21887, A	c 759	7	1.9	507	17	US-10-425-114-15825	Sequence 15825, A
c 687	7	1.9	474	10	US-09-918-995-25135	Sequence 25135, A	c 760	7	1.9	507	18	US-10-424-599-31226	Sequence 31226, A
c 688	7	1.9	474	10	US-09-876-790-7	Sequence 7, Appli	c 761	7	1.9	507	18	US-10-437-963-86776	Sequence 86776, A
c 689	7	1.9	474	18	US-10-888-918-7	Sequence 7, Appli	c 762	7	1.9	509	18	US-10-425-115-13553	Sequence 13553, A
c 690	7	1.9	474	18	US-10-888-918-7	Sequence 7, Appli	c 763	7	1.9	509	18	US-10-425-115-13553	Sequence 13553, A
c 691	7	1.9	474	19	US-10-888-867-7	Sequence 7, Appli	c 764	7	1.9	510	18	US-10-425-115-62975	Sequence 62975, A
c 692	7	1.9	474	19	US-10-888-867-7	Sequence 7, Appli	c 765	7	1.9	511	18	US-10-767-701-5525	Sequence 5525, App
c 693	7	1.9	474	19	US-10-888-931-7	Sequence 7, Appli	c 766	7	1.9	512	14	US-10-198-846-9282	Sequence 9282, App
c 694	7	1.9	476	18	US-10-425-115-165935	Sequence 165935, A	c 767	7	1.9	513	13	US-10-027-632-194004	Sequence 194004, A
c 695	7	1.9	477	9	US-09-740-668A-23	Sequence 23, Appli	c 768	7	1.9	513	13	US-10-027-632-194004	Sequence 194004, A
c 696	7	1.9	477	10	US-09-918-995-26538	Sequence 26538, A	c 769	7	1.9	513	17	US-10-027-632-194004	Sequence 194004, A
c 697	7	1.9	480	18	US-10-357-930-59691	Sequence 59691, A	c 770	7	1.9	513	17	US-10-027-632-194004	Sequence 194004, A
c 698	7	1.9	481	10	US-09-918-995-32827	Sequence 32827, A	c 771	7	1.9	513	17	US-10-424-599-69416	Sequence 69416, A
c 699	7	1.9	481	13	US-10-027-632-90999	Sequence 90999, A	c 772	7	1.9	513	18	US-10-437-963-86804	Sequence 86804, A
c 700	7	1.9	481	13	US-10-027-632-317604	Sequence 317604, A	c 773	7	1.9	514	17	US-10-341-963A-188	Sequence 188, App
c 701	7	1.9	481	17	US-10-027-632-90999	Sequence 90999, A	c 774	7	1.9	514	18	US-10-481-179-31	Sequence 31, Appli
c 702	7	1.9	481	17	US-10-027-632-317604	Sequence 317604, A	c 775	7	1.9	515	16	US-10-029-386-8536	Sequence 8536, App
c 703	7	1.9	482	9	US-09-867-701-10792	Sequence 10792, A	c 776	7	1.9	515	16	US-10-027-632-86724	Sequence 86724, A
c 704	7	1.9	483	17	US-10-424-599-102232	Sequence 102232, A	c 777	7	1.9	517	13	US-10-027-632-86725	Sequence 86725, A
c 705	7	1.9	484	18	US-10-425-115-82025	Sequence 82025, A	c 778	7	1.9	517	13	US-10-027-632-86725	Sequence 86725, A
c 706	7	1.9	486	17	US-10-424-599-133264	Sequence 133264, A	c 779	7	1.9	517	17	US-10-027-632-86725	Sequence 86725, A
c 707	7	1.9	486	18	US-10-767-701-27673	Sequence 27673, A	c 780	7	1.9	518	17	US-10-424-599-13584	Sequence 13584, A
c 708	7	1.9	487	11	US-09-732-627A-551	Sequence 551, App	c 781	7	1.9	519	9	US-09-734-017A-29	Sequence 29, Appli
c 709	7	1.9	488	10	US-09-918-995-27044	Sequence 27044, A	c 782	7	1.9	519	10	US-09-770-961-55	Sequence 55, Appli
c 710	7	1.9	488	13	US-10-027-632-85966	Sequence 85966, A	c 783	7	1.9	519	17	US-10-424-599-24575	Sequence 24575, A
c 711	7	1.9	488	13	US-10-027-632-238139	Sequence 238139, A	c 784	7	1.9	519	18	US-10-021-323-10093	Sequence 10093, A
c 712	7	1.9	488	13	US-10-027-632-316237	Sequence 316237, A	c 785	7	1.9	520	16	US-09-918-995-28356	Sequence 28356, A
c 713	7	1.9	488	17	US-10-027-632-85966	Sequence 85966, A	c 786	7	1.9	520	16	US-10-029-386-10852	Sequence 10852, A
c 714	7	1.9	488	17	US-10-027-632-238139	Sequence 238139, A	c 787	7	1.9	520	18	US-10-767-701-15904	Sequence 15904, A
c 715	7	1.9	488	17	US-10-027-632-316237	Sequence 316237, A	c 788	7	1.9	521	13	US-10-027-632-265935	Sequence 265935, A
c 716	7	1.9	491	13	US-10-027-632-304334	Sequence 304334, A	c 789	7	1.9	521	17	US-10-027-632-265935	Sequence 265935, A
c 717	7	1.9	491	17	US-10-027-632-304334	Sequence 304334, A	c 790	7	1.9	521	9	US-10-424-599-91106	Sequence 91106, A
c 718	7	1.9	492	9	US-09-867-701-5958	Sequence 5958, App	c 791	7	1.9	522	9	US-09-974-300-6617	Sequence 6617, App
c 719	7	1.9	493	17	US-10-424-599-47714	Sequence 47714, A	c 792	7	1.9	523	10	US-09-764-891-1863	Sequence 1863, App
c 720	7	1.9	493	18	US-10-425-115-10108	Sequence 10108, A	c 793	7	1.9	523	11	US-09-732-627A-522	Sequence 522, App
c 721	7	1.9	494	10	US-09-918-995-38027	Sequence 38027, A	c 794	7	1.9	523	13	US-10-027-632-191086	Sequence 191086, A
c 722	7	1.9	494	13	US-10-027-632-245898	Sequence 245898, A	c 795	7	1.9	523	17	US-10-027-632-191086	Sequence 191086, A
c 723	7	1.9	494	17	US-10-027-632-245898	Sequence 245898, A	c 796	7	1.9	523	18	US-10-767-795-2981	Sequence 2981, App
c 724	7	1.9	494	18	US-10-425-115-40738	Sequence 40738, A	c 797	7	1.9	523	18	US-10-425-115-183364	Sequence 183364, A
c 725	7	1.9	495	9	US-09-822-830A-565	Sequence 565, App	c 798	7	1.9	524	18	US-10-021-323-14636	Sequence 14636, A
c 726	7	1.9	495	10	US-09-814-353-13428	Sequence 13428, A	c 799	7	1.9	525	14	US-10-198-846-11871	Sequence 11871, A

800	7	1.9	525	18	US-10-021-323-10401	Sequence 10401, A	c 873	7	1.9	551	9	US-09-764-860-741	Sequence 741, App
801	7	1.9	525	18	US-10-021-323-10401	Sequence 76508, A	c 874	7	1.9	551	9	US-09-764-860-742	Sequence 742, App
802	7	1.9	525	18	US-09-864-761-7378	Sequence 7378, Ap	c 875	7	1.9	551	14	US-10-074-095-741	Sequence 741, App
803	7	1.9	529	18	US-10-021-323-14399	Sequence 14399, A	c 876	7	1.9	551	14	US-10-074-095-742	Sequence 742, App
804	7	1.9	530	18	US-10-021-323-14680	Sequence 14680, A	c 877	7	1.9	551	15	US-10-106-698-2550	Sequence 2550, Ap
805	7	1.9	531	10	US-09-814-353-13041	Sequence 13041, A	c 878	7	1.9	551	17	US-10-212-872-741	Sequence 741, App
806	7	1.9	531	10	US-09-814-353-13041	Sequence 13041, A	c 878	7	1.9	551	17	US-10-212-872-742	Sequence 742, App
807	7	1.9	531	13	US-10-027-632-90686	Sequence 90686, A	c 880	7	1.9	552	13	US-10-027-632-308834	Sequence 308834, A
808	7	1.9	531	13	US-10-027-632-90686	Sequence 90686, A	c 881	7	1.9	552	17	US-10-027-632-308834	Sequence 308834, A
809	7	1.9	531	17	US-10-027-632-90686	Sequence 90686, A	c 882	7	1.9	552	17	US-10-260-238-4263	Sequence 4263, Ap
810	7	1.9	531	17	US-10-027-632-90686	Sequence 90686, A	c 883	7	1.9	552	18	US-10-437-963-83509	Sequence 83509, A
811	7	1.9	533	13	US-10-027-632-92528	Sequence 92528, A	c 884	7	1.9	553	13	US-10-027-632-226732	Sequence 226732, A
812	7	1.9	533	13	US-10-027-632-92528	Sequence 92528, A	c 885	7	1.9	553	13	US-10-027-632-226733	Sequence 226733, A
813	7	1.9	533	13	US-10-027-632-234056	Sequence 234056, A	c 886	7	1.9	553	13	US-10-027-632-226734	Sequence 226734, A
814	7	1.9	533	13	US-10-027-632-234056	Sequence 234056, A	c 887	7	1.9	553	13	US-10-027-632-226735	Sequence 226735, A
815	7	1.9	533	17	US-10-027-632-92528	Sequence 92528, A	c 888	7	1.9	553	17	US-10-027-632-226732	Sequence 226732, A
816	7	1.9	533	17	US-10-027-632-128968	Sequence 128968, A	c 889	7	1.9	553	17	US-10-027-632-226733	Sequence 226733, A
817	7	1.9	533	17	US-10-027-632-234056	Sequence 234056, A	c 890	7	1.9	553	17	US-10-027-632-226734	Sequence 226734, A
818	7	1.9	533	17	US-10-027-632-307628	Sequence 307628, A	c 891	7	1.9	553	17	US-10-027-632-226735	Sequence 226735, A
819	7	1.9	534	13	US-10-095-407-3	Sequence 3, Appli	c 892	7	1.9	553	18	US-10-647-625A-46	Sequence 46, Appli
820	7	1.9	535	18	US-10-021-323-1524	Sequence 1524, Ap	c 893	7	1.9	554	18	US-10-425-115-58000	Sequence 58000, A
821	7	1.9	535	18	US-10-021-323-1524	Sequence 1524, Ap	c 894	7	1.9	555	13	US-10-027-632-87364	Sequence 87364, A
822	7	1.9	535	18	US-10-021-323-1524	Sequence 1524, Ap	c 895	7	1.9	555	13	US-10-027-632-87365	Sequence 87365, A
823	7	1.9	536	13	US-10-425-115-159888	Sequence 159888, A	c 896	7	1.9	555	13	US-10-027-632-269719	Sequence 269719, A
824	7	1.9	536	13	US-10-027-632-130786	Sequence 130786, A	c 897	7	1.9	555	13	US-10-027-632-269720	Sequence 269720, A
825	7	1.9	536	13	US-10-027-632-193388	Sequence 193388, A	c 898	7	1.9	555	13	US-10-027-632-269721	Sequence 269721, A
826	7	1.9	536	13	US-10-027-632-193389	Sequence 193389, A	c 899	7	1.9	555	13	US-10-027-632-303587	Sequence 303587, A
827	7	1.9	536	13	US-10-027-632-193390	Sequence 193390, A	c 900	7	1.9	555	13	US-10-027-632-303588	Sequence 303588, A
828	7	1.9	536	13	US-10-027-632-193391	Sequence 193391, A	c 901	7	1.9	555	13	US-10-027-632-87364	Sequence 87364, A
829	7	1.9	536	17	US-10-027-632-130786	Sequence 130786, A	c 902	7	1.9	555	17	US-10-027-632-87365	Sequence 87365, A
830	7	1.9	536	17	US-10-027-632-193388	Sequence 193388, A	c 903	7	1.9	555	17	US-10-027-632-87366	Sequence 87366, A
831	7	1.9	536	17	US-10-027-632-193389	Sequence 193389, A	c 904	7	1.9	555	17	US-10-027-632-269720	Sequence 269720, A
832	7	1.9	536	17	US-10-027-632-193390	Sequence 193390, A	c 905	7	1.9	555	17	US-10-027-632-269721	Sequence 269721, A
833	7	1.9	537	13	US-10-027-632-193391	Sequence 193391, A	c 906	7	1.9	555	17	US-10-027-632-303587	Sequence 303587, A
834	7	1.9	537	13	US-10-027-632-181646	Sequence 181646, A	c 907	7	1.9	555	17	US-10-027-632-303588	Sequence 303588, A
835	7	1.9	537	13	US-10-027-632-318797	Sequence 318797, A	c 908	7	1.9	557	10	US-09-918-995-26912	Sequence 26912, A
836	7	1.9	537	13	US-10-027-632-318798	Sequence 318798, A	c 909	7	1.9	557	10	US-09-814-353-267	Sequence 267, App
837	7	1.9	537	17	US-10-027-632-318797	Sequence 318797, A	c 910	7	1.9	557	10	US-09-814-353-267	Sequence 267, App
838	7	1.9	537	17	US-10-027-632-318798	Sequence 318798, A	c 911	7	1.9	558	18	US-10-425-115-11233	Sequence 11233, A
839	7	1.9	537	18	US-10-027-632-318799	Sequence 318799, A	c 912	7	1.9	559	9	US-09-864-761-16511	Sequence 16511, A
840	7	1.9	538	18	US-10-027-632-318799	Sequence 318799, A	c 913	7	1.9	559	18	US-10-425-115-124033	Sequence 124033, A
841	7	1.9	539	16	US-10-029-386-10882	Sequence 10882, A	c 914	7	1.9	559	18	US-10-425-115-158315	Sequence 158315, A
842	7	1.9	542	9	US-09-974-300-4868	Sequence 4868, Ap	c 915	7	1.9	559	18	US-10-425-115-158315	Sequence 158315, A
843	7	1.9	542	13	US-10-027-632-299072	Sequence 299072, A	c 916	7	1.9	560	13	US-10-027-632-108918	Sequence 108918, A
844	7	1.9	542	13	US-10-027-632-306625	Sequence 306625, A	c 917	7	1.9	560	13	US-10-027-632-13290	Sequence 13290, A
845	7	1.9	542	13	US-10-027-632-306626	Sequence 306626, A	c 918	7	1.9	560	17	US-10-027-632-108918	Sequence 108918, A
846	7	1.9	542	17	US-10-027-632-299072	Sequence 299072, A	c 919	7	1.9	560	17	US-10-027-632-313290	Sequence 313290, A
847	7	1.9	542	17	US-10-027-632-306625	Sequence 306625, A	c 920	7	1.9	561	13	US-10-027-632-74099	Sequence 74099, A
848	7	1.9	542	17	US-10-027-632-306626	Sequence 306626, A	c 921	7	1.9	561	13	US-10-027-632-74099	Sequence 74099, A
849	7	1.9	543	13	US-10-027-632-289460	Sequence 289460, A	c 922	7	1.9	561	18	US-10-021-323-16973	Sequence 16973, A
850	7	1.9	544	13	US-10-027-632-289460	Sequence 289460, A	c 923	7	1.9	561	18	US-10-425-115-94301	Sequence 94301, A
851	7	1.9	544	17	US-10-027-632-289460	Sequence 289460, A	c 924	7	1.9	563	17	US-10-027-632-45651	Sequence 45651, A
852	7	1.9	545	13	US-10-027-632-40156	Sequence 40156, A	c 925	7	1.9	563	17	US-10-027-632-45651	Sequence 45651, A
853	7	1.9	545	17	US-10-027-632-40156	Sequence 40156, A	c 926	7	1.9	563	18	US-10-021-323-16691	Sequence 16691, A
854	7	1.9	546	17	US-10-027-632-40156	Sequence 40156, A	c 927	7	1.9	563	18	US-10-021-323-16691	Sequence 16691, A
855	7	1.9	547	10	US-09-997-003-18	Sequence 18, Appli	c 928	7	1.9	564	13	US-10-027-632-92940	Sequence 92940, A
856	7	1.9	547	13	US-10-027-632-116133	Sequence 116133, A	c 929	7	1.9	564	13	US-10-027-632-92941	Sequence 92941, A
857	7	1.9	547	13	US-10-027-632-253039	Sequence 253039, A	c 930	7	1.9	564	13	US-10-027-632-137712	Sequence 137712, A
858	7	1.9	547	17	US-10-027-632-116133	Sequence 116133, A	c 931	7	1.9	564	13	US-10-027-632-217638	Sequence 217638, A
859	7	1.9	547	17	US-10-027-632-253039	Sequence 253039, A	c 932	7	1.9	564	13	US-10-027-632-217639	Sequence 217639, A
860	7	1.9	547	17	US-10-027-632-253039	Sequence 253039, A	c 933	7	1.9	564	16	US-10-334-385A-33	Sequence 33, Appli
861	7	1.9	547	18	US-10-357-930-21420	Sequence 21420, A	c 934	7	1.9	564	17	US-10-027-632-92940	Sequence 92940, A
862	7	1.9	547	18	US-10-357-930-21420	Sequence 21420, A	c 935	7	1.9	564	17	US-10-027-632-92941	Sequence 92941, A
863	7	1.9	548	13	US-10-425-115-136172	Sequence 136172, A	c 936	7	1.9	564	17	US-10-027-632-137712	Sequence 137712, A
864	7	1.9	549	13	US-10-027-632-283605	Sequence 283605, A	c 937	7	1.9	564	17	US-10-027-632-217638	Sequence 217638, A
865	7	1.9	549	16	US-10-029-386-8947	Sequence 8947, Ap	c 938	7	1.9	564	17	US-10-027-632-217639	Sequence 217639, A
866	7	1.9	549	16	US-10-029-386-8947	Sequence 8947, Ap	c 939	7	1.9	564	17	US-10-027-632-217639	Sequence 217639, A
867	7	1.9	549	17	US-10-027-632-283605	Sequence 283605, A	c 940	7	1.9	564	17	US-10-425-115-63698	Sequence 63698, A
868	7	1.9	549	17	US-10-260-238-5635	Sequence 5635, Ap	c 941	7	1.9	564	18	US-10-425-115-63698	Sequence 63698, A
869	7	1.9	550	13	US-10-027-632-130449	Sequence 130449, A	c 942	7	1.9	565	9	US-10-357-930-60527	Sequence 60527, A
870	7	1.9	550	17	US-10-027-632-130449	Sequence 130449, A	c 943	7	1.9	565	13	US-09-864-761-9830	Sequence 9830, Ap
871	7	1.9	550	18	US-10-425-115-23805	Sequence 23805, A	c 944	7	1.9	566	13	US-10-027-632-93735	Sequence 93735, A
872	7	1.9	550	18	US-10-425-115-23805	Sequence 23805, A	c 945	7	1.9	566	13	US-10-027-632-93735	Sequence 93735, A
						Sequence 150227,		7	1.9	566	17	US-10-027-632-93735	Sequence 93735, A

```
946 7 1.9 566 17 US-10-027-632-318293, Sequence 318293,
947 7 1.9 566 17 US-10-242-535A-46367, Sequence 46367, A
948 7 1.9 566 17 US-10-085-783A-46367, Sequence 46367, A
949 7 1.9 566 18 US-10-357-930-50406, Sequence 50406, A
950 7 1.9 567 17 US-10-369-493-29136, Sequence 29136, A
951 7 1.9 567 17 US-10-424-599-57070, Sequence 57070, A
952 7 1.9 567 18 US-10-425-115-102573, Sequence 102573, A
953 7 1.9 568 17 US-10-424-599-27796, Sequence 27796, A
954 7 1.9 569 9 US-09-864-761-12731, Sequence 12731, A
955 7 1.9 569 14 US-10-181-642-17, Sequence 17, Appl
956 7 1.9 569 17 US-10-257-294-70, Sequence 70, Appl
957 7 1.9 569 17 US-10-257-294-71, Sequence 71, Appl
958 7 1.9 569 18 US-10-809-654-17, Sequence 17, Appl
959 7 1.9 569 18 US-10-809-655-17, Sequence 17, Appl
960 7 1.9 570 18 US-10-425-115-110416, Sequence 110416, A
961 7 1.9 571 13 US-10-027-632-81990, Sequence 81990, A
962 7 1.9 571 17 US-10-027-632-81990, Sequence 81990, A
963 7 1.9 571 18 US-10-653-047-3969, Sequence 3969, Ap
964 7 1.9 572 13 US-10-027-632-220249, Sequence 220249, A
965 7 1.9 572 13 US-10-027-632-320963, Sequence 320963, A
966 7 1.9 572 17 US-10-027-632-220249, Sequence 220249, A
967 7 1.9 572 17 US-10-027-632-320963, Sequence 320963, A
968 7 1.9 573 13 US-10-002-344A-28, Sequence 28, Appl
969 7 1.9 573 13 US-10-027-632-19226, Sequence 19226, A
970 7 1.9 573 17 US-10-027-632-19226, Sequence 19226, A
971 7 1.9 574 9 US-09-864-761-7102, Sequence 7102, Ap
972 7 1.9 574 16 US-10-029-386-6596, Sequence 6596, Ap
973 7 1.9 574 17 US-10-424-599-83722, Sequence 83722, A
974 7 1.9 574 18 US-10-425-115-119468, Sequence 119468, A
975 7 1.9 575 17 US-10-424-599-105472, Sequence 105472, A
976 7 1.9 575 18 US-10-437-963-86598, Sequence 86598, A
977 7 1.9 576 9 US-09-778-320-146, Sequence 146, App
978 7 1.9 576 9 US-09-770-152-215, Sequence 215, App
979 7 1.9 576 9 US-09-864-761-7169, Sequence 7169, Ap
980 7 1.9 576 9 US-09-910-689-146, Sequence 146, App
981 7 1.9 576 13 US-10-010-742-146, Sequence 146, App
982 7 1.9 576 18 US-10-714-389-146, Sequence 146, App
983 7 1.9 576 18 US-10-717-296-146, Sequence 213527, A
984 7 1.9 577 13 US-10-027-632-213527, Sequence 213527, A
985 7 1.9 577 13 US-10-027-632-213528, Sequence 213528, A
986 7 1.9 577 17 US-10-027-632-213527, Sequence 213527, A
987 7 1.9 577 17 US-10-027-632-213528, Sequence 213528, A
988 7 1.9 578 13 US-10-027-632-198019, Sequence 198019, A
989 7 1.9 578 13 US-10-027-632-225913, Sequence 225913, A
990 7 1.9 578 16 US-10-029-386-12911, Sequence 12911, A
991 7 1.9 578 17 US-10-027-632-198019, Sequence 198019, A
992 7 1.9 578 17 US-10-027-632-225913, Sequence 225913, A
993 7 1.9 578 18 US-10-425-115-45179, Sequence 45179, A
994 7 1.9 579 10 US-09-876-790-1, Sequence 1, Appli
995 7 1.9 579 17 US-10-282-122A-37838, Sequence 37838, A
996 7 1.9 579 18 US-10-425-115-112778, Sequence 112778, A
997 7 1.9 579 18 US-10-888-918-1, Sequence 1, Appli
998 7 1.9 579 19 US-10-888-779-1, Sequence 1, Appli
999 7 1.9 579 19 US-10-888-867-1, Sequence 1, Appli
1000 7 1.9 579 19 US-10-888-780-1, Sequence 1, Appli
```

ALIGNMENTS

RESULT 1

```
US-09-736-250-2
; Sequence 2, Application US/09736250
; Publication No. US20050014139A1
; GENERAL INFORMATION:
; APPLICANT: SUMITOMO ELECTRIC INDUSTRIES, LTD.
; APPLICANT: NAKAMURA, Takeshi
; TITLE OF INVENTION: HUMAN CYCLIN I AND GENES ENCODING THE SAME
; FILE REFERENCE: 050212-0278
; CURRENT APPLICATION NUMBER: US/09/736,250
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 09/054,492
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: PCT/JP96/02905
```

```
; PRIOR FILING DATE: 1996-10-07
; PRIOR APPLICATION NUMBER: 284663/1995
; PRIOR FILING DATE: 1995-10-05
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 1134
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-736-250-2

Alignment Scores:
Pred. No.: 0 Length: 1134
Score: 377.00 Matches: 377
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-09-736-250-1 (1-377) x US-09-736-250-2 (1-1134)

Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuGluLysAlaIle 20
Db 1 ATGAAGTTTCAGGGCCCTTTGGAAACACAGAGATTGCTTTCTCTGTTGGAAAGGCAATC 60
Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 61 ACTAGGAGACACAGATGTGGAAAGTGAATGTGGGAAATGCTTCAATCAGAAATGTT 120
Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn 60
Db 121 TCTCCATCCAGAGAGATGAATTAATCAATGGCTGCCAAACCTCAAGTACCAATTCAC 180
Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 181 CTTTACCAGCAACATTTGCTGGCTAGCAGAGTCTTTTGGATAGGTTTGTAGCTACCGTA 240
Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaAlaLys 100
Db 241 AAGGCTCATCCAAATACTATTGAGTTGTATTGCAATCAGCTGTTTCTTCTAGCTGCCAAG 300
Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 301 ACTGTTGAGGAAGATGAGAAATTCAGTACTAAGGTAATTTGGCAGACAGACAGATTCTGT 360
Qy 121 GlyCysSerSerSerGluIleLeuAlaSerMetGluArgIleLeuAspLysLeuAsnTrp 140
Db 361 GGATGTTCTCATCTGAAATTTTGGAAATGGAGAGAATTTATCTGGATAAGTTGAAATGG 420
Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 421 GATCTTCACACAGCCACACCATTTGGATTTTCTCATATTTTCCATGTCATTCAGTGTCA 480
Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 481 ACTAGGCCTCAGTTACTTTTTCAGTTTCCCAATTTAGGCCCATCTCAACATTTGGCAGTC 540
Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
Db 541 CTTTACCAGCAACATCTACTTCACTGTATGGCTGCCAACCAACTCTTGCATTCAGAGGATCC 600
Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
Db 601 ATGCTTGCTCTGGCCATGGTTAGTCTGGAATGGAGAAATCTCATTTCTGATGGCTTCT 660
Qy 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuLeuHisCysArg 240
Db 661 CTTTACAATTTGAATGCTTTCAGAAAGACAGATGATAGTCCCAAGTTCATTCATTCATTGCG 720
Qy 241 GluLeuValAlaHisHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
Db 721 GAGCTTGTGGCACATCACCTTTTCTACTCTGAGTCTTCTCCCTGCTCTGAAATTCGTTAT 780
```

```
QY 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db 781 GTCTACCGTCCCTCAAGCACACCCCTGGTGTGACAAAGGAGTCTTCAGATTACAT 840
QY 281 ProSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
Db 841 CCTCTCTGTGCCCAGGCCAGACTTCTCCAGGACCAACAGCAGCCAGAGTGCAGTC 900
QY 301 ArgGlyThrAlaAlaPheTyrHisHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
Db 901 AGAGGTACAGCAGCCCTTTTACCATCATCTCCAGCTGCAGTGGGTGCAAGCAGACCTCT 960
QY 321 ThrLysArgLysValGluGluMetGluValAspAspPheTyrAspGlyLysValArgLeu 340
Db 961 ACTAAACCAAGTAGAGAAATGGAAGTGATGACTTCTATGATGGAAATCAAAACGGGTC 1020
QY 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
Db 1021 TATATGAAGATAATGTCTCAGAAATGTGGTCTGTGTGGCAGCTGATTTATCAAGA 1080
QY 361 GlnGluGlyHisAlaSerProCysProLeuGlnProValSerValMet 377
Db 1081 CAAGAGGACATGCTTCCCTTGTCCACCTTGCAGCCCTGTTCTGTCTCATG 1131

RESULT 2
US-10-172-118-1326
; Sequence 1326, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 1326
; LENGTH: 1260
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM_006835
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-1326

Alignment Scores:
Pred. No.: 0 Length: 1260
Score: 377.00 Matches: 377
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Db: 17 Gaps: 0

US-09-736-250-1 (1-377) x US-10-172-118-1326 (1-1260)
QY 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuGluLysAlaIle 20
Db 1 ATGAAGTTTCCAGGCCCTTGGAAACACAGAGATTGTCTTTCCTGTGGAAAGGCATC 60
QY 21 ThrArgGluAlaGlnMetTyrLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 61 ACTAGGAAGCACAGATGTGGAAGTGAATGTGCGGAAATGCCCTTCAATCAGAATGTT 120
QY 41 SerProSerGlnArgAspGluValIleGlnTyrPheAlaLysLeuLysTyrGlnPheAsn 60
Db 1131 TATATGAAGATAATGTCTCAGAAATGTGGTCTGTGTGGCAGCTGATTTATCAAGA 1080
```

```
Db 121 TCTCCATCCCAGAGAGATGAAGTAATTCATGGCTGGCCAAACTCAAGTACCAATTCAAC 180
QY 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 181 CTTTACCAGAGAAACATTTGCTCTGGCTAGCAGTCTTTTGGATAGATGTTTGTAGCTACCCTA 240
QY 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPheLeuAlaAlaLys 100
Db 241 AAGGCTCATCCAAATACTTTGAGTTGATTGCAATCAGCTGTTTTTCTAGCTGCCAAG 300
QY 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 301 ACTGTTGAGGAAGATGAGAGAAATCCAGTACTAAAGGATTTGGCAGAGACAGTTTCTGT 360
QY 121 GlyCysSerSerGluIleLeuArgMetGluArgIleLeuLeuAspLysLeuAsnTrp 140
Db 361 GGATGTTCTCATCTGAAATTTTTCAGAAATGAGAGAAATTAATCTGGATAAGTTGAATGG 420
QY 141 AspleuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 421 GATCTTACACAGCCACCATTCGATTTTCTCATATTTTCCATGTCATTCAGTGTCA 480
QY 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 481 ACTAGGCTCAGTTACTTTTTCAGTTTGGCCAAATGAGCCCATCTCAACATTTGGCAGTC 540
QY 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
Db 541 CTTACCAAGCAACTACTTCTACTGTATGCGCTGCAACCAACTCTCTGCAATTCAGAGATCC 600
QY 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
Db 601 ATGCTTGTCTGCGCCATGGTTAGTCTGGAATGAGAAACTCATTCCTGATGGCTTTCT 660
QY 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
Db 661 CTTACATTTGACTGCTTTCAGAAAGCACAGATGATAGTCTCCAGTTCATTCATTTGTCGG 720
QY 241 GluLeuValAlaHisHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
Db 721 GAGCTTGTGGCACATCACCTTTTCTACTCTGCAGTCTTCCCTGCTCTGAAATTCGGTTAT 780
QY 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db 781 GTCTACCGTCCCTCAAGCACACCCCTGGTGTGACCTGTGACAAAGGAGTGTTCAGATTACAT 840
QY 281 ProSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
Db 841 CCTCTCTGTGCCAGGCCACAGACTTCTCCAGGACCAACAGCAGCCAGAGTGCAGTC 900
QY 301 ArgGlyThrAlaAlaPheTyrHisHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
Db 901 AGAGGTACAGCAGCCCTTTTACCATCATCTCCAGCTGCAGTGGGTGCAAGCAGACCTCT 960
QY 321 ThrLysArgLysValGluGluMetGluValAspAspPheTyrAspGlyLysValArgLeu 340
Db 961 ACTAAACCAAGTAGAGAAATGGAAGTGATGACTTCTATGATGGAAATCAAAACGGGTC 1020
QY 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
Db 1021 TATATGAAGATAATGTCTCAGAAATGTGGTCTGTGTGGCAGCTGATTTATCAAGA 1080
QY 361 GlnGluGlyHisAlaSerProCysProLeuGlnProValSerValMet 377
Db 1081 CAAGAGGACATGCTTCCCTTGTCCACCTTGCAGCCCTGTTCTGTCTCATG 1131

RESULT 3
US-10-342-887-1326
; Sequence 1326, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
```


APPLICANT: Linsley, Peter S.
APPLICANT: Mao, Mao
APPLICANT: Roberts, Christopher J.
APPLICANT: Van 't Veer, Laura Johanna
APPLICANT: Van de Vijver, Marc J.
APPLICANT: Bernards, Rene
TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
FILE REFERENCE: 9301-188-999
CURRENT APPLICATION NUMBER: US/10/342,887
PRIOR FILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: 60/298,918
PRIOR FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: 60/380,710
PRIOR FILING DATE: 2002-05-14
PRIOR APPLICATION NUMBER: 10/172,118
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 2699
SEQ ID NO 1326
LENGTH: 1260
TYPE: DNA
ORGANISM: Homo sapiens
US-10-342-887-1326

Alignment Scores:
Pred. No.: 0 Length: 1260
Score: 377.00 Matches: 377
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-09-736-250-1 (1-377) x US-10-342-887-1326 (1-1260)

Qy 1 MetLysPheProGluProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle 20
Db 1 ATGAAGTTTCAGGGCCCTTGGAAACCCAGAGATTGTTCTTCTGTTGGAAAGCCAAATC 60

Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 61 ACTAGGGAAGCACAGATGGAAGTGAATGTGGGAAATGCTTCAATCAGATGTT 120

Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyTrpPheAsn 60
Db 121 TCTCCATCCAGAGAGATGAAGTAAATCAATGGCTGGCCAAACTCAAGTACCAATTCAC 180

Qy 61 LeuTyTrpGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 181 CTTTACCAGAAACATTTGCTGGCTAGCAGTCTTTGGTAGTATTTAGCTACCGTA 240

Qy 81 LysAlaHisProLysTyTrpLeuSerCysIleAlaIleSerCysPhePheLeuAlaLys 100
Db 241 AAGGCTCATCCAAATACTTGAGTTGATTTGCAATCAGCTGTTTCTTCTAGCTGCCAAG 300

Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 301 ACTGTTGAGGAAGATGAGAGAAATCCAGTACTAAGGTATTGGCAAGACAGATTCTGT 360

Qy 121 GlyCysSerSerSerGluLeuLeuArgMetGluArgIleLeuLeuAspLysLeuAsnTrp 140
Db 361 GGATGTTCTCATCTGAAATTTTGAAGATGAGAGAAATTTCTGGATAAGTCAATTGG 420

Qy 141 AspleuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 421 GATCTTCACAGCCACACCAATGGAATTTCTCATATTTTCCATGTCATTCAGTGTCA 480

Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 481 ACTAGGCTCAGTACTTTTCAGTTTGCCAAATTTGAGCCCATCTCAACATTTGGCAGTC 540

Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
Db 541 CTTACCAAGCAACTACTTCACTGTATGGCTGTGCAACCAACTTCTGCAATTCAGAGGATCC 600

Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
Db 601 ATGCTTGCTCTGGCCATGGTTAGTCTGAAATGGAGAACTCATTTCTGATTGCTTCT 660

Qy 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
Db 661 CTTACAAATTGAATGCTTCAGAAAGCACAGATGATAGTCCCATGTTGATCCATTGTCGG 720

Qy 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyTrp 260
Db 721 GAGCTTGTGGCACAATCACCTTTTACTCTGAGTCTTCCCTGCTCTGAATTCGGTTTAT 780

Qy 261 ValTyArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db 781 GTCTACCGTCCCTCAAGCACACCTGTGTGACCTGTGACAAAGAGGTTCAGATTACAT 840

Qy 281 ProSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
Db 841 CCTCTCTCTGTCCAGGCCAGACTTCTCCAGGACAAACAGCAAGCCAGAGTCCAGTC 900

Qy 301 ArgGlyThrAlaAlaPheTyTrpHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
Db 901 AGAGTACAGAGCCCTTTTACCATCATCTCCAGCTGCCAGTGGTGGTCAAGACACTCT 960

Qy 321 ThrLysArgLysValGluGluMetGluValAspAspPheTyTrpAspGlyIleLysArgLeu 340
Db 961 ACTAAACGCAAGTAGAGGAAATGGAGTGGATGACTTCTATGATGGAATCAACGCTC 1020

Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
Db 1021 TATAATGAAGATAATGTCTCAGAAATATGGGTCTGTGTGTGCTGACTGATTTATCAAGA 1080

Qy 361 GlnGluGlyHisAlaSerProCysProLeuGlnProValSerValMet 377
Db 1081 CAAGAGGAGACATGCTTCCCTTTGTCACCTTTCAGCTTGTCTGTCATG 1131

RESULT 4
US-10-641-643-899
Sequence 899, Application US/10641643
Publication No. US20040077003A1
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
Susan G. Stuart
Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
GENE EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/641,643
FILING DATE: 14-Aug-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166

; INFORMATION FOR SEQ ID NO: 899:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1260 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; IMMEDIATE SOURCE:

; LIBRARY: GENBANK

; CLONE: g1183161

; SEQUENCE DESCRIPTION: SEQ ID NO: 899 :

US-10-641-643-899

Alignment Scores:

Pred. No.:	0	Length:	1260
Score:	377.00	Matches:	377
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	17	Gaps:	0

US-09-736-250-1 (1-377) x US-10-641-643-899 (1-1260)

```

Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuGluLysAlaIle 20
Db 1 ATGAAGTTTCAGGGCCTTGGAAACACAGAGATTGCTTTCCTGTTGGAAGGCAATC 60

Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 61 ACTAGGGAAGCACAGATGTGGAAGTGAATGTGGGAAATGCCTTCAATCAGATGTT 120

Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn 60
Db 121 TCTCCATCCAGAGAGATGAAGTAAATCAATGGTGGCCAAACTCAAGTACCAATCAAC 180

Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 181 CTTTACCAGAAACATTTGCTCTGGTAGCAGTCTTTTGGATAGTCTTTAGCTACCGTA 240

Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaLys 100
Db 241 AAGGCTCATCCAAATACTTCAAGTGTATTGCAATCAGCTGTTTTTCTAGCTGCCAAG 300

Qy 101 ThrValGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 301 ACTGTGAGGAAGATGAGAGAAATTCAGTACTAAGGTATTGGCAAGACAGATTTCTGT 360

Qy 121 GlyCysSerSerGluIleLeuArgMetGluArgIleLeuAspLysLeuAsnTrp 140
Db 361 GGATGTTCTCATCTGAATTTTGGAGATGGAGAGAAATATTCTGGATAAGTTGAATGG 420

Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 421 GATCTTCACAGCCACACACCATGATGATTTTCTTATATTTTCCATGTCATGCGATGCA 480

Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 481 ACTAGGCTCAGTACTTTTCAAGTTTGGCCAAATTTGAGCCCATCTCAACATTTGGCAGTC 540

Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
Db 541 CTTACCAAGCAACTACTTCACTGTATGGCTTGCACCAACTTCTGCAATTCAGAGGATCC 600

Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
Db 601 ATGCTTGCTCTGGCCATGTTAGTCTGGAATGGAGAACTCATTTCTGATGGCTTTCT 660

Qy 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuLeuIleHisCysArg 240
Db 661 CTTCAATTTGAATGCTTTTCAAGAAAGCACAGATGATAGTCTCCCAAGTTCATTTGTCGG 720

Qy 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
Db 721 GAGCTTGGGCACATCACCTTTTCTACTCTGCAGCTCTTCCCTGCTGCAATTCGTTAT 780

```

RESULT 5

US-09-867-701-10907
 ; Sequence 10907, Application US/09867701
 ; Patent No. US20020132237A1

; GENERAL INFORMATION:

; APPLICANT: Aglate, Paul A.
 ; APPLICANT: Jones, Robert
 ; APPLICANT: Harlocker, Susan L.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; FILE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
 ; FILE REFERENCE: 210121.497
 ; CURRENT APPLICATION NUMBER: US/09/867,701
 ; CURRENT FILING DATE: 2001-05-29
 ; NUMBER OF SEQ ID NOS: 10912
 ; SOFTWARE: Fast-Seq for Windows Version 4.0
 ; SEQ ID NO 10907
 ; LENGTH: 1889
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-867-701-10907

Alignment Scores:

Pred. No.:	0	Length:	1889
Score:	377.00	Matches:	377
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-736-250-1 (1-377) x US-09-867-701-10907 (1-1889)

```

Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuGluLysAlaIle 20
Db 544 ATGAAGTTTCAGGGCCTTGGAAACACAGAGATTGCTTTCCTGTTGGAAGGCAATC 603

Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 604 ACTAGGGAAGCACAGATGTGGAAGTGAATGTGGGAAATGCCTTCAATCAGATGTT 663

Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn 60
Db 664 TCTCCATCCAGAGAGATGAAGTAAATTCATGCTGGCCAAACTCAAGTACCAATTCAC 723

Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 724 CTTTACCAGAAACATTTGCTCTGCTGCTAGCAGTCTTTTGGATAGTCTTTTACGTCACGTA 783

Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaLys 100

```

```
Db 784 AAGGCTCATCCAAATACCTGAGTTGATTGCAATCAGCTGTTTCTAGCTGCCAAG 843
Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 844 ACTGTTGAGGAAGATGAGAGAATCCAGTACTAAAGGTATTGGCAAGAGACAGATTTCTGT 903
Qy 121 GlyCysSerSerGluIleLeuArgMetGluArgIleLeuAspLysLeuAsnTrp 140
Db 904 GGATGTTCTCATCTGAAATTTGAGATGGAGAGATTAATCTGGATAGTTGAATGG 963
Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 964 GATCTTCACAGCCACACCATGATGATTTCTTCATATTTCCATGTCATTCAGTGTC 1023
Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 1024 ACTAGGCTTCAGTTACTTTTCAGTTGGCCAAATGGCCAAATGGCCATCTCAACATTTGGCAGTC 1083
Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
Db 1084 CTTACCAAGCACTACTTCACTGTATGGCTGCAACCACTTCTGCAATTCAGAGGATCC 1143
Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
Db 1144 ATGCTTGCTCTGGCCATGGTGTAGTCTGGAATGGAGAACTCAITTCCTGATGGCTTCT 1203
Qy 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuLeuHisCysArg 240
Db 1204 CTTACATTTGAACTGCTTCAGAACGACAGATGGATGCTCCAGTTGATCCATTTGCTGG 1263
Qy 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTrp 260
Db 1264 GAGCTTGTTGGCACATCACCTTTCTACTCTGCAGTCTTCCCTGCCTCTGAATTCGTTAT 1323
Qy 261 ValTrpArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db 1324 GTCTACCGTCCCTCAACGACACCCCTGGTGACCTGTGTGACAAAGGAGTGTTCAGATTACAT 1383
Qy 281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
Db 1384 CCCTCTCTGTCGCGCCGAGACTTCTCCAGAGACACACAGCCAGGAGTCCAGTC 1443
Qy 301 ArgGlyThrAlaAlaPheTyriHisLeuProAlaSerGlyCysLysGlnThrSer 320
Db 1444 AGAGTACAGCAGCGCTTTTACCATCATCTCCAGCTGCCAGTGGGTGCAAGCAGACCTCT 1503
Qy 321 ThrLysArgLysValGluGluMetGluValAspPhePheTyriAspGlyIleLysArgLeu 340
Db 1504 ACTAAACCAAGTAGAGAAATGGAATGGAGTGATGACTTCTATGATGAATCAACGCGTC 1563
Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
Db 1564 TATAATGAAGATATGCTCAGAAATGTGGTCTCTGTGTGGCATGATTTATCAAGA 1623
Qy 361 GlnGluGlyHisAlaSerProCysProProLeuGlnProValSerValMet 377
Db 1624 CAAGGGGACATGCTTCCCTTGTCCACCTTTGCAGCGCTGTTTCTGTCAATG 1674
```

RESULT 6

```
US-09-814-353-21586
; Sequence 21586, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
```

```
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21586
; LENGTH: 2755
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-814-353-21586
```

Alignment Scores:

```
Pred. No.: 3,73e-263 Length: 2755
Score: 266.00 Matches: 266
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 70.56% Indels: 0
DB: 10 Gaps: 0
```

US-09-736-250-1 (1-377) x US-09-814-353-21586 (1-2755)

```
Qy 103 GluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCysGlyCys 122
Db 1099 GAGGAGATGAGAGATTTCCAGTACTAAAGTATTGGCAAGAGACAGATTTCTGTGATGT 1158
Qy 123 SerSerSerGluIleLeuArgMetGluArgIleLeuAspLysLeuAsnTrpAspLeu 142
Db 1159 TCCTCATCTGAAATTTTGAATGGAGAGAAATATTCTGATAAATGGAATGGATCTT 1218
Qy 143 HisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSerThrArg 162
Db 1219 CACACAGCCACACATTTGGATTTTTCATATTTTTCATGCCAATTCAGTGTCAACTAGG 1278
Qy 163 ProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaValLeuThr 182
Db 1279 CCTCAGTACTTTTTCAGTTTGGCCAAATGGAGCCATCTCAACATTTGGCAGTCTTACC 1338
Qy 183 LysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySerMetLeu 202
Db 1339 AAGCAACTACTTCACTGTATGGCTGCAACCAACTTCTGCAATTCAGAGGATCCATGCTT 1398
Qy 203 AlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSerLeuThr 222
Db 1399 GCTCTGGCCATGGTTAGTCTGGAAATGGAGAAACTCATCTCTGATTTGGCTTTCTCTACA 1458
Qy 223 IleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArgGlyLeu 242
Db 1459 ATTGAATCGCTTCAGAAAGCACAGATGGATAGTCCAGTTGATCCATTTGTCGGAGCTT 1518
Qy 243 ValAlaHisIleLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTrpValTrp 262
Db 1519 GTGGCATCATCACCTTTCTACTCTGCGAGTCTTCCCTGCCCTCTGAAATTCGATATGTCTAC 1578
Qy 263 ArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHisProSer 282
Db 1579 CGTCCCTCAAGCACACCTTGGTGACTCTGACAAAGGAGTGTTCAGATTACATCCCTCC 1638
Qy 283 SerValProGlyProAspPheSerLysAspAsnSerLysProGluValProValArgGly 302
Db 1639 TCTGTCCCGAGGCCAGACTTCTCAAGGACCAACAGCAAGGAGTGTTCAGATTACATCCCTCC 1698
Qy 303 ThrAlaAlaPheTyriHisIleLeuProAlaAlaSerGlyCysLysGlnThrSerThrLys 322
Db 1699 ACAGCAGCCTTTTACCATCATCTCCAGCTGCCAGTGGGTGCAAGCAGACCTCTACTAAA 1758
```

Qy 323 ArgLysValGluMetGluValAspPheTyrAspGlyLeuLysArgLeuTyrAsn 342
Db 1759 CGCAAGTAGAGAAATGGAAGTGGATGACTTCTATGATGGAATCAACCGGCTCTATAAT 1818
Qy 343 GluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArgGlnGlu 362
Db 1819 GAAGATAATGCTCAGAAATGTTGGTCTGTGTGGCACTGATTATCAAGACAAGAG 1878
Qy 363 GlyHisAlaSerProCys 368
Db 1879 GGACATGCTTCCCTTGT 1896

RESULT 7

US-10-242-535A-16032
; Sequence 16032, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16032
; LENGTH: 444
; TYPE: DNA
; ORGANISM: Human
US-10-242-535A-16032

Alignment Scores:

Pred. No.: 3,84e-133 Length: 444
Score: 139.00 Matches: 139
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 36.87% Indels: 0
DB: 17 Gaps: 0

US-09-736-250-1 (1-377) x US-10-242-535A-16032 (1-444)

Qy 124 SerSerGluLeuLeuArgMetGluArgIleLeuAspLysLeuAsnTrpAspLeuHis 143
Db 3 TCATCTGAAATTTTGAGAAATGAGAGAAATTTCTGGATAAGTTGAAATGGATCTTCAC 62
Qy 144 ThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSerThrArgPro 163
Db 63 ACAGCCACACCATTTGGATTTCTTCATATTTTCCATGCAATTCGAGTGTCAACTAGGCGCT 122
Qy 164 GlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaValLeuThrLys 183
Db 123 CAGTTACTTTTCAGTTTGGCCCAATTTGAGCCCACTCTCAACATTTGGCAGTCTTACCAAG 182
Qy 184 GlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySerMetLeuAla 203
Db 183 CAACTACTTCACTGTATGGCCCTGCACCAACTTCTGCAATTCAGAGGATCCATGCTTGT 242
Qy 204 LeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSerLeuThrIle 223
Db 243 CTGGCCATGGTTAGTCTGGAAATGAGAAACTCATTTCTGATTTGGCTTTCTTACAAAT 302
Qy 224 GluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArgGluLeuVal 243
Db 303 GAACTGCTTCAGAAAGCAGATGATAGTCCCAAGTTGATCCATTTGTCGGAGCTTGTG 362

Qy 244 AlaHisHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyrValTyr 262
Db 363 GCACATCACCTTTCTACTCTGCAGTCTTCCCTGCTCTGAATTCGTTTATGTCTAC 419

RESULT 8

US-10-085-783A-16032
; Sequence 16032, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16032
; LENGTH: 444
; TYPE: DNA
; ORGANISM: Human
US-10-085-783A-16032

Alignment Scores:

Pred. No.: 3,84e-133 Length: 444
Score: 139.00 Matches: 139
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 36.87% Indels: 0
DB: 17 Gaps: 0

US-09-736-250-1 (1-377) x US-10-085-783A-16032 (1-444)

Qy 124 SerSerGluLeuLeuArgMetGluArgIleLeuAspLysLeuAsnTrpAspLeuHis 143
Db 3 TCATCTGAAATTTTGAGAAATGAGAGAAATTTCTGGATAAGTTGAAATGGATCTTCAC 62
Qy 144 ThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSerThrArgPro 163
Db 63 ACAGCCACACCATTTGGATTTCTTCATATTTTCCATGCAATTCGAGTGTCAACTAGGCGCT 122
Qy 164 GlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaValLeuThrLys 183
Db 123 CAGTTACTTTTCAGTTTGGCCCAATTTGAGCCCACTCTCAACATTTGGCAGTCTTACCAAG 182
Qy 184 GlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySerMetLeuAla 203
Db 183 CAACTACTTCACTGTATGGCCCTGCACCAACTTCTGCAATTCAGAGGATCCATGCTTGT 242
Qy 204 LeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSerLeuThrIle 223
Db 243 CTGGCCATGGTTAGTCTGGAAATGAGAAACTCATTTCTGATTTGGCTTTCTTACAAAT 302
Qy 224 GluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArgGluLeuVal 243
Db 303 GAACTGCTTCAGAAAGCAGATGATAGTCCCAAGTTGATCCATTTGTCGGAGCTTGTG 362
Qy 244 AlaHisHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyrValTyr 262
Db 363 GCACATCACCTTTCTACTCTGCAGTCTTCCCTGCTCTGAATTCGTTTATGTCTAC 419

RESULT 9

US-10-242-535A-30212
; Sequence 30212, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:

```
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; PRIOR FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 30212
; LENGTH: 490
; TYPE: DNA
; ORGANISM: Human
US-10-242-535A-30212

Alignment Scores:
Pred. No.: 6,34e-127 Length: 490
Score: 133.00 Matches: 133
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 35.28% Indels: 0
DB: 17 Gaps: 0

US-09-736-250-1 (1-377) x US-10-242-535A-30212 (1-490)
Qy 144 ThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSerThrArgPro 163
Db 91 ACAGCCACACCATGGATTTCTTCATATTTTCATGCGCATTCAGTGTCACTAGGCGCT 150
Qy 164 GlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaValLeuThrLys 183
Db 151 CAGTTACTTTTCAGTTTGCCTGAAATGGAGAACTCTCAACATTTGGCAGTCTTACCAAG 210
Qy 184 GlnLeuLeuHisCysMetAlaCysAsnGlnLeuGlnPheArgGlySerMetLeuAla 203
Db 211 CAACTACTTCACTGTATGGCTGCAACCACTTCTGCAATTCAGAGATCCATGCTGCT 270
Qy 204 LeuAlaMetValSerLeuGluMetGluLysLeuLeuProAspTrpLeuSerLeuThrIle 223
Db 271 CTGGCCATGGTTAGTCTGGAATGGAGAACTCTTCTGATTCGCTTCTTACAAAT 330
Qy 224 GluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuLeuHisCysArgGluLeuVal 243
Db 331 GAACCTGCTTCAGAAAGCACAGATGATGATGATGATGATGATGATGATGATGATGATG 390
Qy 244 AlaHisHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyrValTyrArg 263
Db 391 GCACATCACCTTTCTACTCTGAGTCTCTCCCTGCTCTGATTCGCTTATGCTACCGT 450
Qy 264 ProLeuLysHisThrLeuValThrCysAspLysGlyVal 276
Db 451 CCCCTCAAGCACACCCCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 489

RESULT 10
US-10-085-783A-30212
; Sequence 30212, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
```

```
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 30212
; LENGTH: 490
; TYPE: DNA
; ORGANISM: Human
US-10-085-783A-30212

Alignment Scores:
Pred. No.: 6,34e-127 Length: 490
Score: 133.00 Matches: 133
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 35.28% Indels: 0
DB: 17 Gaps: 0

US-09-736-250-1 (1-377) x US-10-085-783A-30212 (1-490)
Qy 144 ThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSerThrArgPro 163
Db 91 ACAGCCACACCATGGATTTCTTCATATTTTCATGCGCATTCAGTGTCACTAGGCGCT 150
Qy 164 GlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaValLeuThrLys 183
Db 151 CAGTTACTTTTCAGTTTGCCTGAAATGGAGAACTCTCAACATTTGGCAGTCTTACCAAG 210
Qy 184 GlnLeuLeuHisCysMetAlaCysAsnGlnLeuGlnPheArgGlySerMetLeuAla 203
Db 211 CAACTACTTCACTGTATGGCTGCAACCACTTCTGCAATTCAGAGATCCATGCTGCT 270
Qy 204 LeuAlaMetValSerLeuGluMetGluLysLeuLeuProAspTrpLeuSerLeuThrIle 223
Db 271 CTGGCCATGGTTAGTCTGGAATGGAGAACTCTTCTGATTCGCTTCTTACAAAT 330
Qy 224 GluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuLeuHisCysArgGluLeuVal 243
Db 331 GAACCTGCTTCAGAAAGCACAGATGATGATGATGATGATGATGATGATGATGATGATG 390
Qy 244 AlaHisHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyrValTyrArg 263
Db 391 GCACATCACCTTTCTACTCTGAGTCTCTCCCTGCTCTGATTCGCTTATGCTACCGT 450
Qy 264 ProLeuLysHisThrLeuValThrCysAspLysGlyVal 276
Db 451 CCCCTCAAGCACACCCCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 489

RESULT 11
US-09-814-353-21294
; Sequence 21294, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
```

```
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21294
; LENGTH: 2146
; TYPE: DNA
; ORGANISM: Homo sapiens
; OTHER INFORMATION: n is a, c, g, or t
US-09-814-353-21294

Alignment Scores:
Pred. No.: 5,01e-116 Length: 2146
Score: 123.00 Matches: 149
Percent Similarity: 98.68% Conservative: 0
Best Local Similarity: 98.68% Mismatches: 0
Query Match: 32.63% Indels: 2
DB: 10 Gaps: 0

US-09-736-250-1 (1-377) x US-09-814-353-21294 (1-2146)
Qy 229 AlaGlnMetAspSerGlnLeuLeuHisCysArgGluLeuValAlaHisHisLeuSer 248
Db 869 GCCCAGATGGATAGCTCCAGCTTGATCCATGTGCGGAGCTTGTGGCACAATCACTTTCT 928
Qy 249 ThrLeuGlnSerSerLeuProLeuAsnSerValTyrValTyrArgProLeuLeuHisThr 268
Db 929 ACTCTGCAGTCTTCCCTGCCTCTGAATTCCTTTATGTCTACCGTCCCTCAAGCACACC 988
Qy 269 LeuValThrCysAspLysGlyValPheArgLeuHisProSerSerValProGlyProAsp 288
Db 989 CTGTGTACCTGTGCACAAAGAGTGTTCAGATTACCTCCTCTGTGCCAGGCCAGAC 1048
Qy 289 PheSerLysAspAsnSerLysProGluValProValArgGlyThrAlaAlaPheTyrHis 308
Db 1049 TTCTCCAGGACACACGACGAGAGTGCCAGTCAGAGGTACAGAGCCTTTTACCAT 1108
Qy 309 HisLeuProAlaAla-SerGlyCysLysGlnThrSer-ThrLysArgLysValGluLum 328
Db 1109 CATCTCCAGCTGCCAGTGGGTGCAAGACGACCTCTTACTAAACGCAAGTAGAGGAAA 1168
Qy 328 etGluValAspAspPheTyrAspGlyIleTyrAspGlyLeuTyrAsnGluAspAsnValSerG 348
Db 1169 TGAAGTGGATGAGCTTCTATGATGAATCAACCGCTCTATAATGAAGATATATGTCAG 1228
Qy 348 luAsnValGlySerValCysGlyThrAspLeuSerArgGlnGluGlyHisAlaSerProC 368
Db 1229 AAAATGGGTCTGTGTGGCACTGATTTATCAAGACAGAGGAGCATGCTTCCCTT 1288
Qy 368 ysProProLeuGlnProValSerValMet 377
Db 1289 GTCCACCTTTGCAGCCTGTTTCTGTCTCATG 1317

RESULT 12
US-10-242-535A-6834
; Sequence 6834, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liaw, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242.535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6834
; LENGTH: 389
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (358)..(358)
; OTHER INFORMATION: n is a, c, g, or t
US-10-085-783A-6834

; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6834
; LENGTH: 389
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (358)..(358)
; OTHER INFORMATION: n is a, c, g, or t
US-10-242-535A-6834

Alignment Scores:
Pred. No.: 1.42e-111 Length: 389
Score: 118.00 Matches: 118
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 31.30% Indels: 0
DB: 17 Gaps: 0

US-09-736-250-1 (1-377) x US-10-242-535A-6834 (1-389)
Qy 2 LysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIleThr 21
Db 2 AAGTTTCCAGGGCCTTTGGAAACCCAGAGATTGCTTCTTCTGTTGGAAAGGCCAATCACT 61
Qy 22 ArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnValSer 41
Db 62 AGGGAAGCACAGATGTGGAAGTGAATGTGCGGAAAAATGCCCTTCAAAATCAGAAATGTTTCT 121
Qy 42 ProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsnLeu 61
Db 122 CCATCCAGAGAGATGAAGTAATTCATGTGCTGCCCAAACTCAAGTACCAATCAACCTT 181
Qy 62 TyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrValLys 81
Db 182 TACCCAGAAACATTTGCTTGGCTAGCAGCTTTTGGATAGTTTGTAGTACCGTAAAG 241
Qy 82 AlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaLysThr 101
Db 242 GCTCATCCAAAATACTTGAAGTTGATTGCAATCAGCTGTTTCTTCTAGCTGCCAAGACT 301
Qy 102 ValGluLysAspGluArgIleProValLeuLysValLeuAlaArgAspSerPhe 119
Db 302 GTTGAGGAAGATGAGAGATTCAGAGTAAAGGATATTGGCAAGAGACAGATTTC 355

RESULT 13
US-10-085-783A-6834
; Sequence 6834, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liaw, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085.783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6834
; LENGTH: 389
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (358)..(358)
; OTHER INFORMATION: n is a, c, g, or t
US-10-085-783A-6834
```

Alignment Scores:
Pred. No.: 1.42e-111 Length: 389
Score: 118.00 Matches: 118
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 31.30% Indels: 0
DB: 17 Gaps: 0

US-09-736-250-1 (1-377) x US-10-085-783A-6834 (1-389)

QY 2 LysPheProGluPProLeuGluuGlnArgLeuSerPheLeuLeuGluLysAlaIleThr 21
DB 2 AAGTTTCCAGGGCCCTTTGGAAAACAGAGATTGTCTTCTCTGTTGGAAAAGGCAATCACT 61

QY 22 ArgGluAlaGlnMetTrpLysValAlaValArgLysMetProSerAsnGlnAsnValSer 41
DB 62 AGGGAAGACACAGATGTGGAAAGTGAATGTGGGAAATGCCCTTCAAAATCAGAAATGTTTCT 121

QY 42 ProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrglnPheAsnLeu 61
DB 122 CCATCCAGAGAGATGAAGTATTCAATGGCTGGCCAACTCAAGTACCAATTCACCTT 181

QY 62 TyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrValLys 81
DB 182 TACCAGAAACATTTGCTGTGGTACAGTCTTTTGGATAGTCTTTTACCTACCGTAAAG 241

QY 82 AlaHisProLysTyLeuSerCysIleAlaIleSerCysPhePheLeuAlaLysThr 101
DB 242 GCTCATCCAAATATCTTGATGTGATTCATCAATCAGCTGTTTTTCTAGCTGCCAAGACT 301

QY 102 ValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspPhe 119
DB 302 GTTGAGGAAGATGAGAGAAATCCAGTACTAAAGGTATTGGCAAGAGACAGTTTC 355

RESULT 14
US-10-242-535A-33391

; Sequence 33391, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liaw, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; PRIOR FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 33391
; LENGTH: 369
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2)..(2)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (25)..(25)
; OTHER INFORMATION: n is a, c, g, or t
; US-10-242-535A-33391

Alignment Scores:
Pred. No.: 2.03e-105 Length: 369
Score: 112.00 Matches: 112

Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 29.71% Indels: 0
DB: 17 Gaps: 0

US-09-736-250-1 (1-377) x US-10-242-535A-33391 (1-369)

QY 216 ProAspTrpLeuSerLeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGln 235
DB 28 CCGATTGGCTTTCTCTTCAATTTGAATGCTTTCAGAAAGCACAGATGGATAGCTCCAG 87

QY 236 LeuIleHisCysArgGluLeuValAlaHisHisLeuSerThrLeuGlnSerSerLeuPro 255
DB 88 TTGATTCATTGTCGGAGCTTGTGGACATCACCTTTCTACTCTGCACTCTTCCCTGCT 147

QY 256 LeuAsnSerValTyValTyArgProLeuLysHisThrLeuValThrCysAspLysGly 275
DB 148 CTGAATTCGCTTTATGTCTACCGTCCCTCAAGCACACCTTGTGTGACCTGTGACAAAGGA 207

QY 276 ValPheArgLeuHisProSerSerValProGlyProAspPheSerLysAspAsnSerLys 295
DB 208 GTGTTCAATTTACATCCCTCTCTGTCAGGCCAGACTTCTCCAAGGACACAGCAAG 267

QY 296 ProGluValProValArgGlyThrAlaAlaPheTyHisHisLeuProAlaAlaSerGly 315
DB 268 CCAGAAGTGCAGTCAGAGGTACAGAGCCCTTTTACCATCATCTCCAGCTGCCAGTGG 327

QY 316 CysLysGlnThrSerThrLysArgLysValGluGlu 327
DB 328 TGCAAGCAGACCTCTACTAAACGCAAGTAGAGGAA 363

RESULT 15

US-10-085-783A-33391
; Sequence 33391, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liaw, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 33391
; LENGTH: 369
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2)..(2)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (25)..(25)
; OTHER INFORMATION: n is a, c, g, or t
; US-10-085-783A-33391

Alignment Scores:
Pred. No.: 2.03e-105 Length: 369
Score: 112.00 Matches: 112
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 29.71% Indels: 0
DB: 17 Gaps: 0

US-09-736-250-1 (1-377) x US-10-085-783A-33391 (1-369)

```
Qy 216 ProAspTrpLeuSerLeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGln 235
Db 28 CCTGATTGGCTTTCTCTTACAATTGAACTGCTTCAGAAAGCACAGATGGATAGCTCCAG 87
Qy 236 LeuIleHisCysArgGluLeuValAlaHisIleLeuSerThrLeuGlnSerSerLeuPro 255
Db 88 TTGATCCATTGTGGGAGCTTGTGGCAGATCACCTTTCTACTCTGCAGTCTTCCCTGCCT 147
Qy 256 LeuAsnSerValTyrValTyrArgProLeuLysHisThrLeuValThrCysAspLysGly 275
Db 148 CTGAATTCGGTTTATGTCTACCGTCCCTCAAGCACACCCCTGGTGACCTGTGACAAAGGA 207
Qy 276 ValPheArgLeuHisProSerSerValProGlyProAspPheSerLysAspAsnSerLys 295
Db 208 GTGTTTCAGATTACATCCCTCTCTGTCCAGGCCAGACTTCTCCAAGGACAAAGCAAG 267
Qy 296 ProGluValProValArgGlyThrAlaAlaPheTyrHisLeuProAlaAlaSerGly 315
Db 268 CCAGAGTCCAGTCAGAGGTACAGAGCCCTTTACCATCATCTCCAGCTGCCAGTGGG 327
Qy 316 CysLysGlnThrSerThrLysArgLysValGluGlu 327
Db 328 TGCAAGCAGAGCTCTACTATAACGCAAGTAGAGGAA 363
```

Search completed: February 11, 2005, 17:09:05
Job time : 1020.34 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 11, 2005, 07:42:20 ; Search time 5874.84 Seconds
(without alignments)
2442.660 Million cell updates/sec

Title: US-09-736-250-1
Perfect score: 377
Sequence: 1 MKFPGPLENQLSLLEKAI.....LSRQEGHASPCLPQPVSVM 377

Scoring table:
OLIGO Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Word size: 1

Total number of hits satisfying chosen parameters: 68477535

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-O=/cgn2_1/USPTO_spool/US09736250/runat_07022005_154942_20659/app.query.fasta_1.718
-DB=EST -QFMT=fastap -SUPFIX=oligo.rst -MINMATCH=0.1 -LGOPEL=0 -LGOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi -LIST=1000
-DOCALLIGN=200 -THR SCORE=quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptp
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09736250 @CGN 1 1 4385 @runat_07022005_154942_20659 -NCPU=6 -ICPU=3
-NO_MMAP -LARGOQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

- EST:
1: gb_est1:*
2: gb_est2:*
3: gb_hcc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	261	69.2	903	5	BU956287 AGENCOURT
2	253	67.1	918	5	BQ673252 AGENCOURT
3	252	66.8	899	6	BC358716 AGENCOURT
4	249	66.0	775	4	BM016042 603642469
5	249	66.0	890	4	BI858571 603389030
6	246	65.3	764	6	CB962746 AGENCOURT
7	246	65.3	936	5	BU501311 AGENCOURT
8	246	65.3	963	5	BU538306 AGENCOURT
9	244	64.7	920	5	BQ673277 AGENCOURT

10	243	64.5	862	5	BU149962
11	241	63.9	830	5	EX437607
12	236	62.6	853	5	BU159699
13	235	62.3	764	4	BG205510 RST24889
14	235	62.3	767	4	BG189523 RST8568 A
15	235	62.3	844	4	BG215999 RST35685
16	235	62.3	889	6	CD358161 AGENCOURT
17	235	62.3	891	5	BU151205
18	233	61.8	946	5	BU558083
19	232	61.5	865	5	BU188239 AGENCOURT
20	230	61.0	912	5	BQ670517 AGENCOURT
21	226	59.9	884	5	BU188938 AGENCOURT
22	223	59.2	670	6	CB115197
23	223	59.2	767	4	BG202878 RST22246
24	221	58.6	751	5	EX422046
25	221	58.6	753	4	BI859488 603385338
26	221	58.6	849	4	BG758079
27	221	58.6	959	4	BF972370 602240689
28	220	58.4	662	4	BG830200 602764779
29	220	58.4	803	5	BQ071740 AGENCOURT
30	220	58.4	920	5	BU528295 AGENCOURT
31	218	57.8	752	6	CB998866 AGENCOURT
32	218	57.8	932	5	BQ669046 AGENCOURT
33	217	57.6	914	5	BQ894247 AGENCOURT
34	216	57.3	933	7	CO048817 ILLUMIGEN
35	216	57.3	934	7	CN801970 ILLUMIGEN
36	216	57.3	946	7	CN647001 ILLUMIGEN
37	216	57.3	963	7	CN803219 ILLUMIGEN
38	216	57.3	966	7	CN643780 ILLUMIGEN
39	216	57.3	978	4	BM463752 AGENCOURT
40	216	57.3	978	7	CN641931 ILLUMIGEN
41	216	57.3	983	7	CN646807 ILLUMIGEN
42	215	57.0	674	7	CN403758 170005325
43	213	56.5	674	7	CN403761 170006000
44	212	56.2	639	7	CV026068 3899 Full
45	209	55.4	790	4	BG198062 RST17446
46	208	55.2	640	6	CD699834 EST16358
47	208	55.2	819	5	BU945610 AGENCOURT
48	208	55.2	960	5	BQ930674 AGENCOURT
49	207	54.9	661	6	CD689640 EST6163 h
50	207	54.9	1023	4	BM423081 PLATE1 H1
51	206	54.6	801	4	BG253045 602365568
52	206	54.6	810	5	EX461980
53	206	54.6	841	7	CF552849 AGENCOURT
54	206	54.6	885	5	BQ671998 AGENCOURT
55	204	54.1	909	5	BU975546 AGENCOURT
56	204	54.1	992	7	CO646424 ILLUMIGEN
57	203	53.8	615	5	BU078994 im69c04 Y
58	202	53.6	852	7	CF243019 AGENCOURT
59	202	53.6	888	5	EX433245
60	201	53.3	733	6	CB555746 MMSPO001
61	200	53.1	716	2	BE888060 601511562
62	200	53.1	773	4	BG208600 RST28103
63	200	53.1	957	5	BU956183 AGENCOURT
64	195	51.7	587	6	CB154620 K-EST0212
65	195	51.7	863	4	BG429609 602501290
66	195	51.7	906	6	CD107527 AGENCOURT
67	195	51.7	921	7	CF264864 AGENCOURT
68	194	51.5	584	6	CB164677 K-EST0225
69	194	51.5	726	6	CD642135 AGENCOURT
70	194	51.5	736	2	BE876700 601488265
71	194	51.5	801	5	BQ645542 AGENCOURT
72	194	51.5	931	5	BU501596 AGENCOURT
73	194	51.5	959	7	CN803488 ILLUMIGEN
74	193	51.2	581	5	BP372621 BP372621
75	193	51.2	686	7	CR559762 DKE2p459J
76	193	51.2	706	4	BG924737 HNC29-1-D
77	193	51.2	1060	4	BI758594 603027253
78	193	51.2	1142	4	BM466858 AGENCOURT
79	192	50.9	579	7	CN403760 170004237
80	192	50.9	684	6	CB269635 1008542 H
81	192	50.9	878	4	BI159881 602863704
82	191	50.7	956	5	BQ672234 AGENCOURT

Bette for Dora

83	190	50.4	570	2	BE297106	601177785	156	160	42.4	485	1	AA417175	AA417175	zui3b07.r
c	84	190	50.4	682	2	BF220183	601296732	157	160	42.4	608	4	BM015005	603640960
	85	190	50.4	774	5	BUI501374	AGENCOURT	c	158	42.4	617	2	AW249490	2821433.3
	86	190	50.4	863	4	BG777471	602664794	159	160	42.4	893	4	BI257270	602967201
	87	189	50.1	568	1	AU280181	AU280181	c	160	42.4	893	5	EQ773620	UI-H-EZ1-
	88	189	50.1	913	5	BQ674754	AGENCOURT	161	159	42.2	681	6	CD642085	AGENCOURT
	89	188	49.9	565	4	BM825480	K-EST0097	162	158	41.9	486	5	BU785709	AGENCOURT
	90	188	49.9	682	2	BE383076	601298885	163	158	41.9	547	4	BM857824	1j45c04.y
	91	188	49.9	766	4	BG208089	RST27579	164	157	41.9	784	4	BG337639	1j45c03.y
	92	188	49.9	841	6	CD520278	AGENCOURT	165	158	41.9	506	6	CA861899	1r79e01.y
	93	188	49.9	899	6	CD522597	AGENCOURT	166	157	41.6	567	5	BP259087	BP259087
	94	187	49.6	563	6	CB162617	K-EST0223	167	157	41.6	578	5	BP258271	BP258271
	95	187	49.6	596	7	CA403768	170005313	168	155	41.1	516	1	AA310922	EST181758
	96	186	49.3	569	6	CB115210	K-EST0159	169	155	41.1	691	2	BF337048	602034442
	97	186	49.3	587	5	BP205055	BP205055	c	170	41.1	724	4	BI761713	603046583
	98	186	49.3	629	6	CB381894	TGEST2y2	171	154	40.8	463	2	BE382365	601298668
	99	186	49.3	851	2	BP569230	60185591	172	154	40.8	470	1	AI350283	qo29a05.x
	100	185	49.1	563	2	AW612687	h30e12.x	173	154	40.8	522	1	AA310005	EST181072
	101	184	48.8	553	6	CB149851	K-EST0206	c	174	40.8	982	5	BQ708698	AGENCOURT
	102	184	48.8	577	5	BP255708	BP255708	175	153	40.6	497	1	AA088548	z189c07.r
	103	184	48.8	786	2	BE885933	601507564	c	176	40.6	673	5	BQ182277	UI-H-ED0-
	104	184	48.8	858	4	BG112293	602282442	c	177	40.6	674	5	BM994615	UI-H-DUO-
	105	183	48.5	552	4	BP971793	602240073	c	178	40.6	782	4	EG13628	RST12762
	106	183	48.5	552	5	BP265831	BP265831	179	153	40.6	896	4	EG220577	RST40363
	107	183	48.5	561	2	BE550729	7b58a12.x	180	153	40.6	1134	9	AY412158	Homo sapi
	108	183	48.5	568	7	CA403767	601004245	c	181	40.3	535	5	BQ345444	MR4-NT014
	109	182	48.3	714	2	BE294585	601176160	c	182	40.3	670	5	BM997732	UI-H-D10-
	110	182	48.3	767	6	CD520815	AGENCOURT	c	183	40.3	672	5	BM970544	UI-CF-EC1
	111	181	48.0	748	6	CB963441	AGENCOURT	c	184	40.3	672	5	BU615980	UI-H-DF0-
	112	181	48.0	757	4	EG201812	RST21154	c	185	40.3	676	4	EG762543	603734406
	113	181	48.0	768	4	EG204905	RST24321	c	186	40.3	770	2	CF636200	601458271
	114	180	47.7	629	6	CD675866	6f29b06.y	c	187	40.3	1047	7	CN641956	ILLUMIGEN
	115	179	47.5	718	4	BG929142	HNC59-1-C	c	188	40.1	464	1	AI348410	6034c09.x
	116	179	47.5	746	2	BE515271	601236040	c	189	40.1	663	4	BI917454	603185118
	117	179	47.5	970	2	BE899429	601682204	c	190	40.1	892	4	EG213298	RST32304
	118	178	47.2	538	6	CB156885	K-EST0215	c	191	39.8	541	4	BM312319	IG4H09.y
	119	178	47.2	766	4	EG767215	602740208	c	192	39.8	596	6	CD671336	IG4H09.y
	120	178	47.2	911	2	BE747713	601578166	c	193	39.8	664	5	BU679866	UI-CF-DU1
	121	177	46.9	654	1	AI832925	at73e05.x	c	194	39.8	775	4	EG219146	RST38899
	122	177	46.9	818	4	BG686132	602638411	c	195	39.5	530	2	BF110854	7n41b06.x
	123	177	46.9	909	4	EG199730	RST19024	c	196	39.5	722	2	BF269691	601185835
	124	177	46.9	1068	5	EM923007	AGENCOURT	c	197	39.3	470	1	AA213687	zq2h06.r
	125	176	46.7	754	4	EM479270	AGENCOURT	c	198	39.0	443	6	CB121958	K-EST0169
	126	175	46.4	722	6	CD640899	AGENCOURT	c	199	39.0	492	4	BM509658	IG92e01.y
	127	175	46.4	889	6	CD517935	AGENCOURT	c	200	39.0	586	2	AW411227	fh1b01.y
	128	174	46.2	876	4	EG209664	RST29190	c	201	39.0	636	7	CN483826	hw38g08.y
	129	173	45.9	756	6	CD623343	60233343	c	202	39.0	648	7	CN403762	170004245
	130	172	45.6	736	4	BI861437	603386664	c	203	39.0	654	2	BF792283	602252801
c	131	172	45.6	1109	4	EM462171	AGENCOURT	204	146	38.7	592	5	BP307165	BP307165
	132	171	45.4	607	1	AL044648	DKF2p434P	c	205	38.7	667	6	CA441829	UI-H-ED0-
c	133	171	45.4	938	4	BG387910	602412932	c	206	38.7	694	6	CA441689	UI-H-ED0-
	134	170	45.1	625	5	BU069684	im22f05.y	c	207	38.7	694	7	CN647834	ILLUMIGEN
	135	170	45.1	818	2	BE885777	601508992	c	208	38.5	444	1	AI348472	Q030a09.x
	136	170	45.1	839	4	BG977722	602438783	c	209	38.5	672	6	CB551872	MSP0028
	137	170	45.1	889	4	BP979086	602147596	c	210	38.5	787	6	CB958276	AGENCOURT
	138	169	44.8	515	6	CA948213	iq19c12.y	c	211	38.2	642	5	BU784337	AGENCOURT
	139	169	44.8	735	4	BG199251	RST18532	c	212	38.2	644	2	BF794011	602254657
c	140	167	44.3	535	5	BQ188175	UI-E-BT1-	213	144	38.2	830	4	BI667676	603293024
	141	166	44.0	570	1	AA525154	ni51a08.s	c	214	38.2	904	4	BG185256	1b37h12.y
c	142	166	44.0	694	1	AA703243	zi70e05.s	215	144	38.2	556	2	AG409690	fh01d06.y
	143	165	43.8	534	6	CA867868	ir82d01.y	c	216	37.9	759	4	EG214935	RST4195.A
	144	164	43.5	500	7	CF135196	UI-HF-CB0	c	217	37.9	973	5	BQ650937	AGENCOURT
	145	164	43.5	582	5	BP301192	BP301192	c	218	37.7	453	4	BF999436	CM3-GN007
	146	164	43.5	872	5	BU542568	AGENCOURT	c	219	37.7	556	4	BG656173	1b37h12.y
	147	164	43.5	1214	5	BU539034	AGENCOURT	c	220	37.7	556	2	AG409690	fh01d06.y
	148	163	43.2	842	2	BE885524	601508717	c	221	37.7	609	7	CF363598	833489.MA
	149	162	43.0	767	4	EG213835	RST33455	c	222	37.4	562	1	AA664175	ac04h04.s
	150	162	43.0	866	4	EG393996	602416893	c	223	37.4	644	2	AW972885	EST384980
	151	162	43.0	887	4	EG182156	RST1020.A	c	224	37.4	664	5	BU603028	AGENCOURT
	152	162	43.0	914	4	EM451072	AGENCOURT	c	225	37.4	666	1	AA218918	zr02c03.s
	153	162	43.0	928	7	BN801922	ILLUMIGEN	c	226	37.4	976	4	BG392121	602410213
	154	161	42.7	673	2	AW409798	fh02d12.x	c	227	37.1	421	7	CR525159	DKF2p4590
c	155	161	42.7	1241	4	BG746028	602723467	228	139	36.9	619	4	BM539941	hb16b08.9

C 229	139	36.9	533	5	BM991335	BM991335	UI-H-D10-	C 302	123	32.6	658	1	AI719868	AI719868	as47a04.x
C 230	139	36.9	710	2	B270121	B270121	601185927	303	123	32.6	899	1	BF245597	BF245597	z01863527
C 231	138	36.6	535	1	AA215707	AA215707	zr97h07.r	304	122	32.4	445	1	AA084885	AA084885	en13301.r
C 232	138	36.6	561	4	BF975395	BF975395	602245924	306	122	32.4	562	2	BF437208	BF437208	7p67h12.x
C 233	138	36.6	581	5	BP258977	BP258977	BP258977	C 305	122	32.4	635	2	BF594792	BF594792	7o55d03.x
C 234	138	36.6	611	2	B2323082	B2323082	hu47a07.x	C 307	122	32.4	920	2	BE300217	BE300217	600944220
C 235	138	36.6	744	6	C0522104	C0522104	AGENCOURT	C 308	121	32.1	370	2	AW020950	AW020950	df16g08.y
C 236	138	36.6	775	4	B214936	B214936	RS734591	C 309	121	32.1	388	2	BF851047	BF851047	CM3-EN007
C 237	138	36.6	776	5	BX925342	BX925342	BX925342	C 310	121	32.1	475	1	AI302360	AI302360	qn08h11.x
C 238	138	36.6	906	5	BQ673816	BQ673816	AGENCOURT	C 311	121	32.1	581	1	AW162274	AW162274	au75h05.x
C 239	137	36.3	712	1	AV716842	AV716842	AV716842	C 312	121	32.1	672	6	CD640858	CD640858	AGENCOURT
C 240	137	36.3	827	4	BG032020	BG032020	602300525	C 313	121	32.1	782	1	AI018633	AI018633	ou47h04.x
C 241	137	36.3	856	2	BF130818	BF130818	601818484	C 314	121	32.1	1078	4	BM454194	BM454194	AGENCOURT
C 242	137	36.3	918	4	BG205994	BG205994	RS225429	C 315	120	31.8	484	1	AJ707455	AJ707455	AJ707455
C 243	137	36.3	935	2	BF663243	BF663243	602144361	C 316	120	31.8	484	1	AA487743	AA487743	ab20e06.r
C 244	137	36.3	976	4	BG757286	BG757286	602715271	C 317	120	31.8	511	2	BE709305	BE709305	IL3-HT061
C 245	137	36.3	1220	5	BUI77249	BUI77249	AGENCOURT	C 318	120	31.8	606	5	BU579739	BU579739	im90a11.x
C 246	136	36.1	410	6	CA388900	CA388900	cs03f08.y	C 319	120	31.8	703	1	AI479008	AI479008	tm29g03.x
C 247	136	36.1	526	1	AA604363	AA604363	no79g10.s	C 320	120	31.8	734	2	AW026536	AW026536	wv14f11.x
C 248	136	36.1	757	4	BG211683	BG211683	RS731252	C 321	120	31.8	935	5	BQ673790	BQ673790	AGENCOURT
C 249	136	36.1	1020	5	BQ051750	BQ051750	AGENCOURT	C 322	120	31.8	1010	2	BE612666	BE612666	601452513
C 250	136	36.1	1041	4	BM555910	BM555910	AGENCOURT	C 323	119	31.6	601	1	AA846727	AA846727	aj99a10.s
C 251	135	35.8	438	7	D52239	D52239	HUM072A06B	C 324	119	31.6	673	5	BU738049	BU738049	UI-E-DW1-
C 252	135	35.8	601	1	AA593789	AA593789	nm65d01.s	C 325	119	31.6	1029	4	BM454583	BM454583	AGENCOURT
C 253	135	35.8	617	7	CF365002	CF365002	835601.MA	C 326	118	31.3	405	4	BF945731	BF945731	CM1-NN021
C 254	135	35.8	643	4	BI197962	BI197962	602761927	C 327	118	31.3	559	1	AA521260	AA521260	aa75e06.s
C 255	135	35.8	763	6	C9999367	C9999367	AGENCOURT	C 328	118	31.3	770	4	EG199250	EG199250	RS7185311
C 256	135	35.8	917	2	BF684044	BF684044	602141379	C 329	118	31.3	829	4	BI597323	BI597323	603251617
C 257	134	35.5	408	1	AA578724	AA578724	nh23h11.s	C 330	118	31.3	842	2	BF381815	BF381815	603181067
C 258	134	35.5	444	1	AA130255	AA130255	z129c01.r	C 331	118	31.3	946	4	EG106015	EG106015	602290215
C 259	134	35.5	979	2	BF344340	BF344340	602014715	C 332	118	31.3	952	4	EG340555	EG340555	602462121
C 260	133	35.3	494	5	BX282797	BX282797	RS282797	C 333	117	31.0	449	1	AA864947	AA864947	oh36b04.s
C 261	133	35.3	494	7	CR742450	CR742450	Y07010.F1	C 334	117	31.0	564	1	AI755086	AI755086	cr35c06.x
C 262	133	35.3	554	5	BQ267575	BQ267575	ij90a09.y	C 335	117	31.0	580	2	AW009156	AW009156	w978b05.x
C 263	133	35.3	611	2	BQ273350	BQ273350	im69c04.x	C 336	117	31.0	582	7	CF768669	CF768669	CES001974
C 264	131	34.7	588	5	BU078719	BU078719	AGENCOURT	C 337	117	31.0	588	5	BP362057	BP362057	BP362057
C 265	131	34.7	1109	4	BP980373	BP980373	602288255	C 338	117	31.0	605	1	AA664102	AA664102	ac06a03.s
C 266	130	34.5	509	2	BE084450	BE084450	QV2-BT063	C 339	116	30.8	981	4	EG169354	EG169354	602120902
C 267	130	34.5	513	1	AA443651	AA443651	zw35b10.r	C 340	116	30.8	619	4	BI063996	BI063996	IL3-UT011
C 268	130	34.5	582	5	BP193654	BP193654	BP193654	C 341	116	30.8	703	4	EG616164	EG616164	602642744
C 269	130	34.5	610	2	AW151319	AW151319	KG47h08.x	C 342	116	30.8	748	4	BG220118	BG220118	RS739890
C 270	130	34.5	854	4	EG182134	EG182134	RS7998.At	C 343	115	30.5	398	2	BF857991	BF857991	RC5-PT019
C 271	129	34.2	403	1	AA668695	AA668695	AS668695	C 344	115	30.5	493	2	AW873472	AW873472	hm01h04.x
C 272	129	34.2	603	5	BQ271252	BQ271252	ij90a09.x	C 345	115	30.5	562	4	EG686057	EG686057	602638626
C 273	129	34.2	619	4	BM857651	BM857651	ij69c03.x	C 346	115	30.5	652	6	CB437257	CB437257	684704.MA
C 274	129	34.2	654	1	AI765328	AI765328	w173f10.x	C 347	114	30.2	344	6	CB135336	CB135336	K-EST0187
C 275	129	34.2	668	5	BQ002431	BQ002431	UI-H-E11-	C 348	114	30.2	346	6	CB135453	CB135453	K-EST0187
C 276	129	34.2	671	5	BM980581	BM980581	UI-CF-EN1	C 349	114	30.2	534	2	BF434285	BF434285	7o95b11.x
C 277	129	34.2	673	1	AI928349	AI928349	w096c03.x	C 350	114	30.2	544	2	AW236763	AW236763	xm84f08.x
C 278	129	34.2	690	7	CF135924	CF135924	UI-HF-BN0	C 351	114	30.2	567	1	AA846826	AA846826	aj99h03.s
C 279	129	34.2	724	7	CF135985	CF135985	UI-HF-BN0	C 352	114	30.2	655	2	AA467341	AA467341	he09e10.x
C 280	129	34.2	731	5	BU632784	BU632784	UI-H-FE1-	C 353	114	30.2	955	4	EG341156	EG341156	602462513
C 281	129	34.2	765	7	CF135787	CF135787	UI-HF-BN0	C 354	113	30.0	440	2	BE831205	BE831205	PM4-MT004
C 282	128	34.0	456	1	AI879521	AI879521	au54a08.x	C 355	113	30.0	469	1	AA026942	AA026942	zk04h06.r
C 283	128	34.0	611	4	BM690806	BM690806	UI-E-CX0-	C 356	113	30.0	531	1	AI601273	AI601273	ar89b01.x
C 284	128	34.0	645	4	BM312236	BM312236	ig41h09.x	C 357	113	30.0	550	5	BP306529	BP306529	BP306529
C 285	128	34.0	1021	4	BG261332	BG261332	602373094	C 358	113	30.0	559	4	EG684675	EG684675	602635957
C 286	127	33.7	582	5	BP268725	BP268725	BP268725	C 359	113	30.0	582	5	BP256863	BP256863	BP256863
C 287	127	33.7	587	2	BF725114	BF725114	bx12d04.y	C 360	113	30.0	632	6	CA947959	CA947959	iq19c12.x
C 288	127	33.7	695	1	AA910671	AA910671	ok84a04.s	C 361	113	30.0	815	4	EG182157	EG182157	RS71021.A
C 289	127	33.7	777	7	C0882771	C0882771	BoVGen_11	C 362	112	29.7	337	7	CM403770	CM403770	170006002
C 290	126	33.4	432	7	H43942	H43942	Y07010.F1	C 363	112	29.7	338	1	AA810339	AA810339	nx74h07.s
C 291	126	33.4	443	2	BE295596	BE295596	601176557	C 364	112	29.7	394	7	D52485	D52485	HUM079F08B
C 292	126	33.4	833	5	BU532129	BU532129	AGENCOURT	C 365	112	29.7	409	1	AA044007	AA044007	zk58e02.r
C 293	125	33.2	383	5	BP428997	BP428997	BP428997	C 366	112	29.7	532	1	AA707260	AA707260	ag84d03.r
C 294	125	33.2	569	7	AA595249	AA595249	no33b07.s	C 367	112	29.7	634	1	AA053839	AA053839	zf53c08.r
C 295	125	33.2	569	7	N31918	N31918	Y721g12.bir	C 368	111	29.4	433	1	AA305861	AA305861	EST176862
C 296	125	33.2	863	4	BM011998	BM011998	603636417	C 369	111	29.4	547	2	AW250256	AW250256	2821433.5
C 297	124	32.9	938	5	BQ710910	BQ710910	AGENCOURT	C 370	111	29.4	557	1	AA622207	AA622207	no43a03.s
C 298	124	32.9	449	7	H06771	H06771	Y183e01.r1	C 371	111	29.4	634	2	AW027887	AW027887	w862e08.x
C 299	123	32.6	433	1	AA351545	AA351545	EST59320	C 372	111	29.4	679	2	BE382430	BE382430	601297257
C 300	123	32.6	560	1	AA992575	AA992575	ot97e05.s	C 373	111	29.4	834	2	BF698561	BF698561	602130766
C 301	123	32.6	647	2	BF435610	BF435610	nac33h11.	C 374	111	29.4	921	5	BQ230170	BQ230170	AGENCOURT

C 521 88 23.3 580 1 A1598247 tnl5d02.x
C 522 88 23.3 594 6 CB169351 KYB602702
C 523 88 23.3 757 4 BG777885 602665623
C 524 88 23.3 806 2 BF669925 602118429
C 525 87 23.1 405 4 B1036675 RC6-NT015
C 526 87 23.1 459 1 A1032951
C 527 87 23.1 497 6 CA45832 UI-H-BKO
C 528 87 23.1 491 7 W46580 zc32809.r1
C 529 87 23.1 587 1 AA496420 zV37C03.r
C 530 87 23.1 915 5 BU844745 AGENCOURT
C 531 86 22.8 421 1 AA157562 z068905.s
C 532 86 22.8 424 7 T78365 VC99f11.r1
C 533 86 22.8 461 1 AA054388 zF54f01.r1
C 534 86 22.8 478 4 AA456153 zX74a01.r
C 535 86 22.8 478 4 B1491939 dF17C01.w
C 536 86 22.8 478 4 B1906154 603062603
C 537 86 22.8 479 2 AW020980 dF17C01.y
C 538 86 22.8 484 2 AW403704 UI-HF-BKO
C 539 86 22.8 489 1 AA937188 ok13C10.s
C 540 86 22.8 521 1 AA417071 zU13b07.s
C 541 86 22.8 538 1 AA487524 ab20e06.s
C 542 86 22.8 630 4 BG501836 602548934
C 543 86 22.8 647 2 BF853287 MR2-EN009
C 544 86 22.8 968 2 BF789168 601476292
C 545 85 22.5 341 1 AA209345 zQ82e03.r
C 546 85 22.5 365 7 R75949 Y162b02.r1
C 547 85 22.5 466 1 A1306635 qn45h11.x
C 548 85 22.5 507 7 R88891 YP97b03.r1
C 549 85 22.5 549 1 AA599293 ag35C03.s
C 550 85 22.5 594 1 AU145099 AU145099
C 551 85 22.5 607 1 AA629751 ae63C01.s
C 552 85 22.5 764 1 A1800633 wg12910.x
C 553 85 22.5 839 4 BM014961 603640906
C 554 84 22.3 255 2 BF825099 RC3-HK002
C 555 84 22.3 281 1 AA355875 EST6430
C 556 84 22.3 439 1 A1278881 Q042h11.x
C 557 84 22.3 447 6 CA943599 ir82d01.x
C 558 84 22.3 450 1 A1795935 wg40C11.x
C 559 84 22.3 465 5 BU069467 im22f05.x
C 560 84 22.3 572 1 AU146040 AU146040
C 561 84 22.3 630 6 CB267878 1006784 H
C 562 84 22.3 745 4 BG912921 602807320
C 563 83 22.0 325 4 BG183155 RST2025 A
C 564 83 22.0 388 7 F25987 HSPD13241 H
C 565 83 22.0 439 1 A1051917 ow38907.s
C 566 83 22.0 446 1 A1680686 tx40b07.x
C 567 83 22.0 446 5 BU785406 in45C04.x
C 568 83 22.0 447 1 A1636109 t92h04.x
C 569 83 22.0 685 2 AW301064 xk12b11.x
C 570 82 21.8 356 7 T30826 EST23354 Hu
C 571 82 21.8 423 7 H00488 H00488 Y124b06.r1
C 572 82 21.8 453 7 AA101887 N91218 zai13f01.r1
C 573 82 21.8 456 7 N91218 zai13f01.r1
C 574 82 21.8 459 2 AW403463 BU785406
C 575 82 21.8 611 7 N30602 YW72b06.s1
C 576 82 21.8 643 1 A1679428 t63f12.x
C 577 82 21.8 828 5 BU566387 AGENCOURT
C 578 81 21.5 269 1 AA680208 ac82d11.s
C 579 81 21.5 340 2 AW993907 RC3-BN003
C 580 81 21.5 370 7 T36202 EST98394 Hu
C 581 81 21.5 437 1 AA292432 zt28h02.s
C 582 81 21.5 441 1 A1635372 t994C11.x
C 583 81 21.5 441 2 AW299224 x948a02.x
C 584 81 21.5 487 1 A1813543 wJ8d01.x
C 585 81 21.5 578 5 BP220954 BP220954
C 586 81 21.5 659 2 B8675818 7f16f08.x
C 587 81 21.5 1083 4 EM460353 AGENCOURT
C 588 80 21.2 453 2 AW406913 UI-HF-BKO
C 589 80 21.2 459 1 A1347777 q096C05.s
C 590 80 21.2 501 1 AA533127 nj46g02.s
C 591 80 21.2 627 4 B1250151 602995324
C 592 80 21.2 734 4 BG211729 RST13298
C 593 80 21.2 1091 2 BE894125 601438253

C 594 79 21.0 435 1 AA021376
C 595 79 21.0 453 1 A1377586
C 596 79 21.0 474 2 BE675931 TC18f07.x
C 597 79 21.0 511 1 A1355203 q67h10.x
C 598 79 21.0 568 1 A1144511 Qb73h04.x
C 599 79 21.0 902 5 BQ937545
C 600 79 21.0 937 5 BQ921119
C 601 79 21.0 1011 5 BQ683114
C 602 78 20.7 298 7 H81242 YU73002.r1
C 603 78 20.7 339 6 CD694302 EST10825
C 604 78 20.7 385 4 B1036680
C 605 78 20.7 448 7 T61988 yb96h02.r1
C 606 78 20.7 470 2 AW062552
C 607 78 20.7 482 4 B1063842 IL3-UT011
C 608 78 20.7 504 4 B1063658 IL3-UT011
C 609 78 20.7 504 4 B1063676 IL3-UT011
C 610 78 20.7 504 4 B1063677 IL3-UT011
C 611 78 20.7 504 4 B1063980 IL3-UT011
C 612 78 20.7 505 4 B1063693 IL3-UT011
C 613 78 20.7 506 4 B1063678 IL3-UT011
C 614 78 20.7 506 4 B1063687 IL3-UT011
C 615 78 20.7 507 4 B1063663 IL3-UT011
C 616 78 20.7 507 4 B1063665 IL3-UT011
C 617 78 20.7 524 4 B1063679 IL3-UT011
C 618 78 20.7 812 9 AY412159 Pan trogl
C 619 78 20.7 853 2 BF666533 602123987
C 620 77 20.4 287 4 B1036693 RC6-NT015
C 621 77 20.4 427 1 AA961959 q092C10.s
C 622 77 20.4 427 7 N68425
C 623 77 20.4 499 1 AA827740 OB54h11.s
C 624 77 20.4 584 5 BP367260
C 625 77 20.4 625 2 BF229960 PM3-CS003
C 626 77 20.4 712 4 B1153367 602918645
C 627 77 20.4 916 4 BF981165 602310440
C 628 77 20.4 1024 5 BQ071597 AGENCOURT
C 629 77 20.4 1458 4 BM473295
C 630 76 20.2 228 7 T34505 EST69511 Hu
C 631 76 20.2 231 2 AW602562
C 632 76 20.2 277 1 AA484896 N88322 K3097F Huma
C 633 76 20.2 335 7 N88322 K3097F Huma
C 634 76 20.2 407 1 AA146795
C 635 76 20.2 486 1 A1017489 ou29a09.x
C 636 76 20.2 922 5 BU846202 AGENCOURT
C 637 76 20.2 952 5 BQ499999 AGENCOURT
C 638 75 19.9 348 4 BG943235 AGENCOURT
C 639 75 19.9 400 1 A1140742 qa02h06.x
C 640 75 19.9 411 6 CA868145 ir78e02.y
C 641 75 19.9 417 1 A1023061 ow65d10.s
C 642 75 19.9 418 7 N41846 yw72b06.r1
C 643 75 19.9 423 1 A1002297 q086f06.s
C 644 75 19.9 445 1 AA102742 zn75C10.s
C 645 75 19.9 452 1 AA411127 zt28g02.r
C 646 75 19.9 539 2 AW197146 xB16d03.x
C 647 75 19.9 546 1 A1914392 wd48d05.x
C 648 75 19.9 558 6 CB265551 1004456 H
C 649 75 19.9 680 4 BG661032 N335 SSH-
C 650 75 19.9 683 4 BG470735 602511674
C 651 74 19.6 368 1 AJ573253 AJ573253
C 652 74 19.6 395 2 AA780047 hm96g06.x
C 653 74 19.6 414 1 AA057383 zF59d06.s
C 654 74 19.6 451 1 A1301708 qn36h05.x
C 655 74 19.6 466 7 W21065 zB55a09.r1
C 656 74 19.6 486 1 A1298533 qn02a11.x
C 657 74 19.6 490 1 A1609708 tF82b11.x
C 658 74 19.6 504 1 AA677163 zj56f06.s
C 659 74 19.6 526 2 BF061159 y181g09.x
C 660 74 19.6 549 1 A1339407 qT02d03.x
C 661 74 19.6 572 5 BQ127440 i60a03.y
C 662 74 19.6 582 4 BM476598 UI-E-EJ0-
C 663 74 19.6 583 1 AA401892 zt44d09.s
C 664 74 19.6 595 5 BQ127196 i557a06.y
C 665 74 19.6 701 4 B1395164 TUDPEc139
C 666 74 19.6 733 2 BF030624 601559595

AA021376 ze68c10.r
A1377586 7c18f07.x
BE675931 q67h10.x
A1355203 qb73h04.x
A1144511 Qb73h04.x
BQ937545 AGENCOURT
BQ921119 AGENCOURT
BQ683114 AGENCOURT
H81242 YU73002.r1
CD694302 EST10825
B1036680 RC6-NT015
T61988 yb96h02.r1
AW062552 IL3-UT007
B1063842 IL3-UT011
B1063658 IL3-UT011
B1063676 IL3-UT011
B1063677 IL3-UT011
B1063980 IL3-UT011
B1063693 IL3-UT011
B1063678 IL3-UT011
B1063687 IL3-UT011
B1063663 IL3-UT011
B1063665 IL3-UT011
B1063679 IL3-UT011
AY412159 Pan trogl
BF666533 602123987
B1036693 RC6-NT015
AA961959 q092C10.s
N68425 zai13e08.s1
AA827740 OB54h11.s
BP367260 BP367260
BF229960 PM3-CS003
B1153367 602918645
BF981165 602310440
BQ071597 AGENCOURT
BM473295 AGENCOURT
T34505 EST69511 Hu
AW602562 RC3-BT056
AA484896 ne81g10.s
N88322 K3097F Huma
AA146795 z035h12.s
A1017489 ou29a09.x
BU846202 AGENCOURT
BQ499999 AGENCOURT
BG943235 ax35C01.x
A1140742 qa02h06.x
CA868145 ir78e02.y
A1023061 ow65d10.s
N41846 yw72b06.r1
A1002297 q086f06.s
AA102742 zn75C10.s
AA411127 zt28g02.r
AW197146 xB16d03.x
A1914392 wd48d05.x
CB265551 1004456 H
BG661032 N335 SSH-
BG470735 602511674
AJ573253 AJ573253
AA780047 hm96g06.x
AA057383 zF59d06.s
A1301708 qn36h05.x
W21065 zB55a09.r1
A1298533 qn02a11.x
A1609708 tF82b11.x
AA677163 zj56f06.s
BF061159 y181g09.x
A1339407 qT02d03.x
BQ127440 i60a03.y
BM476598 UI-E-EJ0-
AA401892 zt44d09.s
BQ127196 i557a06.y
B1395164 TUDPEc139
BF030624 601559595

667	74	13.6	837	1	AU119783	AU119783	740	66	17.5	552	2	AW176627	AW176627	IL4-CT007
668	73	19.4	283	2	BF828336	MR1-HN006	741	66	17.5	557	2	BE855565	BE855565	7910C04.X
669	73	19.4	283	2	BF828372	MR1-HN006	742	66	17.5	585	1	AA191621	AA191621	zp19109.S
670	73	19.4	358	6	CD678566	hp09h12.Y	743	66	17.5	761	4	BI185194	BI185194	UNL-P-PN-
671	73	19.4	446	1	AA443595	zw35b10.S	744	66	17.2	959	5	BQ230627	BQ230627	AGENCOURT
672	73	19.4	488	1	R90728	Ym02a05.S1	745	65	17.2	247	5	BQ565115	BQ565115	q130h07.Y
673	73	19.4	565	1	AA455699	aa22c12.X	746	65	17.2	324	2	BE766760	BE766760	IL4-NT010
674	73	19.4	597	6	CA865837	ir78e02.X	747	65	17.2	421	1	AI952335	AI952335	wx27c10.X
675	73	19.4	776	7	CNA03759	CNA03759	748	65	17.2	461	1	N25815	N25815	YK22D02.r1
676	73	19.4	860	4	BG685185	BG685185	749	65	17.2	481	2	R90752	R90752	Ym22A05.r1
677	72	19.1	399	7	H18197	H18197	750	65	17.2	542	2	AW265239	AW265239	xq54a01.X
678	72	19.1	413	7	N24351	Yx14a05.r1	751	65	17.2	822	4	BG716298	BG716298	602676557
679	72	19.1	424	7	R10180	R10180	752	65	17.2	822	4	AA778982	AA778982	ac37f07.S
680	72	19.1	436	1	AA021071	AA021071	753	64	17.0	278	1	BE300959	BE300959	db10h11.X
681	72	19.1	453	1	AI311374	AI311374	754	64	17.0	367	2	BE300959	BE300959	db10h11.X
682	72	19.1	465	1	AI811927	AI811927	755	64	17.0	382	1	AA088582	AA088582	z64b06.X
683	72	19.1	468	2	BF927593	CM2-NT019	756	64	17.0	390	2	AA040398	AA040398	UI-HF-BK0
684	72	19.1	475	1	AA459535	AA459535	757	64	17.0	428	1	AA525244	AA525244	n152f05.S
685	72	19.1	487	4	BI063801	BI063801	758	64	17.0	442	7	R53807	R53807	Y103C05.S1
686	72	19.1	522	6	CD465666	CD465666	759	64	17.0	451	7	H86415	H86415	y893e05.r1
687	72	19.1	563	5	BU579991	BU579991	760	64	17.0	460	1	AA021650	AA021650	z6e9d06.X
688	72	19.1	583	5	BF376806	BF376806	761	64	17.0	461	7	R87382	R87382	ym88f06.r1
689	72	19.1	736	2	BE743763	BE743763	762	64	17.0	468	1	AA018844	AA018844	z129c01.S
690	72	19.1	766	4	BG110301	BG110301	763	64	17.0	476	1	AA018844	AA018844	z657h10.S
691	72	19.1	766	4	BG110301	BG110301	764	64	17.0	493	2	BE769362	BE769362	PM2-FT002
692	71	18.8	415	1	AA018940	AA018940	765	64	17.0	564	1	AA088443	AA088443	z189c07.S
693	71	18.8	418	1	AA857209	AA857209	766	64	17.0	592	6	CD623342	CD623342	56016114H
694	71	18.8	419	1	AA632379	AA632379	767	63	16.7	245	5	BQ324040	BQ324040	CM2-C1013
695	71	18.8	488	2	BF832652	BF832652	768	63	16.7	354	2	BF825103	BF825103	RC3-HN002
696	71	18.8	494	1	AI268435	AI268435	769	63	16.7	402	1	AA010834	AA010834	z634d03.S
697	71	18.8	564	5	BF259054	BF259054	770	63	16.7	410	7	N23295	N23295	Yx77e10.S1
698	71	18.8	582	1	AU147052	AU147052	771	63	16.7	415	6	CB799998	CB799998	AMGNNUC:N
699	71	18.8	643	2	BF116024	BF116024	772	63	16.7	422	4	AI036659	AI036659	RC6-NT015
700	71	18.8	644	5	BU689348	BU689348	773	63	16.7	430	7	H28392	H28392	Y152f04.r1
701	71	18.8	663	2	BE613480	BE613480	774	63	16.7	502	4	BM663687	BM663687	UI-E-CK0-
702	71	18.8	674	6	CA448476	CA448476	775	63	16.7	556	1	AA001183	AA001183	z648f01.X
703	71	18.8	724	2	BF667981	BF667981	776	63	16.7	661	2	BF925989	BF925989	MR2-NT013
704	71	18.8	745	5	BQ000493	BQ000493	777	63	16.7	673	4	BI653500	BI653500	603300485
705	71	18.8	800	2	BF205634	BF205634	778	63	16.7	718	7	CO559445	CO559445	AGENCOURT
706	71	18.8	1064	4	BG495262	BG495262	779	63	16.7	727	7	CO403221	CO403221	AGENCOURT
707	70	18.6	336	7	Z28780	Z28780	780	63	16.7	752	7	CO401140	CO401140	AGENCOURT
708	70	18.6	474	1	AA188000	AA188000	781	63	16.7	757	7	CV111060	CV111060	AGENCOURT
709	70	18.6	477	1	AI805925	AI805925	782	63	16.7	760	4	BI906096	BI906096	603062484
710	70	18.6	558	1	AU159472	AU159472	783	63	16.7	762	7	CK476853	CK476853	AGENCOURT
711	70	18.6	611	1	AA188001	AA188001	784	63	16.7	807	7	CO394917	CO394917	AGENCOURT
712	70	18.6	642	1	AA573290	AA573290	785	63	16.7	809	7	CO394917	CO394917	AGENCOURT
713	70	18.6	734	4	EG254346	EG254346	786	63	16.7	815	7	CV117459	CV117459	AGENCOURT
714	70	18.6	1059	4	AG254346	AG254346	787	63	16.7	855	5	BU527460	BU527460	AGENCOURT
715	69	18.3	215	1	AA628593	AA628593	788	63	16.7	886	4	BG198262	BG198262	RST17406
716	69	18.3	321	2	BE767779	BE767779	789	63	16.7	896	5	BQ879445	BQ879445	AGENCOURT
717	69	18.3	321	2	BE767779	BE767779	790	63	16.7	1085	7	CR754276	CR754276	CR754276
718	69	18.3	355	1	AA299052	AA299052	791	62	16.4	438	2	BF825097	BF825097	RC3-HN002
719	69	18.3	402	1	AA505973	AA505973	792	62	16.4	542	1	AV591749	AV591749	AV591749
720	69	18.3	1015	5	BQ066739	BQ066739	793	62	16.4	849	2	BF577160	BF577160	602135454
721	68	18.0	268	2	AW843279	AW843279	794	61	16.2	208	2	AW901060	AW901060	CM0-NN101
722	68	18.0	277	2	BE766649	BE766649	795	61	16.2	277	2	AW299229	AW299229	x648b02.X
723	68	18.0	395	1	AI265892	AI265892	796	61	16.2	347	1	AA248313	AA248313	CSG2469.S
724	68	18.0	435	7	W96274	W96274	797	61	16.2	386	7	H40555	H40555	Ym87b09.S1
725	68	18.0	493	1	AI446228	AI446228	798	61	16.2	406	1	AI797547	AI797547	w654h06.X
726	67	17.8	243	7	R10208	R10208	799	61	16.2	408	6	CD512156	CD512156	AGENCOURT
727	67	17.8	326	7	R10179	R10179	800	61	16.2	420	1	AA704015	AA704015	ag80b04.X
728	67	17.8	426	1	AA043972	AA043972	801	61	16.2	448	1	AA027118	AA027118	z604h06.S
729	67	17.8	441	7	H30847	H30847	802	61	16.2	459	1	AA001081	AA001081	z647a01.X
730	67	17.8	476	4	BI063844	BI063844	803	61	16.2	462	1	AI708106	AI708106	AI708106
731	67	17.8	801	2	BE620803	BE620803	804	61	16.2	526	1	AA758596	AA758596	ah58a08.S
732	67	17.8	834	2	BF308244	BF308244	805	61	16.2	526	1	AA758596	AA758596	ah58a08.S
733	67	17.8	913	5	BQ221930	BQ221930	806	61	16.2	571	5	BQ773013	BQ773013	UI-H-FEO-
734	66	17.5	414	1	AI370280	AI370280	807	61	16.2	722	7	BG183268	BG183268	RST2142.A
735	66	17.5	437	1	AA121443	AA121443	808	60	15.9	384	4	BI048432	BI048432	MR4-TN011
736	66	17.5	468	4	BI063827	BI063827	809	60	15.9	524	4	BI102257	BI102257	603068487
737	66	17.5	469	2	AW859789	AW859789	810	60	15.9	540	1	AA225516	AA225516	nc25b10.X
738	66	17.5	498	2	AW302456	AW302456	811	60	15.9	656	4	BI861443	BI861443	603386672
739	66	17.5	517	1	AI288797	AI288797	812	60	15.9	688	4	BG422324	BG422324	602448979

813	60	15.9	793	4	BG205511	RST24890	886	54	14.3	562	2	BF852812	MR3-EN009
814	60	15.9	803	1	AUL43082	AUL43082	887	54	14.3	701	1	AI568713	ch14g08.x
815	60	15.9	903	2	BF306450	601893337	888	53	14.1	349	1	AA639531	nq91c02.s
816	60	15.9	906	2	BE784177	6014711391	889	53	14.1	352	2	BE539946	601060601
817	60	15.9	946	2	BG031336	6032299031	890	53	14.1	353	1	AA443086	x74a01.s
818	59	15.6	935	2	BE707784	QV3-HT054	891	53	14.1	354	1	AA443122	xt74d06.s
819	59	15.6	232	4	BG218606	RST38346	892	53	14.1	361	2	AA493228	UI-M-BH3-
820	59	15.6	273	6	CD673801	IS04g10.Y	893	53	14.1	413	1	AA766630	oa38b09.s
821	59	15.6	327	2	BF8293970	6013112309	894	53	14.1	444	2	BF469374	UI-M-BH3-
822	59	15.6	362	2	BF825091	RC3-HN002	895	53	14.1	452	2	AA464684	BP230016B
823	59	15.6	388	1	AA019589	ze60c09.s	896	53	14.1	464	2	BE137044	u959a07.Y
824	59	15.6	550	6	CB554966	MMSP0031	897	53	14.1	509	1	AA050559	mj20g08.Y
825	59	15.6	910	5	BQ942748	AGENCOURT	898	53	14.1	514	2	AW227144	um66e04.Y
826	59	15.6	933	5	BQ669200	AGENCOURT	899	53	14.1	516	2	AI836101	UI-M-AJ1-
827	59	15.6	953	5	BUS26745	AGENCOURT	900	53	14.1	519	2	BF456625	BX511532
828	58	15.4	292	7	R71979	VJ84g03.r1	901	53	14.1	521	6	CD806120	UI-M-GW0-
829	58	15.4	275	7	T35540	EST86969.Hu	902	53	14.1	521	6	CD806120	UI-M-GW0-
830	58	15.4	296	7	H45224	V003e04.r1	903	53	14.1	526	6	CA034473	CA034473
831	58	15.4	300	2	BE833056	RC6-ET008	904	53	14.1	588	2	BF041384	BP250025B
832	58	15.4	383	6	CB703771	AMGNNUC:N	905	53	14.1	600	4	BG803120	0221-16.M
833	58	15.4	395	7	W03594	za02b11.r1	906	53	14.1	620	7	CF764690	CES003367
834	58	15.4	440	7	H40679	YP50f06.s1	907	53	14.1	680	5	BQ442736	UI-M-EV0-
835	58	15.4	673	4	BG188438	RST7456.A	908	53	14.1	688	6	CD807159	UI-M-GW0-
836	58	15.4	964	4	BG164089	602341131	909	53	14.1	693	6	CD806096	UI-M-GW0-
837	57	15.1	197	1	AA659220	nt92c11.s	910	53	14.1	717	7	CO890616	BovGen.18
838	57	15.1	247	7	N55813	J2985F.Huma	911	53	14.1	722	7	CN837718	AGENCOURT
839	57	15.1	321	7	R87368	Ym88d08.r1	912	53	14.1	726	6	CB952709	AGENCOURT
840	57	15.1	409	1	AA021333	ze68b08.r	913	53	14.1	728	5	BQ178754	UI-M-EV0-
841	57	15.1	409	2	AA01698	UI-HF-BK0	914	53	14.1	729	7	CF750534	UI-M-HJ0-
842	57	15.1	411	7	H45216	V003c07.r1	915	53	14.1	741	7	CF724469	UI-M-G20-
843	57	15.1	411	7	T15517	I81478.Infa	916	53	14.1	747	5	BQ178962	UI-M-EV0-
844	57	15.1	416	2	BF222344	7p51f01.x	917	53	14.1	747	7	CK943550	4067471.B
845	57	15.1	420	7	H48467	Y890M07.r1	918	53	14.1	759	5	BQ164402	UI-M-FR0-
846	57	15.1	441	2	BF109033	7149d03.x	919	53	14.1	798	5	BU706227	UI-M-EV0-
847	57	15.1	454	2	AW15630	UI-B-B11-	920	53	14.1	798	7	CF950351	UI-M-HJ0-
848	57	15.1	455	7	CN403769	170006001	921	53	14.1	833	7	CO796221	AGENCOURT
849	57	15.1	457	7	N32671	Yx77e10.r1	922	53	14.1	900	5	BQ951632	AGENCOURT
850	57	15.1	501	5	B0430243	UI-HF-ENO	923	53	14.1	936	5	BQ712467	AGENCOURT
851	57	15.1	505	4	B1063845	IL3-UT011	924	53	14.1	2045	3	AK050465	Mus.muscu
852	57	15.1	538	4	BM505258	IG92e01.x	925	53	14.1	2739	3	AK079476	AK079476
853	57	15.1	576	5	BM996837	UI-H-DH0-	926	52	13.8	359	7	F36711	HSPD34599.H
854	56	14.9	323	1	AA985180	am79c06.s	927	52	13.8	380	1	AA813533	ai65g10.s
855	56	14.9	330	6	CA891650	B0167B05-	928	52	13.8	384	2	BE128724	DEPA2474
856	56	14.9	368	2	BF919657	RC6-NT015	929	52	13.8	414	7	N36758	Y734a01.s1
857	56	14.9	384	4	BI490970	dfo1h03.w	930	52	13.8	418	1	AA861003	aj90f10.s
858	56	14.9	384	4	BM666783	UI-B-CL1-	931	52	13.8	435	1	AA121968	zm25c09.s
859	56	14.9	403	1	AA018037	zes1d04.r	932	52	13.8	446	1	AA284509	zt20f06.s
860	56	14.9	432	7	CN645730	ILJUMIGEN	933	52	13.8	454	7	R87486	Ym90c07.s1
861	56	14.9	437	4	B1063825	IL3-UT011	934	52	13.8	457	1	AI360680	qx64f03.x
862	56	14.9	485	1	AA157999	zo57d09.s	935	52	13.8	505	4	B1063998	IL3-UT011
863	56	14.9	504	4	B1063987	IL3-UT011	936	52	13.8	545	1	AA894835	oj61f10.s
864	56	14.9	509	4	B1063979	IL3-UT011	937	52	13.8	610	2	BF243478	601879503
865	56	14.9	554	2	AW515055	xu83b04.x	938	52	13.8	901	5	BQ686351	AGENCOURT
866	56	14.9	743	2	BF797400	602257046	939	52	13.8	910	5	BQ643059	AGENCOURT
867	56	14.9	750	4	BG428886	602494673	940	52	13.8	931	5	BQ709316	AGENCOURT
868	55	14.6	262	4	BG209161	RST28675	941	51	13.5	344	7	R84956	Yc40d06.s1
869	55	14.6	350	1	AA730298	nw41c12.s	942	51	13.5	386	5	BI133769	BY133769
870	55	14.6	388	7	H85576	Y890h07.s1	943	51	13.5	423	1	AA146787	zo35g12.s
871	55	14.6	402	1	AI492331	ti23b03.x	944	51	13.5	431	7	R93806	Yt72a08.s1
872	55	14.6	424	2	BF197808	7p92g06.x	945	51	13.5	463	7	CF896236	A0208B12-
873	55	14.6	430	7	R85113	Yc43f02.s1	946	51	13.5	492	6	CA896306	B0198B10-
874	55	14.6	444	1	AI342973	qo27c04.x	947	51	13.5	511	7	CN674363	A0947F11-
875	55	14.6	459	7	N29011	Yx40b06.r1	948	51	13.5	541	6	CD542845	B024AB08-
876	55	14.6	460	6	CD287048	14.K2.abd	949	51	13.5	585	7	CF895975	A0204G04-
877	55	14.6	506	1	AA215708	xr57h07.s	950	51	13.5	597	7	N58511	Yv72f08.s1
878	55	14.6	693	1	AUL134091	AUL134091	951	51	13.5	600	4	BG805121	0613-68.M
879	55	14.6	1022	5	BQ059268	AGENCOURT	952	51	13.5	600	4	BI988307	3223-72.M
880	54	14.3	344	1	AI735109	as76a02.x	953	51	13.5	600	4	BI990483	4071-72.M
881	54	14.3	440	1	AA164577	zo92d11.s	954	51	13.5	600	5	BU923128	7044-59.M
882	54	14.3	462	1	AI499883	tn97c04.x	955	51	13.5	600	6	CA527854	8053-56.M
883	54	14.3	475	1	AI801762	to95b05.x	956	51	13.5	604	1	AA882230	Vx42d03.x
884	54	14.3	486	2	BF842750	QV3-HT101	957	51	13.5	604	4	BI916177	603178061
885	54	14.3	514	4	B1063978	IL3-UT011	958	51	13.5	611	5	BU787194	il55b12.Y

```

959 51 13.5 614 7 CF898290
c 960 51 13.5 626 1 AA057586
c 961 51 13.5 653 6 CB426708
51 13.5 654 6 CB435983
963 51 13.5 692 2 BB877738
51 13.5 809 6 CB599544
964 51 13.5 844 4 BG246428
965 51 13.5 846 2 BG246428
966 51 13.5 846 2 B159549
967 51 13.5 920 5 BU529002
968 51 13.5 1110 9 AY412160
969 50 13.3 253 4 B1036115
970 50 13.3 253 4 B1036116
971 50 13.3 336 4 BG200248
c 972 50 13.3 353 1 AA558174
c 973 50 13.3 370 1 AA225844
c 974 50 13.3 379 7 R43432
c 975 50 13.3 420 4 B1063843
c 976 50 13.3 437 1 AA758948
c 977 50 13.3 441 7 W46581
c 978 50 13.3 505 4 B1063973
979 50 13.3 750 4 B1855507
980 49 13.0 151 6 CB116617
981 49 13.0 157 7 N56413
982 49 13.0 246 4 BG180306
c 983 49 13.0 357 7 N45919
984 49 13.0 380 7 N33478
985 49 13.0 444 2 AW512453
986 49 13.0 460 7 H39028
987 49 13.0 486 1 AA434421
988 49 13.0 487 7 H28367
989 49 13.0 544 7 H28143
990 49 13.0 563 1 AA528021
991 49 13.0 600 5 BU920931
992 49 13.0 601 2 BE891426
993 49 13.0 617 1 AA020986
994 49 13.0 731 2 BF241617
995 49 13.0 836 4 B1155031
996 49 13.0 913 2 BE562867
997 49 13.0 933 4 B1695196
998 49 13.0 1013 5 BQ055815
999 48 12.7 336 1 AA975283
c1000 48 12.7 352 7 H38301

ALIGNMENTS
BU956287 903 bp mRNA linear EST 21-OCT-2002
AGENCOURT 10613307 NIH MGC 107 Homo sapiens cDNA clone
IMAGE:6729846 5', mRNA sequence.
BU956287
BU956287.1 GI:24185959
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 903)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLC3053 row: 1 column: 05
High quality sequence stop: 695.

FEATURES             Location/Qualifiers
     source            1..903
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6729846"
                     /tissue_type="adenocarcinoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH MGC 107"
                     /note="Organ: breast; Vector: pOTB7; Site: 1: EcoRI;
                     Site: 2: XhoI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GCCACGAG(G). Library constructed by
                     Ling Hong in the laboratory of Gerald M. Rubin (University
                     of California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."

ORIGIN
Alignment Scores:      4.24e-247      Length:      903
Pred. No.:            261.00          Matches:     261
Score:                100.00%          Conservative: 0
Percent Similarity:   100.00%          Mismatches:  0
Best Local Similarity: 69.23%          Indels:      0
Query Match:         69.23%          Gaps:        0
DB:                  5

US-09-736-250-1 (1-377) x BU956287 (1-903)

Oy 2 LysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuGluLysAlaIleThr 21
Db 3 AAGTTTCAGGGCCTTTGGAAACACAGAGATTGCTTTCTGTGTGGAAAGGCAATCACT 62

Oy 22 ArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnValSer 41
Db 63 AGGGAACACAGATGTGGAAAGTAATGCGGGAATGCTTCAATCAGATGTTCT 122

Oy 42 ProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLysTyrGlnPheAsnLeu 61
Db 123 CCATCCAGAGAGATGAATTAATCAATGCTGCGCCAACTCAAGTACCAATTCACCTT 182

Oy 62 TyrProGlnThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrValLys 81
Db 183 TACCACCAAAACATTTGCTCTGGCTAGCAGCTTTTGGATAGGTTTTTAGCTACCGTAAG 242

Oy 82 AlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaAlaLysThr 101
Db 243 GCTCATCCAAATACTTGTAGTTGTTGCAATCAGCTGTTTTTCTTAGCTGCCAAGACT 302

Oy 102 ValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCysGly 121
Db 303 GTTCAGGAAGATGAGAGAATTCAGTACTAAGGTATTGGCAAGAGACAGTTTCTGTGGA 362

Oy 122 CysSerSerSerGluIleLeuAtgMetGluArgIleIleLeuAspLysLeuAsnTrpAsp 141
Db 363 TGTTCCTCATCTGAATTTTGAAGTGAAGAAATTAATCTCGAATAGTTGAATGGAT 422

Oy 142 LeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSerThr 161
Db 423 CTTCCACAGCCACACCATTCGATTTTCTTATATTTCCATATTTCCATGCAATGCACTGCACT 482

Oy 162 ArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaValLeu 181
Db 483 AGGCCTCAGTTACTTTTTCAGTTTCCCAAAATGAGCCCATCTCAACATTTGGCAGTCTCTT 542

Oy 182 ThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySerMet 201
Db 543 ACCAAGCAACTACTTCTACTGTATGGCTGCAACCAACTTCTGCAATTCAGAGGATCCATG 602

Oy 202 LeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSerLeu 221
Db 603 CTTGCTCTGGCCATGGTTAGTCTGGAATGAGAAACTCATTTCTCTGATGTTGCTTTCTCTT 662

```



```

Qy 222 ThrileGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuLeuHisCysArgGlu 241
Db 663 ACAATTGAACGCTTCAGAAAGCACAGATGATAGTCCCTCCAGTTGATCCATTGTCGGGAG 722
Qy 242 LeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyrVal 261
Db 723 CTTGTGGACATACCTTTCTACTCTGACGCTCTCCCTGGCTCTGAAATTCGTTATGTC 782
Qy 262 Tyr 262
Db 783 TAC 785

RESULT 2
LOCUS BQ673252 918 bp mRNA linear EST 15-JUL-2002
DEFINITION AGENCOURT 8349250 NIH_MGC_102 Homo sapiens cDNA clone IMAGE:6276033
5', mRNA sequence.
ACCESSION BQ673252
VERSION BQ673252.1 GI:21784086
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 918)
AUTHORS NIH-MGC http://mgs.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC

FEATURES
source
cDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L12CM2460 row: c column: 10
High quality sequence stop: 708.
Location/Qualifiers
1..918
/organism="Homo sapiens"
/mo_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6276033"
/tissue type="epidermoid carcinoma, cell line"
/lab host="DH10B (phage-resistant)"
/clone lib="NIH MGC 102"
/note="Organ: salivary gland; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed
by Ling Hong in the laboratory of Gerald M. Rubin
(University of California, Berkeley) using ZAP-cDNA
synthesis kit (Stratagene) and Superscript II RT (Life
Technologies). Note: this is a NIH_MGC Library."

ORIGIN
Alignment Scores:
Pred. No.: 3,526-239 Length: 918
Score: 253.00 Matches: 253
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 67.11% Indels: 0
Gaps: 5

US-09-736-250-1 (1-377) x BQ673252 (1-918)

Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle 20
Db 108 ATGAAGTTTCCAGGCGCTTGGAAACACAGAGATTGCTTTCTTCCTGTTGGAAAGGCAATC 167
Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40

```

```

Db 168 ACTAGGGAACACAGATGTGAAAGTGAATGTCGGAATAATGCCTTCAATCAGAAATGTT 227
Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysLeuLysGlnPheAsn 60
Db 228 TCTCCATCCAGAGAGATGAAGTAATTAATCAATGGCTGGCCAACTCAAGTACCAATTCAAC 287
Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 288 CTTTACCAGAAACATTGCTCTGGCTAGCAGTCTTTTGGATAGGTTTTCAGCTACCCTGA 347
Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaAlaLys 100
Db 348 AGGCTCATCTCAAAATACTTGGATTGATTGCAATCAGCTGTTTTCCTAGCTGCCAAG 407
Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 408 ACTGTTGAGGAAGATGAGAGAAATTCAGTAGTACTAAAGGATATTGGCAGAGACAGTTCTGT 467
Qy 121 GlyCysSerSerSerGluIleLeuArgMetGluArgIleIleLeuAspLysLeuAsnTrp 140
Db 468 GGATGTTTCTCATCTGAAATTTTGGAAATGGAGAGAAATATTCTGGATAAGTTGAATTGG 527
Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 528 GATCTTCACAGCCACCATTTGGATTCTTCATATTTTCCATGTCATTCGATTCGAGTGCA 587
Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 588 ACTAGGCTCAGTTACTTTTCAGTTTCCCAAAATTTAGGCCCATCTCAACATTTGGCAGTC 647
Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuGlnPheArgGlySer 200
Db 648 CTTACCAAGCAACTACTTCACTGTATGGCTTGCACCACTCTGCAATTCAGAGATCC 707
Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
Db 708 ATGCTTGCTCTGGCCATGGTTAGTCTGGAATGGAGAACTCATCTCTGATTGCTTCT 767
Qy 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuLeuHisCysArg 240
Db 768 CTTACATTTGAACCTGCTTCAGAAAGCACAGATGATAGTCCCAAGTTGATCCATTGTCGG 827
Qy 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSer 253
Db 828 GAGCTTGTGGCACATCACCTTTCTACTCTGCGAGTCCTCC 866

RESULT 3
CD358716 899 bp mRNA linear EST 29-MAY-2003
DEFINITION AGENCOURT 14284919 NIH_MGC_180 Homo sapiens cDNA clone
IMAGE:30390835 5', mRNA sequence.
ACCESSION CD358716
VERSION CD358716.1 GI:31130127
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS 1 (bases 1 to 899)
TITLE NIH-MGC http://mgs.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be

```

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: NDAM466 row: 1 column: 20

High quality sequence start: 28

High quality sequence stop: 640.

FEATURES

source

1..899
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30390835"
/lab_host="DH10B-Ton A (T1 and T5 phage resistances)"
/clone_lib="NIH_MGC_180"
/note="Organ: Testis; Vector: pCMV-SPORT6.1; Site.1: NotI; Site.2: EcoRV (destroyed); Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.68 kb. Library was constructed by (Invitrogen). Note: this is a NIH_MGC Library."

ORGANISM

Alignment Scores:
Pred. No.: 3,366-238 Length: 899
Score: 252.00 Matches: 252
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 66.84% Indels: 0
DB: 6 Gaps: 0

US-09-736-250-1 (1-377) x CD358716 (1-899)

Qy 116 ArgAspSerPheCysGlyCysSerSerSerGluLeuLeuArgMetGluArgIleLeu 135
Db 38 AGAGACATTTCTGTGGATGTTCTCATCTCAATTTTGAATGGAGAAATTTCTG 97
Qy 136 AspLysLeuAenTtpAspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHis 155
Db 98 GATAGTTGAATGGGATCTTACACAGCCACACCATTTGGATTTTCTCATATTTCCAT 157
Qy 156 AlaIleAlaValSerThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSer 175
Db 158 GCCATTGAGTGTCACTAGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 217
Qy 176 GlnHisLeuAlaValLeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeu 195
Db 218 CAACATTTGGCAGCTCTTACCAAGCAACTCTTCACTGTATGGCTGCAACCACTTCTG 277
Qy 196 GlnPheArgGlySerMetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuLeu 215
Db 278 CAATTCAGAGATTCATGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 337
Qy 216 ProAspTrpLeuSerLeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGln 235
Db 338 CCTGATTGGCTTTCTCTTACATTTGAATGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 397
Qy 236 LeuLeuHisCysArgGluLeuValAlaHisHisLeuSerThrLeuGlnSerSerLeuPro 255
Db 398 TTGATTCATTTCTGGGAGCTTGTGGCAGCATCACCTTTCTACTCTGAGCTTCTTCTGCT 457
Qy 256 LeuAsnSerValTyrValTyrArgProLeuLysHisThrLeuValThrCysAspLysGly 275
Db 458 CTGAATTCGGTTTATGCTTACCGTCCCTCAAGCACACCTTGGTGGAGCTGTGCAAGGA 517
Qy 276 ValPheArgLeuHisProSerSerValProGlyProAspPheSerLysAspAsnSerLys 295
Db 518 GTGTTTCAGATTACATCCCTCTCTGTCCTGAGCCAGCATCTTCTTCTTCTTCTTCTTCTTCT 577
Qy 296 ProGluValProValArgGlyThrAlaAlaPheTyrHisLeuProAlaAlaSerGly 315
Db 578 CCAGAGTGCAGTCAGAGGTACAGAGCCCTTTTACCATCATCTTCCAGCTGCGAGTGGG 637
Qy 316 CysLysGlnThrSerThrLysArgLysValGluGluMetGluValAspAspPheTyrAsp 335

Db 638 TGCAAGCAGACCTCTACTAAACGCAAGTAGAGAAATGGAAGTGGAGTACTTCTATGAT 697
Qy 336 GlyIleLysArgLeuTyrAsnGluAspAsnValSerGluAsnValGlySerValCysGly 355
Db 698 GGAATCAACAGCGCTCTATAATGAAGATAATGTCTCAGAAAAATGTGGTCTTGTGTGGC 757
Qy 356 ThrAspLeuSerArgGlnGluGlyHisAlaSerPro 367
Db 758 ACTGATTATCAACAGCAAGAGGACATGCTTCCCT 793
RESULT 4
BM016042
LOCUS
DEFINITION 603642469P1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:5418352 5',
mRNA sequence.
ACCSSION BM016042
VERSION BM016042.1 GI:16530396
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 775)
TITLE NIH-MGC http://mgs.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12067 row: j column: 17
High quality sequence stop: 771.
Location/Qualifiers
1..775
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5418352"
/tissue_type="mammary adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_87"
/note="Organ: breast; Vector: pCMV-SPORT6; Site.1: NotI;
Site.2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.383 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

Alignment Scores:
Pred. No.: 2,686-235 Length: 775
Score: 249.00 Matches: 249
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 66.05% Indels: 0
DB: 4 Gaps: 0

US-09-736-250-1 (1-377) x BM016042 (1-775)

Qy 54 LysLeuLysTyrGlnPheAsnLeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeu 73
Db 2 AACTCAAGTACCAATTCACCTTTACCCAGAAACATTTGCTCTGGCTAGCAGTCTTTG 61
Qy 74 AspArgPheLeuAlaThrValLysAlaHisProLysTyrLeuSerCysIleAlaIleSer 93
Db 62 GATAGTTTTTGTAGTACCTACCGTAAAGGCTCATCAAAATCTTGGATTGTATTCATCAGC 121
Qy 94 CysPhePheLeuAlaAlaLysThrValGluGluAspGluArgIleProValLeuLysVal 113

```

Db      122 TGTTCCTTCTAGTCGCAAGACTGTTGAGGAAGATGAGAAATTCAGTACTAAAGTA 181
Qy      114 LeuAlaArgAspSerPheCysGlyCysSerSerSerGluLeuLeuArgMetGluArgIle 133
Db      182 TTGGCAAGACAGACAGTTCTCTGTGGATGTTCTCTCATCTGAAATTTTGGAGATGGAGAAAT 241
Qy      134 IleLeuAspLysLeuAsnTrpAspLeuHisThrAlaThrProLeuAspPheLeuHisIle 153
Db      242 ATTCTGGATAGTTGAATTTGGATCTTCACAGACCCACACATTTGATGATTTCTTCATATT 301
Qy      154 PheHisAlaIleAlaValSerThrArgProGlnLeuLeuPheSerLeuProLysLeuSer 173
Db      302 TTCCATGCGATTCAGTGTCTCACTAGGCTCAGTTACTTTTCAGTTTGCCCAATTTGAGC 361
Qy      174 ProSerGlnHisLeuAlaValLeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGln 193
Db      362 CCATCTCAACATTTGGCAGTCTTACCAAGCAACTTACTTCACTGATGGCTGCAACCAA 421
Qy      194 LeuLeuGlnPheArgGlySerMetLeuAlaLeuAlaMetValSerLeuGluMetGluLys 213
Db      422 CTTCTGCAATTCAGAGGATCCATGCTTCTGTGGCCATGGTTAGTCTGGAAATGGAGAA 481
Qy      214 LeuLeuProAspTrpLeuSerLeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSer 233
Db      482 CTCAATCTCGATTTGGCTTTCTTACATTTGACTGCTTCAGAAAGCACAGATGGATAGC 541
Qy      234 SerGlnLeuIleHisCysArgGluLeuValAlaHisLeuSerThrLeuGlnSerSer 253
Db      542 TCCAGATTGATCCATTTGTGGGAGCTTGTGGCAGATCACCTTTCTACTCTGCAGTCTTCC 601
Qy      254 LeuProLeuAsnSerValTyrValTyrArgProLeuLysHisThrLeuValThrCysAsp 273
Db      602 CTGCTCTGAAATTCGGTTTATGTCTACCGTCCCTCAAGACACACCTGGTGACCTGTGAC 661
Qy      274 LysGlyValPheArgLeuHisProSerSerValProGlyProAspPheSerLysAspAsn 293
Db      662 AAAGAGTTGTCAGATTACATCCCTCTCTGTCCAGGCCCCAGAGCTTCTCCAGAGCAAC 721
Qy      294 SerLysProGluValProValArgGly 302
Db      722 AGCAAGCCAGAAAGTCCAGTCCAGAGG 748

RESULT 5
BI858571
LOCUS   603389030P1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:5398038 5',
DEFINITION mRNA sequence.
ACCESSION BI858571
VERSION   BI858571.1 GI:15999318
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 890)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12014 row: 1 column: 07
High quality sequence stop: 855.
Location/Qualifiers
1. 890
/organism="Homo sapiens"
/mol_type="mRNA"
FEATURES
source

```

```

ORIGIN
Alignment Scores:
Pred. No.:      3,09e-235      Length:      890
Score:          249.00        Matches:    249
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches:    0
Query Match:     66.05%       Indels:     0
DB:              4           Gaps:       0

US-09-736-250-1 (1-377) x BI858571 (1-890)

```

```

Qy      91 AlaIleSerCysPhePheLeuAlaAlaLysThrValGluGluAspGluArgIleProVal 110
Db      3 GCATCAGCTGTTTTTCTTAGCTGCCAAGACTGTTGAGGAGATGAGAAATTCAGTA 62
Qy      111 LeuLysValLeuAlaArgAspSerPheCysGlyCysSerSerSerGluLeuLeuArgMet 130
Db      63 CTTAAAGGTTATGGCAAGACAGTTCCTGTGGATGTTCTCATCTGAAATTTTGAATG 122
Qy      131 GluArgIleIleLeuAspLysLeuAsnTrpAspLeuHisThrAlaThrProLeuAspPhe 150
Db      123 GAGAGAAATTTATTCGGATTAAGTTGAATTTGGATCTTCACACAGCACACCATTTGGATTTT 182
Qy      151 LeuHisIlePheHisAlaIleAlaValSerThrArgProGlnLeuLeuPheSerLeuPro 170
Db      183 CTTCAATATTTTCCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTC 242
Qy      171 LysLeuSerProSerGlnHisLeuAlaValLeuThrLysGlnLeuLeuHisCysMetAla 190
Db      243 AAATTTAGGCCCATCTCAACATTTGGCAGTCTTACCAAGCAACTTACTTCACTGATGGCC 302
Qy      191 CysAsnGlnLeuLeuGlnPheArgGlySerMetLeuAlaLeuAlaMetValSerLeuGlu 210
Db      303 TGCAACCAACTTCTGCAATTCAGAGGATCCATGCTGCTCTGGCCATGGTTAGTCTGGAA 362
Qy      211 MetGluLysLeuIleProAspTrpLeuSerLeuThrIleGluLeuLeuGlnLysAlaGln 230
Db      363 ATGGAGAAATCATCTCTGATTTGGCTTTCTTACAAATTTGACTGCTTCAGAAAGCACAG 422
Qy      231 MetAspSerSerGlnLeuIleHisCysArgGluLeuValAlaHisLeuSerThrLeu 250
Db      423 ATGGATAGTCTCCCATGTTGATCCATTTGCGGAGCTTGTGGCAGCATCACCTTTCTACTCTG 482
Qy      251 GlnSerSerLeuProLeuAsnSerValTyrValTyrArgProLeuLysHisThrLeuVal 270
Db      483 CAGCTTTCCCTGCTCTGAAATTCGGTTTATGTCTACCGTCCCTCAAGACACACCTGCTG 542
Qy      271 ThrCysAspLysGlyValPheArgLeuHisProSerSerValProGlyProAspPheSer 290
Db      543 ACCTGTGACAAAGAGTGTTCAGATTACATCCCTCTCTGTCCAGGCCAGACTTCTTCC 602
Qy      291 LysAspAsnSerLysProGluValProValArgGlyThrAlaAlaPheTyrHisLeu 310
Db      603 AAGGACAAACAGCAAGCCAGAAAGTCCAGTCCAGAGTACAGAGCTTACAGAGCTTTTACCATCATCTC 662
Qy      311 ProAlaAlaSerGlyCysLysGlnThrSerThrLysArgLysValGluGluMetGluVal 330
Db      663 CCAGCTCCCAAGTGGTGCAGAGCAGACCTCTACTAAACGCAAAAGTAGAGGAATGGAAGTG 722
Qy      331 AspAspPheTyrAspGlyIleLysArg 339
Db      723 GATGACTTCTATGATGGAATCAAAACGG 749

```

```

/db_xref="taxon:9606"
/clones IMAGE:5398038"
/tissue_type="mammary adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_87"
/notes="Organ: breast; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.383 Kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

```

```

RESULT 6
CB962746
LOCUS
DEFINITION
CB962746 764 bp mRNA linear EST 29-APR-2003
AGENCOURT_1345224 NIH_MGC_187 Homo sapiens cdna clone
IMAGE:30319383 5', mRNA sequence.
ACCESSION
CB962746
VERSION
CB962746.1 GI:30218864
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 764)
NIH-MGC http://mgi.nci.nih.gov/
AUTHORS
National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE
Unpublished (1999)
JOURNAL
Contact: Robert Strausberg, Ph.D.
COMMENT
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
cdna Library Preparation: CLONTECH Laboratories, Inc.
cdna Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDCW115 row: h column: 16
High quality sequence stop: 676.
Location/Qualifiers
1..764
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30319383"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH MGC 187"
/note="Organ: Blood vessels - aorta, basilar and artery;
Vector: pDNR-LIB; Site: 1: SfiI (ggccattatggcc); Site 2:
SfiI (ggccgcctcgcc); 5' and 3' adaptors were used in
cloning as follows: 5' adaptor sequence:
5'-CACGCCCATTTATGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCGCGGCGGCACATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.4 kb
(range 0.5-4.0 kb). 14/15 colonies contained inserts by
PCR. This library was enriched for full-length clones and
was constructed by Clontech Laboratories (Palo Alto, CA).
Note: this is a NIH_MGC Library."
ORIGIN
Alignment Scores:
Pred. No.: 2,45e-232 Length: 764
Score: 246.00 Matches: 246
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 65.25% Indels: 0
DB: 6 Gaps: 0
US-09-736-250-1 (1-377) x CB962746 (1-764)
QY 118 SerPheCysGlyCysSerSerGluLeuArgMetGluArgilleLeuAspLys 137
Db 3 AGTTTCGTGGATGTTCTCATCTGGAATTTTGAGATGGAGAGATTTCTGGATAG 62
QY 138 LeuAsnTrpAspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIle 157
Db 63 TTGAATTGGGATCTTCACAGCCACACACCATTCGATTTCTTCATATTTTCCATGCCATT 122
QY 158 AlaValSerThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHis 177
Db 123 GCAGTGCACTAGGCTTCAGTTACTTTTCATGTTGCCAAATTCAGCCCATCTCAACAT 182
QY 178 LeuAlaValLeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPhe 197

```

/clone_lib="NIH_MGC_43"
/note="Organ: eye; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library. |"

ORIGIN

Alignment Scores:
Pred. No.: 3,02e-232 Length: 936
Score: 246.00 Matches: 246
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 65.25% Indels: 0
DB: 5 Gaps: 0

US-09-736-250-1 (1-377) x BU501311 (1-936)

Qy 79 ThrVallyslAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPheLeuAla 98
Db 1 ACCGTAAAGGCTCATCAAAATCTGAGTTGTATGCAATCAGCTGTTTTCTTAGCT 60
Qy 99 AlalysThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSer 118
Db 61 GCCAAGACTGTTGAGGAAGATGAGAGATTCCAGTACTTAAAGGTATTGGCAAGAGACAGT 120
Qy 119 PheCysGlyCysSerSerGluIleLeuArgMetGluArgIleLeuAspLysLeu 138
Db 121 TTCTGTGATGTTCTCTCATCTGAAATTTGAGATGGAGAGAAATTTCTGGATAAGTTG 180
Qy 139 AsnTrpAspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAla 158
Db 181 AATTGGGATCTTCACAGCCACACCATTTGATTTCTTATATTTCCATGCAATTCGA 240
Qy 159 ValSerThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeu 178
Db 241 GTGTCAACTAGGCTCAGTACTTTTCAAGTTGTTGCCAAATTTGAGCCCATCTCAACATTTG 300
Qy 179 AlaValLeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuGlnPheArg 198
Db 301 GCAGTCTTTACCAAGCAACTACTTCTACGTATGGCTGCAACCAACTTCTGCAATTCAGA 360
Qy 199 GlySerMetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrp 218
Db 361 GGATCCATGCTGCTCTGGCCATGTTAGTCTGGAAATGGAGAACTCATTTCTGATTGG 420
Qy 219 LeuSerLeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHis 238
Db 421 CTTTCTCTTCAATTTGAATGCTCTCAGAAAGCACAGATGGATGCTCCAGTTGATCCAT 480
Qy 239 CysArgGluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSer 258
Db 481 TGTGGGAGCTGTGGGCACATCACCCTTTCTACTCTGCAGTCTCCCTGCCCTCGAATTC 540
Qy 259 ValTrpValTrpArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArg 278
Db 541 GTTTATGTCACCGTCCCTCAGACACACCTGTGTGACCTGTGACAAAGGAGTGTTCAGA 600
Qy 279 LeuHisProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluVal 298
Db 601 TTACATCCCTCTCTGTCCAGGCCACAGCTTCTCCAAAGGCAACAGCAAGCCAGAGTG 660
Qy 299 ProValArgGlyThrAlaAlaPheTyrrhisLeuProAlaAlaSerGlyCysIleGln 318
Db 661 CCAGTCAGAGGTACAGACGCTTTTACCATCATCTCCAGCTGCCAGTGGGTGCAAGCAG 720
Qy 319 ThrSerThrLysArgLys 324
Db 721 ACCTCTACTAAACGCAAG 738

RESULT 8

BU538306
LOCUS
DEFINITION
AGENCOURT 10181155 NIH MGC 107 Homo sapiens cDNA clone
IMAGE:6568838 5', mRNA sequence.
BU538306
ACCESSION
BU538306.1 GI:22848747
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 963)
REFERENCE
AUTHORS
TITLE
NIH-MGC <http://mgs.nci.nih.gov/>.
JOURNAL
National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbe-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LUCM2755 row: c column: 14
High quality sequence stop: 646.

FEATURES

source
1..963
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6568838"
/tissue_type="adenocarcinoma, cell line"
/lab_hosts="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_107"
/notes="Organ: breast; Vector: pOTB7; Site 1: EcoRI;
Site 2: XhoI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:
Pred. No.: 3,11e-232 Length: 963
Score: 246.00 Matches: 246
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 65.25% Indels: 0
DB: 5 Gaps: 0

US-09-736-250-1 (1-377) x BU538306 (1-963)

Qy 2 LysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuGluLysAlaIleThr 21
Db 3 AAGTTTCACGGCCCTTGGAAACACAGATGTTCTTCTGTTGGAAAGGCAATCACT 62
Qy 22 ArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnValSer 41
Db 63 AGGGAAGCACAGATGTGGAAAGTGAATGTGGGAAAATGCCCTTCAAAATCAGATGTTTCT 122
Qy 42 ProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsnLeu 61
Db 123 CCATCCAGAGAGATGAAGTAATTCATGCTGCCAAACTCAAGTACCAATTCACACTT 182
Qy 62 TyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrValLys 81
Db 183 TACCCAGAACATTTGCTCTGGCTAGCAGTCTTTTGGTAGTGTTCCTACCGTAAAG 242
Qy 82 AlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaAlaLysThr 101

Db 243 GCTCATCAAAATACCTTGGATTGATTCGAATCAGCTGTTTTCCTAGCTGCCAAGACT 302
 Qy 102 ValGluGluAspGluuArgGluProValLeuLysValLeuAlaArgAspSerPheCysGly 121
 Db 303 GTTGAAGGAGATGAGAGAAATCCAGTACTAAGGTAATGGCAAGAGACAGTTTCTGTGA 362
 Qy 122 CysSerSerGluLeuLeuArgMetGluArgLleLeuLeuAspLysLeuAsnTrpAsp 141
 Db 363 TGTTCCTCATCTGAAATTTTCAGAAATGAGAGAAATTAATCTGGATAAGTTGGGAT 422
 Qy 142 LeuHisThrAlaThrProLeuAspPheLeuHisLlePheHisAlaLleAlaValSerThr 161
 Db 423 CTTACACAGCCACACCACTTGGATTTCTTCATATTTTCCATGCAATTCGCAAGTGTCACT 482
 Qy 162 ArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaValLeu 181
 Db 483 AGGCTCAGTTACTTTTCAGTTTGGCCAAATGAGCCCATCTCAACATTTGGCAGTCTCT 542
 Qy 182 ThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySerMet 201
 Db 543 ACCAAGCAACTACTTCACTGTATGGCTGCAACCAACTTCTGCAATTCAGAGGATCCATG 602
 Qy 202 LeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuLleProAspTrpLeuSerLeu 221
 Db 603 CTTGCTCTGGCCATGGTTAGTCTGGAATGAGAAACTCATTCCTGATTTGCTTCTCTT 662
 Qy 222 ThrLleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuLleHisCysArgGlu 241
 Db 663 ACAATTGAACTGCTTCAGAAAGCAGATGATAGTCCCAAGTTGATCCATTTGTGGGAG 722
 Qy 242 LeuValAlaHisHisLeu 247
 Db 723 CTTGTGGCACATCACCTT 740

RESULT 9

BQ673277
 LOCUS
 DEFINITION AGNCOURT 8354951 NIH_MGC_102 Homo sapiens cDNA clone IMAGE:6275333
 5', mRNA sequence.

ACCESSION BQ673277

VERSION BQ673277.1 GI:21784111

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 740)

AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Rubin Laboratory

cDNA Arrayed by: The I.M.A.G.E. Consortium (LML)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LML at:

<http://image.llnl.gov>

Plate: LUCM2458 row: f column: 06

High quality sequence stop: 691.

Location/Qualifiers

1. .920

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:6275333"

/tissue type="epidermoid carcinoma, cell line"

/lab host="DH10B (phage-resistant)"

/clone lib="NIH MGC 102"

/notes="Organ: salivary gland; Vector: pOTB7; Site_1: XhoI;

Site_2: EcoRI; cDNA made by oligo-dT priming.

FEATURES

source

Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCACGAG(G). Library constructed
 by Ling Hong in the laboratory of Gerald M. Rubin
 (University of California, Berkeley) using ZAP-cDNA
 synthesis kit (Stratagene) and Superscript II RT (Life
 Technologies). Note: this is a NIH_MGC Library. "

ORIGIN

Alignment Scores:
 Pred. No.: 2,82e-230 Length: 920
 Score: 244.00 Matches: 244
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 64.72% Indels: 0
 DB: 5 Gaps: 0

US-09-736-250-1 (1-377) x BQ673277 (1-920)

Qy 22 ArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnValSer 41
 Db 42 AGGAAGCACAGATGTGGAAGTGAATGTGGGAAATGCTTCAATCAGATGTTCT 101
 Qy 42 ProSerGlnArgAspGluValLleGlnTrpLeuAlaLysLeuLysTrpGlnPheAsnLeu 61
 Db 102 CCATCCAGAGAGATGAAGTAATTCATGGCTGGCCAACTCAAGTACCAATTCACCTT 161
 Qy 62 TyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrValLys 81
 Db 162 TACCCAGAAACATTTGCTCTGGCTAGCAGCTTTTGGATAGGTTTTCAGTACCGTAAG 221
 Qy 82 AlaHisProLysTrpLeuSerCysLleAlaLleSerCysPhePheLeuAlaAlaLysThr 101
 Db 222 GCTCATCAAAATACTTTGAGTTGTTATTCATCAGCTGTTTTCCTAGCTGCCAAGACT 281
 Qy 102 ValGluGluAspGluuArgLleProValLeuLysValLeuAlaArgAspSerPheCysGly 121
 Db 282 GTTGAGGAAGATGAGAGAAATTCAGTACTAAAGTATTTGGCAAGACAGTTTCTGTGGA 341
 Qy 122 CysSerSerGluLleLeuArgMetGluArgLleLleLeuAspLysLeuAsnTrpAsp 141
 Db 342 TGTTCCTCATCTGAAATTTTGAGATGAGAGAAATTAATCTGGATAGTGAATGGAT 401
 Qy 142 LeuHisThrAlaThrProLeuAspPheLeuHisLlePheHisAlaLleAlaValSerThr 161
 Db 402 CTTACACAGCCACACCATTTGGATTTTCATATTTCCATATTCATGTCAGTGTCAACT 461
 Qy 162 ArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaValLeu 181
 Db 462 AGGCCTCAGTTACTTTTCAGTTTGGCCAAATTTGAGCCCATCTCAACATTTGGCAGT 521
 Qy 182 ThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgLysMet 201
 Db 522 ACCAAGCAACTACTTCACTGTATGGCTGTCAACCAACTTTCCGATTCAGAGGATCCATG 581
 Qy 202 LeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuLleProAspTrpLeuSerLeu 221
 Db 582 CTTGCTCTGGCCATGGTTAGTCTGGAATGGAGAACTCATTCCTGATGGCTTCTCTT 641
 Qy 222 ThrLleGluLeuGlnLysAlaGlnMetAspSerSerGlnLeuLleHisCysArgGlu 241
 Db 642 ACAATTTGAATGCTTCAGAAAGCAGATGATGATGATGATGATGATGATGATGATGAT 701
 Qy 242 LeuValAlaHisHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyrVal 261
 Db 702 CTTGTGGCACATCACCTTTTCTACTCTGAGTCTTCCCTGCTCTGATTCGTTTATGTC 761

262 TyrArgProLeu 265
 762 TACCGTCCCTC 773

RESULT 10

BUI49962

LOCUS

862 bp

mRNA

linear

EST 03-SEP-2002

/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

ORIGIN

Alignment Scores:

Pred. No.: 2.35e-227 Length: 830
Score: 241.00 Matches: 273
Percent Similarity: 99.27% Conservative: 0
Best Local Similarity: 99.27% Mismatches: 1
Query Match: 63.93% Indels: 2
DB: 5 Gaps: 0

US-09-736-250-1 (1-377) x BX437607 (1-830)

Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuGluLysAlaIle 20
Db 9 ATGAAGTTTCCAGGGCTTTGCAAAACCCAGAGATTGTCTTCTCTGTGGAAAGGCAATC 68
Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 69 ACTAGGGAAGCACAGATGTGAAAGTGAATGTGGGAAATGCGCTTCAAAATCAGAAATGTT 128
Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn 60
Db 129 TCTCATCCAGAGAGATGAAGTAATTCATAGCTGGCCAACTCAAGTACCAATTCAC 188
Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 189 CTTTACCAGAAACATTTGCTCTGGTAGCAGTCTTTTGGATAGTGTATTTAGCTACCGTA 248
Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaAlaLys 100
Db 249 AAGGCTCATCAAAATCTTGAAGTTGATTCGAATCAGCTGTCTTTCTAGCTGGCCAAAG 308
Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 309 ACTGTGTGAGGAAGATGAGAGATTTCCAGTACTAAAGGTATTGGCAAGACAGATTTCTGT 368
Qy 121 GlyCysSerSerGluIleLeuArgMetGluArgIleLeuLeuAspLysLeuAsnTrp 140
Db 369 GGATGTCTCTCATCTGAAATTTTGAAGATGAGAGAAATTTCTGGATAGATTCGAATGG 428
Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 429 GATCTTACAGCCACACCATTTGATTTCTTATATTTTCCATGCAATTCAGAGTGTCA 488
Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 489 ACTAGGCTCAGTTACTTTTTCAGTTTGCCTAAATTTGAGCCCATCTCAACATTTGGCAGTC 548
Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgLysSer 200
Db 549 CTTTACCAGCACTACTTCACTGTATGCTGCAACCACTTCTGCAATTCAGAGGATCC 608
Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
Db 609 ATGCTTGTCTGGCCATGGTTAGTCTGGAATGGAGAACTCATCTCTGATGGCTTCT 668
Qy 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
Db 669 CTTACAAATGAATGCTTTCAGAAAGCACAGATGATAGTCTCCAGTTGATTCATTGTGCG 728
Qy 241 GluLeuValAlaHisIleLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTy 260
Db 729 GAGCK-TGTGGCAATCACCTTTCTACTCTGAGTCTTCCCTGCTCTGGAATTCGGTTA 787
Qy 260 rValTyrArgProLeuLysHisThrLeuValThrCysAspLys 274
Db 788 TGTATTCCGTCCTCAGACACACCTTGGTGGCTGTGACCTGTGACNA 830

RESULT 12

BUI59699

LOCUS

DEFINITION

S, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BUI59699 853 bp mRNA linear EST 04-SEP-2002
AGENCOURT 7888352 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:6141567

BUI59699.1 GI:22673609

BUI59699

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 853)

NIH-MGC <http://mgs.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-x@mail.nih.gov.

Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM13461 row: p column: 16

High quality sequence stop: 681.

FEATURES

source

1. 853

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:6141567"

/tissue_type="retinoblastoma"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_67"

/notes="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI;

Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 1.75 kb. Library constructed by Life

Technologies."

ORIGIN

Alignment Scores:

Pred. No.: 2.13e-222 Length: 853
Score: 236.00 Matches: 269
Percent Similarity: 99.26% Conservative: 0
Best Local Similarity: 99.26% Mismatches: 1
Query Match: 62.60% Indels: 2
DB: 5 Gaps: 0

US-09-736-250-1 (1-377) x BUI59699 (1-853)

Qy 48 ValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsnLeuTyrProGluThrPheAla 67

Db 2 GTAATTAATGGGTGGCCAACTCAAGTACCAATTCACCTTACCCAGAAACATTTGCT 61

Qy 68 LeuAlaSerSerLeuLeuAspArgPheLeuAlaThrValLysAlaHisProLysTyrLeu 87

Db 62 CTGGCTAGCAGTCTTTTGGATAGTCTTTTACCTACCGTAAGGCTCATCCAAATACCTG 121

Qy 88 SerCysIleAlaIleSerCysPhePheLeuAlaAlaLysThrValGluGluAspGluArg 107

Db 122 AGTTGATTGCAATCAGCTGTTTTTCTAGCTGCCAAGACTGTTGAGGAAGATGAGAGA 181

Qy 108 IleProValLeuLysValLeuAlaArgAspSerPheCysGlyCysSerSerSerGluIle 127

Db 182 ATTCCAGTACTAAAGGTATTGGCAAGACAGACAGTTCTCTGTGGATGTTCTCATCTGAAT 241

Qy 128 LeuArgMetGluArgIleLeuLeuAspLysLeuAsnTrpAspLeuHisThrAlaThrPro 147

Db 242 TTGAGATGGAGAGAAATTTCTGGATAGTGAATGGATCTTACACAGCCACCA 301

Qy 148 LeuAspPheLeuHisIlePheHisAlaIleAlaValSerThrArgProGlnLeuLeuPhe 167

Db 302 TTGGATTTTCATATTTTCATGCCATTCAGGTCACATAGGCTTCAGTTACTTTTC 361
Qy 168 SerLeuProLysLeuSerProSerGlnHisLeuAlaValLeuThrLysGlnLeuLeuHis 187
Db 362 AGTTTGCCCAATGAGCCCACTCAACATTTGGCAGTCCTTACCAAGCACTACTTCAC 421
Qy 188 CysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySerMetLeuAlaLeuAlaMetVal 207
Db 422 TGTATGGCTGCAACCACTTCCTGCAATTCAGAGGATCCATGCTTGCTCTGGCCATGTT 481
Qy 208 SerLeuGluMetGluLeuLeuLeuProAspTrpLeuSerLeuThrLysGlnLeuGln 227
Db 482 AGCTGGAAATGGGAAACTCATCTCTGATTTGGCTTTCTTACAAATGAACTGCTTCAG 541
Qy 228 LysAlaGlnMetAspSerSerGlnLeuLeuHisCysArgGluLeuValAlaHisLeu 247
Db 542 AAAGCACAGATGATAGTCCAGTTGATCCATTTGCGGAGCTTGTGGCACATCACCTT 601
Qy 248 SerThrLeuGlnSerSerLeuProLeuAsnSerValTrpValArgProLeuLysHis 267
Db 602 TCTACTCTGCACTCTCCCTGCTGCAATTCGCTTTATGTTACCGTCCCTCAAGCAC 661
Qy 268 ThrLeuValThrCysAspLysGlyValPheArgLeuHisProSerSerVal-ProGlyPr 287
Db 662 ACCCTGGTGAAGTGTGCAAGAGTGTTCAGATTACATCCCTCTCTGNG-TCCAGGCC 720
Qy 287 oAspPheSerLysAspAsnSerLysProGluValProValArgGlyThrAlaAlaPheTy 307
Db 721 AGACTTCTCCAGGACACACAGCCAGAGAGTGCAGTTCAGAGTACAGAGCTTTTA 780
Qy 307 rHisLeuProAlaAlaSerGlyCysLys 317
Db 781 CCATCATCTCCAGCTGCGAGTGGTGCAAA 811

RESULT 13

BG205510 764 bp mRNA linear EST 21-APR-2001
LOCUS RST24889 Athersys RAGE Library Homo sapiens cdna, mRNA sequence.

DEFINITION BG205510

ACCESSION BG205510.1 GI:13727148

VERSION EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 764)

Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R.,

Cain, S., Leventhal, C., Thornton, M., Ramchandran, R.,

Whittington, J., Lerner, L., Costanzo, D., McElligott, K., Booser, S.,

Mays, R., Smith, E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K.,

Offenbacher, J., Danzig, J. and Ducar, M.

Creation of genome-wide protein expression libraries using random

activation of gene expression

Nat. Biotechnol. 19 (5), 440-445 (2001)

21227151

11329013

Contact: Scott J. Cain

Athersys, Inc.

3201 Carnegie Ave, Cleveland, OH 44115, USA

Tel: 216 431 9900

Fax: 216 361 9596

Email: scain@atersys.com

High quality sequence stop: 551.

Location/Qualifiers

1. 764

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/cell_line="HT1080"

/clone_lib="Athersys RAGE Library"

/note="See 'Creation of Genome-wide Protein Expression

Libraries using Random Activation of Gene Expression',

Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."

ORIGIN

Alignment Scores:
Pred. No.: 1.86e-221 Length: 764
Score: 235.00 Matches: 235
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 62.33% Indels: 0
DB: 4 Gaps: 0

US-09-736-250-1 (1-377) x BG205510 (1-764)

Qy 39 AsnValSerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTrpGln 58
Db 3 ANTGTTCCTCATCCAGAGAGATGAAGTAATTCATGGCTGGCCAAACTCAAGTACCA 62
Qy 59 PheAsnLeuTyProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAla 78
Db 63 TTCAACCTTTACCAGAAACATTTGCTCTGGTAGCAGTCTTTTGGATAGGTTTTAGCT 122
Qy 79 ThrValLysAlaHisProLysTyLeuSerCysIleAlaIleSerCysPhePheLeuAla 98
Db 123 ACCGTAAAGGCTCATCCAAATATCTGAGTTGTAATTCGAATCAGCTGTTTTCTTAGCT 182
Qy 99 AlalysThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSer 118
Db 183 GCCAAGACTGTTGAGGAAGATGAGAGATTCAGTGTCTAAAGTATTGGCAGAGACAGT 242
Qy 119 PheCysGlyCysSerSerSerGluIleLeuArgMetGluArgIleLeuLeuAspLysLeu 138
Db 243 TTCTGTGATGTTCTCTCATCTGAAATTTTGAATGAGAGAAATTTTCTGATAAGTTG 302
Qy 139 AsnTrpAspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAla 158
Db 303 AATTGGGATCTTCACAGCCACACCACTTGGATTTCTTCATATTTTCCATGTCATGCA 362
Qy 159 ValSerThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeu 178
Db 363 GTGTCACTAGGCTCAGTTACTTTTCAGTTTGGCCAAATGAGCCCATCTCAACATTTG 422
Qy 179 AlaValLeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArg 198
Db 423 GCAGTCTCTTACCAAGCAACTTCTCAGTGTATGGCTGCAACCAACTTCTGCAATTCAGA 482
Qy 199 GlySerMetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrp 218
Db 483 GGATCCCATGCTTGCTCTGGCCATGGTTAGTCTGGAAATGGAGAAACTCATTCCTGATTGG 542
Qy 219 LeuSerLeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHis 238
Db 543 CTTTCTCTTACATTTGAATGCTTTCAGAAAGCAGATGATAGTCTCCAGTTGATCCAT 602
Qy 239 CysArgGluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSer 258
Db 603 TGTGGGAGCTTGTGGCACATCACCTTTCTACTCTGAGTCTTCCCTGCTCTGAAATTC 662
Qy 259 ValTrpValTrpArgProLeuLysHisThrLeuValThrCysAsp 273
Db 663 GTTTATGCTACCGTCCCTCAAGCACACCCCTGGTGTGAC 707

RESULT 14

BG189523

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

BG189523 767 bp mRNA linear EST 21-APR-2001

RST8568 Athersys RAGE Library Homo sapiens cdna, mRNA sequence.

BG189523

BG189523.1 GI:13711210

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

1 (bases 1 to 767)
Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R., Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J., Lerner, L., Costanzo, D., McElligott, K., Booser, S., Mays, R., Smith, E., Veloso, N., Klika, A., Hess, U., Cothren, K., Lo, K., Offenbacher, J., Danzig, J. and Ducar, M.
Creation of genome-wide protein expression libraries using random activation of gene expression

Nat. Biotechnol. 19 (5), 440-445 (2001)
21227151
11329013
Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@athersys.com
High quality sequence stop: 550.
Location/Qualifiers
1..767
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_line="HT1080"
/clone_lib="Athersys RAGE Library"
/notes="See 'Creation of Genome-wide Protein Expression' Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."

ORIGIN

Alignment Scores:
Pred. No.: 1,86e-221 Length: 767
Score: 235.00 Matches: 235
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 62.33% Indels: 0
DB: 4 Gaps: 0

US-09-736-250-1 (1-377) x BG189523 (1-767)

QY 39 AsnValSerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGln 58
Db 3 AATGTTTCTCCATCCCGAGAGATGAAGTAATTCATGGCTGGCCAACTCAAGTACCA 62
QY 59 PheAsnLeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAla 78
Db 63 TTCACGCTTTACCAGAGAAACATTTGCTCTGGCTAGCAGTCTTTTGGATAGGTTTTAGCT 122
QY 79 ThrValLysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAla 98
Db 123 ACCGTAAGGCTCATCCAAATACTTGAGTTGATGCAATCAGCTGTTTTTCCTAGCT 182
QY 99 AlaLysThrValGluAspGluArgIleProValLeuLysValLeuAlaArgAspSer 118
Db 183 GCCAAGACTGTTGAGGAAGATGAGAGAAATCCAGTACTAAAGCTATTGGCAAGACAGT 242
QY 119 PheCysGlyCysSerSerGluIleLeuArgMetGluArgIleIleLeuAspLysLeu 138
Db 243 TTTCTGTGGATGTTTCCCTCATCTGAAATTTTGAGAAATGGAGAGAAATATTCTCGGATAAGTTG 302
QY 139 AsnTrpAspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAla 158
Db 303 AATTGGGATCTTCACACAGCCACACCATTTGGATTTCTTCATATTTCCATGCCATTGCA 362
QY 159 ValSerThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeu 178
Db 363 GTGTCAACTAGGCGCTCAGTTACTTTTCAGTTTGCCTCCCAATTTGAGCCCATCTCAACATTG 422

```
Qy 108 IleProValLeuLysValLeuAlaArgAspSerPheCysGlyCysSerSerSerGluIle 127
Db |||||
7 ATTCAGTACTAAAGGATTGCGAAGACAGAGTTTCTGTGGATGTTCTCATCTGAAATT 66
Qy 128 LeuArgMetGluArgIleLeuAspLysLeuAsnTrpAspLeuHisThrAlaThrPro 147
Db |||||
67 TTGAGATGGAGAGAAATTAATCTCGATAAGTTGAATTGGGATCTTCACACAGCCACACCA 126
Qy 148 LeuAspPheLeuHisIlePheHisAlaIleAlaValSerThrArgProGlnLeuLeuPhe 167
Db |||||
127 TTGGATTTCCTTCATATTTCCATGGCCATTGCAGTGTCAACTAGGCCTCAGTTACTTTTC 186
Qy 168 SerLeuProLysLeuSerProSerGlnHisLeuAlaValLeuThrLysGlnLeuLeuHis 187
Db |||||
187 AGTTTGCCCAAAATTGAGCCCATCTCAACATTTGGCAGTCTTACCAAGCAACTACTTCAC 246
Qy 188 CysMetAlaCysAenGlnLeuLeuGlnPheArgGlySerMetLeuAlaLeuAlaMetVal 207
Db |||||
247 TGTATGGCCTGCAACCAACTTCTGCAATTGAGAGATCCATGCTGTGCTCTGGCCATGGTT 306
Qy 208 SerLeuGluMetGluLysLeuIleProAspTrpLeuSerLeuThrIleGluLeuLeuGln 227
Db |||||
307 AGTCTGGAATGGAGAACTCATTCCTGATTGGCTTCTTACAAATTGAATGACTGCTTCAG 366
Qy 228 LysAlaGlnMetAspSerSerGlnLeuIleHisCysArgGluLeuValAlaHisHisLeu 247
Db |||||
367 AAAGCACAGATGGATAGTCCAGTTGATCCATTGTGGAGCTTGTGGCACATCACCTT 426
Qy 248 SerThrLeuGlnSerSerLeuProLeuAsnSerValTyrValTyrArgProLeuLysHis 267
Db |||||
427 TCTACTCTGCAGTCTCTCCCTGCCCTTGAAATTCGGTTATGTCTACCGTCCCTCAAGCAC 486
Qy 268 ThrLeuValThrCysAspLysGlyValPheArgLeuHisProSerSerValProGlyPro 287
Db |||||
487 ACCCTGGTGACTGTGACAAAGGAGTGTTCAGATTACATCCCTCTCTGTCCAGGCCCA 546
Qy 288 AspPheSerLysAspAsnSerLysProGluValProValArgGlyThrAlaAlaPheTyr 307
Db |||||
547 GACTTCTCCAAGGACAAACAGCAAGCCAGAGTGCAGTCCAGGTACAGCAGCCTTTTAC 606
Qy 308 HisHisLeuProAlaAlaSerGlyCysLysGlnThrSerThrLysArgLysValGluGlu 327
Db |||||
607 CATCATCTCCAGCTGCCAGTGGGTGCAAGCAGACCTCTACTAAACGCAAGTAGAGGAA 666
Qy 328 MetGluValAspPheTyrAspGlyIleLysArgLeuTyrAsn 342
Db |||||
667 ATGGAAGTGGATGACTTCTATGATGAATCAACGGCTCTATAT 711
```

Search completed: February 11, 2005, 12:21:04
Job time : 6017.84 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 11, 2005, 07:56:46 ; Search time 7689.45 Seconds
(without alignments)
2375.673 Million cell updates/sec

Title: US-09-736-250-1
Perfect score: 377
Sequence: 1 MKFPGLNQLSLLEKAI.....LSRQGHASCPPLQPVSM 377

Scoring table:
OLIGO Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Word size: 1

Total number of hits satisfying chosen parameters: 9408497

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlh
-Q=/cgn2.1/usPTO.apool/US09736250/runat.07022005.154942.20650/app.query.fasta.1.718
-DB=GenEmbl -QWMT=fastap -SUFFIX=oligo.rge -MINMATCH=0.1 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi -LIST=1000
-DOCALIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09736250 @CGN 1 1 3890 @runat.07022005.154942.20650 -NCPU=6 -ICPU=3
-NO.MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

GenEmbl.*
1: gb.ba.*
2: gb.htg.*
3: gb.in.*
4: gb.om.*
5: gb.ov.*
6: gb.pat.*
7: gb.ph.*
8: gb.pl.*
9: gb.pr.*
10: gb.ro.*
11: gb.sts.*
12: gb.sv.*
13: gb.un.*
14: gb.vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	377	100.0	1133	6	AR145734 Sequence
2	377	100.0	1260	6	AR087353 Sequence
3	377	100.0	1260	6	CQ812312 Sequence
4	377	100.0	1260	6	AR281918 Sequence

5	377	100.0	1260	6	AR380354 Sequence
6	377	100.0	1260	9	HUMCYI
7	377	100.0	1384	9	AF135162
8	377	100.0	1817	9	BC000420 Homo sapi
9	377	100.0	1889	6	CQ468129 Sequence
10	377	100.0	1889	9	BC004975 Homo sapi
11	266	70.6	2755	6	CQ414515 Sequence
12	240	63.7	1131	9	CR541783 Homo sapi
13	230	61.0	690	6	CQ721727 Sequence
14	149	39.5	29867	9	AY207372 Homo sapi
15	149	39.5	35191	9	AC111196 Homo sapi
16	149	39.5	178916	2	AF002874 Homo sapi
17	149	39.5	179443	2	AC079051 Homo sapi
18	144	38.2	444	6	AX886044 Sequence
19	144	38.2	444	6	BD025654 Sequence
20	133	36.9	444	6	CQ671106 Sequence
21	133	35.3	490	6	CQ685286 Sequence
22	129	34.2	804	6	BD079737 Cancer-as
23	126	33.4	601	11	BV180201 sqnm10841
24	123	32.6	2146	6	CQ414223 Sequence
25	118	31.3	389	6	CQ661908 Sequence
26	112	29.7	369	6	CQ688465 Sequence
27	99	26.3	601	11	BV167473 sqnm5620
28	90	23.9	536	6	AX780652 Sequence
29	90	23.9	1535	10	AF005886 Mus muscu
30	90	23.9	2348	10	BC003290 Mus muscu
31	88	23.3	1493	6	BD194541 Human nuc
32	88	23.3	1493	6	AX015395 Sequence
33	84	22.3	409	6	AX779269 Sequence
34	77	20.4	350	6	CQ675890 Sequence
35	75	19.9	486	6	CQ410226 Sequence
36	65	17.2	447	6	AX198885 Sequence
37	65	17.2	447	6	AX209412 Sequence
38	62	16.4	889	6	CQ468128 Sequence
39	50	13.3	200850	2	AC101881 Mus muscu
40	50	13.3	202228	2	AC124646 Mus muscu
41	49	13.0	426	6	CQ397543 Sequence
42	49	13.0	426	6	CQ403842 Sequence
43	47	12.5	590	11	G51451 SHGC-80948
44	46	12.2	11793	10	AF228739S2
45	46	12.2	193811	2	AC134827 Mus muscu
46	46	12.2	241543	2	AC099472 Rattus no
47	46	12.2	260517	2	AC111318 Rattus no
48	46	12.2	270068	2	AC113213 Rattus no
49	43	11.4	145795	2	AC022548 Homo sapi
50	43	11.4	145795	9	AC104771 Homo sapi
51	41	10.9	288	6	CQ712652 Sequence
52	40	10.6	477	6	CQ398303 Sequence
53	40	10.6	477	6	CQ404590 Sequence
54	40	10.6	516	6	CQ410974 Sequence
55	38	10.1	136	6	A74835 Sequence 52
56	38	10.1	136	6	A77814 Sequence 52
57	37	9.8	444	6	AX397198 Sequence
58	36	9.5	179333	2	AC117658 Mus muscu
59	34	9.0	304	6	AX914031 Sequence
60	34	9.0	304	6	BD049564 Sequence
61	34	9.0	308	6	CQ696855 Sequence
62	29	7.7	1553	5	BC075116 Xenopus t
63	29	7.7	1658	5	BC061670 Xenopus l
64	25	6.6	368	11	G53823 SHGC-85345
65	24	6.4	244	6	CQ713942 Sequence
66	22	5.8	183	6	A74629 Sequence 31
67	22	5.8	183	6	A77608 Sequence 31
68	21	5.6	818	5	BX930648 Gallus ga
69	20	5.3	200	6	CQ660642 Sequence
70	19	5.0	60	6	CQ543223 Sequence
71	15	4.0	251	6	CQ689968 Sequence
72	14	3.7	65	6	CQ558861 Sequence
73	13	3.4	135	6	A74630 Sequence 31
74	13	3.4	135	6	A77609 Sequence 31
75	13	3.4	790	5	BX930233 Gallus ga
76	13	3.4	1850	5	BX950469 Gallus ga
77	13	3.4	2166	5	BC044400 Danio rer

78	13	3.4	2339	5	BC068369	BC068369	Danio rer	151	9	2.4	228736	2	AC097228	AC097228	Pan trogl
79	13	3.4	15161	10	AF228739	Mus muscu	152	9	2.4	229252	2	AC096043	AC096043	Rattus no	
80	12	3.2	183	6	C0704042	Sequence	153	9	2.4	231580	2	AC136817	AC136817	Rattus no	
81	10	2.7	227524	2	AC126180	Rattus no	154	9	2.4	236974	2	AC095207	AC095207	Rattus no	
82	10	2.7	23219	2	AC136572	Rattus no	155	9	2.4	240797	2	AC098388	AC098388	Rattus no	
83	9	2.4	756	8	AY050319	Arabidops	156	9	2.4	244637	2	AC109053	AC109053	Rattus no	
84	9	2.4	1608	8	AF139807	Dolichos	157	9	2.4	247119	2	AC126868	AC126868	Rattus no	
85	9	2.4	1643	6	AR237858	Sequence	158	9	2.4	249490	2	AC126561	AC126561	Rattus no	
86	9	2.4	2215	8	AY340621	Aspergill	159	9	2.4	252988	2	AC121550	AC121550	Mus muscu	
87	9	2.4	3023	10	AF207742	Mus muscu	160	9	2.4	257451	2	AC098508	AC098508	Rattus no	
88	9	2.4	6265	6	AR237859	Sequence	161	9	2.4	259629	2	AC119553	AC119553	Rattus no	
89	9	2.4	7006	14	AF296094	Porcine t	162	9	2.4	275688	2	AC111722	AC111722	Rattus no	
90	9	2.4	7008	14	AF296100	Porcine t	163	9	2.4	279908	2	AC151281	AC151281	Mus muscu	
91	9	2.4	7018	14	AF296117	Porcine t	164	9	2.4	296820	10	AF312033	AF312033	Mus muscu	
92	9	2.4	7019	14	AF296109	Porcine t	165	9	2.4	300312	2	AC111822	AC111822	Rattus no	
93	9	2.4	18544	2	AC020199	Drosophil	166	9	2.4	301136	3	AE003591	AE003591	Drosophil	
94	9	2.4	24389	6	C0612992	Sequence	167	9	2.4	335551	2	AC115496	AC115496	Rattus no	
95	9	2.4	37144	1	MICB2492	Z98756	168	9	2.4	348950	1	MLEPRTN7	MLEPRTN7	Mycobacte	
96	9	2.4	74613	8	AB005230	Arabidops	169	8	2.1	236	8	ATH521114	ATH521114	Arabidops	
97	9	2.4	83178	2	AC117537	Magnaport	170	8	2.1	277	6	AR244739	AR244739	Sequence	
98	9	2.4	98546	2	AC149146	Xenopus t	171	8	2.1	279	6	AX916767	AX916767	Sequence	
99	9	2.4	99708	2	AC149531	Xenopus t	172	8	2.1	279	6	BD052300	BD052300	Sequence	
100	9	2.4	101981	9	AC003001	Homo sapi	173	8	2.1	282	8	AY233739	AY233739	Clavispor	
101	9	2.4	104002	9	HS388N15	Z99571	174	8	2.1	324	11	G60347	G60347	SHGC-150259	
102	9	2.4	110000	2	AC130075	Continuation (3 of	175	8	2.1	324	11	HSA065YD5	HSA065YD5	H.sapiens (
103	9	2.4	114279	2	AC083907	Homo sapi	176	8	2.1	367	11	BV105444	BV105444	MARC 2148	
104	9	2.4	130260	2	AC083907	Mus muscu	177	8	2.1	377	11	BV128386	BV128386	PZA00411	
105	9	2.4	138761	2	CR790366	Danio rer	178	8	2.1	382	6	AR521433	AR521433	Sequence	
106	9	2.4	142189	2	AC148072	Daelypus n	179	8	2.1	400	6	AR355411	AR355411	Sequence	
107	9	2.4	142948	9	AC147025	Pan trogl	180	8	2.1	400	6	AR536967	AR536967	Sequence	
108	9	2.4	146813	2	BX927104	Danio rer	181	8	2.1	400	11	BV128405	BV128405	PZA00411	
109	9	2.4	149461	2	AC019282	Homo sapi	182	8	2.1	403	11	BV128385	BV128385	PZA00411	
110	9	2.4	157410	2	AC021341	Homo sapi	183	8	2.1	407	11	BV128397	BV128397	PZA00411	
111	9	2.4	157657	2	AL353742	Human DNA	184	8	2.1	408	11	BV128395	BV128395	PZA00411	
112	9	2.4	160972	2	AC011673	Homo sapi	185	8	2.1	411	11	BV128398	BV128398	PZA00411	
113	9	2.4	163382	6	C0869778	Sequence	186	8	2.1	412	11	BV128382	BV128382	PZA00411	
114	9	2.4	164183	9	AC079233	Homo sapi	187	8	2.1	413	8	AY656922	AY656922	Unculture	
115	9	2.4	164434	2	AC009841	Drosophil	188	8	2.1	418	11	BV128389	BV128389	PZA00411	
116	9	2.4	164457	8	AC013850	Medicago	189	8	2.1	421	11	BV128383	BV128383	PZA00411	
117	9	2.4	167519	9	AC013727	Homo sapi	190	8	2.1	421	11	BV128404	BV128404	PZA00411	
118	9	2.4	168037	2	AC150211	Otolemur	191	8	2.1	422	11	BV128387	BV128387	PZA00411	
119	9	2.4	168176	2	AC121101	Mus muscu	192	8	2.1	424	11	BV128396	BV128396	PZA00411	
120	9	2.4	168414	2	AC106815	Homo sapi	193	8	2.1	424	11	BV128408	BV128408	PZA00411	
121	9	2.4	169118	2	AC073313	Homo sapi	194	8	2.1	424	11	BV128410	BV128410	PZA00411	
122	9	2.4	169405	9	AC092800	Homo sapi	195	8	2.1	428	11	BV128390	BV128390	PZA00411	
123	9	2.4	170552	2	AC139659	Rattus no	196	8	2.1	428	11	BV128406	BV128406	PZA00411	
124	9	2.4	171790	2	AC011106	Homo sapi	197	8	2.1	434	11	BV128411	BV128411	PZA00411	
125	9	2.4	174588	9	AC011841	Homo sapi	198	8	2.1	435	6	AX779282	AX779282	Sequence	
126	9	2.4	175645	9	AC073114	Homo sapi	199	8	2.1	435	11	BV128409	BV128409	PZA00411	
127	9	2.4	176446	9	AC142327	Pan trogl	200	8	2.1	437	11	BV128392	BV128392	PZA00411	
128	9	2.4	177855	9	AC013718	Homo sapi	201	8	2.1	438	11	BV128384	BV128384	PZA00411	
129	9	2.4	178965	3	AC010117	Drosophil	202	8	2.1	438	11	BV128399	BV128399	PZA00411	
130	9	2.4	182896	2	AC011043	Homo sapi	203	8	2.1	441	11	BV128388	BV128388	PZA00411	
131	9	2.4	184795	2	AC150640	Bos tauru	204	8	2.1	441	11	BV128394	BV128394	PZA00411	
132	9	2.4	184829	2	AC133506	Mus muscu	205	8	2.1	450	11	G37490	G37490	SHGC-57864	
133	9	2.4	186059	10	AC130826	Mus muscu	206	8	2.1	463	1	AY261408	AY261408	Unculture	
134	9	2.4	188901	2	AC132886	Mus muscu	207	8	2.1	493	8	AY190539	AY190539	Clavispor	
135	9	2.4	192510	10	AC121999	Mus muscu	208	8	2.1	494	8	AY190541	AY190541	Clavispor	
136	9	2.4	192919	10	AL732464	Mouse DNA	209	8	2.1	495	8	AJ786246	AJ786246	Clavispor	
137	9	2.4	198468	9	AC098477	Homo sapi	210	8	2.1	511	11	G73397	G73397	ATM, exon3 R	
138	9	2.4	198649	8	AY534123	Aegilops	211	8	2.1	512	6	AR503348	AR503348	Sequence	
139	9	2.4	200033	9	HSA21973	Homo sapi	212	8	2.1	512	6	AR518630	AR518630	Sequence	
140	9	2.4	201997	2	AC141220	Rattus no	213	8	2.1	517	8	CLU44817	CLU44817	Clavispora	
141	9	2.4	202914	2	AC078939	Homo sapi	214	8	2.1	558	11	G63060	SHGC-140653		
142	9	2.4	203100	9	AC145965	Pan trogl	215	8	2.1	599	11	BV054827	BV054827	S212P6038	
143	9	2.4	208840	2	CR318658	Danio rer	216	8	2.1	605	11	G85721	G85721	S209P6387RG	
144	9	2.4	209611	5	BX001058	Zebrafish	217	8	2.1	612	8	AY497690	AY497690	Clavispor	
145	9	2.4	209888	2	AC146462	Saimiri s	218	8	2.1	624	5	CR389084	CR389084	Gallus ga	
146	9	2.4	210148	10	AL928791	Mouse DNA	219	8	2.1	656	11	PM6C4B	PM6C4B	AL684917 Penicilli	
147	9	2.4	210336	2	AC128830	Rattus no	220	8	2.1	664	11	PM10G5B	PM10G5B	AL684055 Penicilli	
148	9	2.4	213776	2	AC126092	Rattus no	221	8	2.1	675	9	HS428112	HS428112	Homo sapi	
149	9	2.4	217080	10	AC110519	Mus muscu	222	8	2.1	681	11	PM6F10B	PM6F10B	AL684978 Penicilli	
150	9	2.4	218631	2	AC109532	Rattus no	223	8	2.1	737	9	HSRGL14	HSRGL14	AF186793 Homo sapi	

224	8	2.1	740	5	D14314	D14314 Gallus gall	297	8	2.1	1967	8	S81897	S81897 OsNramp1-Nr
225	8	2.1	773	8	AF362992	AF362992 Fucus ves	298	8	2.1	1987	8	R1CNRAMP	L41217 Oryza sativ
c 226	8	2.1	852	6	BD147371	BD147371 Primer fo	c 299	8	2.1	1989	8	CQ599940	CQ599940 Sequence
227	8	2.1	852	6	AX867309	AX867309 Sequence	c 300	8	2.1	1992	6	AX319765	AX319765 Sequence
228	8	2.1	879	6	CQ735521	CQ735521 Sequence	c 301	8	2.1	2000	6	AX654926	AX654926 Sequence
229	8	2.1	912	6	AX393979	AX393979 Sequence	c 302	8	2.1	2000	6	AX656434	AX656434 Sequence
230	8	2.1	912	6	AX366951	AX366951 Sequence	c 303	8	2.1	2001	6	BD193228	BD193228 Novel fam
231	8	2.1	915	1	AF503437	AF503437 Bacillus	c 304	8	2.1	2007	6	AX621706	AX621706 Sequence
232	8	2.1	915	1	AV084076	AV084076 Bacillus	c 305	8	2.1	2021	6	AX432742	AX432742 Sequence
233	8	2.1	921	11	BV05803	BV05803 BARC0051	c 306	8	2.1	2071	6	CQ842600	CQ842600 Sequence
c 234	8	2.1	1053	6	AR550723	AR550723 Sequence	c 307	8	2.1	2071	9	AK123972	AK123972 Homo sapi
c 235	8	2.1	1053	6	AX594468	AX594468 Sequence	c 308	8	2.1	2083	8	AK121534	AK121534 Oryza sat
c 236	8	2.1	1053	6	AX818588	AX818588 Sequence	c 309	8	2.1	2100	9	BC043385	BC043385 Homo sapi
c 237	8	2.1	1053	6	AX829618	AX829618 Sequence	c 310	8	2.1	2126	8	AB042550	AB042550 Oryza sat
c 238	8	2.1	1053	8	AX557694	AX557694 Saccharom	c 311	8	2.1	2136	5	BC053303	BC053303 Danio rer
c 239	8	2.1	1059	8	AF229410	AF229410 Brassica	c 312	8	2.1	2161	6	AX695726	AX695726 Sequence
c 240	8	2.1	1060	8	AF229412	AF229412 Brassica	c 313	8	2.1	2161	9	S57212	S57212 hMEF2C=MYOC
c 241	8	2.1	1069	8	AF229409	AF229409 Brassica	c 314	8	2.1	2165	6	AX339095	AX339095 Sequence
c 242	8	2.1	1070	8	AF229408	AF229408 Brassica	c 315	8	2.1	2187	6	AX346253	AX346253 Sequence
243	8	2.1	1073	5	GHWG2A	X63463 G.gallus HM	c 316	8	2.1	2218	8	AK066495	AK066495 Oryza sat
244	8	2.1	1089	6	AX339097	AX339097 Sequence	c 317	8	2.1	2248	8	D87042	D87042 Zea mays mR
245	8	2.1	1099	6	AX109688	AX109688 Sequence	c 318	8	2.1	2254	8	AK061881	AK061881 Oryza sat
246	8	2.1	1109	5	CR388627	CR388627 Gallus ga	c 319	8	2.1	2287	6	CQ841613	CQ841613 Sequence
247	8	2.1	1119	9	HUMG3FEFA	M69023 Homo sapien	c 320	8	2.1	2287	6	AK123255	AK123255 Homo sapi
c 248	8	2.1	1125	6	AR375643	AR375643 Sequence	c 321	8	2.1	2341	3	D86741	D86741 Caenorhabdi
249	8	2.1	1127	8	AF402076	AF402076 Zygosacch	c 322	8	2.1	2365	5	AY256908	AY256908 Danio rer
250	8	2.1	1127	8	AF402085	AF402085 Kluyverom	c 323	8	2.1	2390	5	AJ721043	AJ721043 Gallus ga
c 251	8	2.1	1174	5	GGU24675	U24675 Gallus gall	c 324	8	2.1	2420	5	AB096039	AB096039 Gallus ga
252	8	2.1	1176	6	AX339096	AX339096 Sequence	c 325	8	2.1	2431	3	D86740	D86740 Nematode mR
253	8	2.1	1231	6	AR505948	AR505948 Sequence	c 326	8	2.1	2450	9	HSSEC232	X97065 H.sapiens m
c 254	8	2.1	1233	6	AR451000	AR451000 Sequence	c 327	8	2.1	2451	6	CQ719441	CQ719441 Sequence
c 255	8	2.1	1245	10	AY288422	AY288422 Mus muscu	c 328	8	2.1	2464	9	AK027078	AK027078 Homo sapi
c 256	8	2.1	1245	10	AY633765	AY633765 Mus muscu	c 329	8	2.1	2498	9	BC042553	BC042553 Homo sapi
257	8	2.1	1252	5	AY423005	AY423005 Danio rer	c 330	8	2.1	2516	8	AB034803	AB034803 Pisum sat
258	8	2.1	1267	6	AR504358	AR504358 Sequence	c 331	8	2.1	2562	11	AF356180S2	AF356181 Hordeum v
259	8	2.1	1267	6	AR519640	AR519640 Sequence	c 332	8	2.1	2589	8	ATH296275	AJ296275 Arabidops
c 260	8	2.1	1315	5	CR352412	CR352412 Gallus ga	c 333	8	2.1	2602	9	BC052802	BC052802 Homo sapi
261	8	2.1	1320	9	HSM801208	AL122064 Homo sapi	c 334	8	2.1	2622	9	BC082968	BC082968 Homo sapi
c 262	8	2.1	1332	6	CQ604506	CQ604506 Sequence	c 335	8	2.1	2641	9	BSM808198	BX684052 Homo sapi
263	8	2.1	1338	6	CQ735120	CQ735120 Sequence	c 336	8	2.1	2655	8	POS430697	AJ430697 Pleurotus
264	8	2.1	1347	5	BC067660	BC067660 Danio rer	c 337	8	2.1	2658	1	AF087018	AF087018 Aetobact
265	8	2.1	1358	8	AK103557	AK103557 Oryza sat	c 338	8	2.1	2787	10	BC057212	BC057212 Mus muscu
c 266	8	2.1	1437	1	AF297010	AF297010 Pseudomon	c 339	8	2.1	2790	6	AR322399	AR322399 Sequence
c 267	8	2.1	1449	6	CQ745861	CQ745861 Sequence	c 340	8	2.1	2797	9	AK123396	AK123396 Homo sapi
c 268	8	2.1	1505	3	AY058667	AY058667 Drosophil	c 341	8	2.1	2800	6	AX832899	AX832899 Sequence
c 269	8	2.1	1510	8	BT015739	BT015739 Arabidops	c 342	8	2.1	2800	9	AK094119	AK094119 Homo sapi
c 270	8	2.1	1527	6	AR347066	AR347066 Sequence	c 343	8	2.1	2826	10	MMU23922	U23922 Mus musculu
c 271	8	2.1	1543	3	DROALDO	D10762 Drosophila	c 344	8	2.1	2833	10	BC003469	BC003469 Mus muscu
272	8	2.1	1550	6	CQ413710	CQ413710 Sequence	c 345	8	2.1	2881	5	AJ621377	AJ621377 Tetraodon
273	8	2.1	1566	8	AK110468	AK110468 Oryza sat	c 346	8	2.1	2882	8	AK067110	AK067110 Oryza sat
c 274	8	2.1	1621	3	AF035229	AF035229 Leishmani	c 347	8	2.1	2986	6	AX705334	AX705334 Sequence
c 275	8	2.1	1650	14	AY362031	AY362031 Ovine pro	c 348	8	2.1	3027	9	AB005590	AB005590 Homo sapi
c 276	8	2.1	1654	6	CQ585105	CQ585105 Sequence	c 349	8	2.1	3076	8	ENU07031	U07031 Emericella
c 277	8	2.1	1662	1	BSF010057	AJ010057 Burkholde	c 350	8	2.1	3079	8	D89010	D89010 Aspergillus
c 278	8	2.1	1699	6	BD156074	BD156074 Primer fo	c 351	8	2.1	3249	10	AF123388	AF123388 Mus muscu
c 279	8	2.1	1699	6	AX876334	AX876334 Sequence	c 352	8	2.1	3253	8	AB087620	AB087620 Aspergill
c 280	8	2.1	1700	9	AK001249	AK001249 Homo sapi	c 353	8	2.1	3272	8	AK110021	AK110021 Oryza sat
c 281	8	2.1	1705	10	RN113G2	X03914 Rattus norv	c 354	8	2.1	3275	6	CQ491966	CQ491966 Sequence
282	8	2.1	1711	6	AR258007	AR258007 Sequence	c 355	8	2.1	3394	6	CQ604505	CQ604505 Sequence
283	8	2.1	1711	6	AR282901	AR282901 Sequence	c 356	8	2.1	3407	9	AB022434	AB022434 Homo sapi
284	8	2.1	1711	6	AK401358	AK401358 Sequence	c 357	8	2.1	3426	5	AJ719795	AJ719795 Gallus ga
c 285	8	2.1	1715	6	BD136399	BD136399 95 human	c 358	8	2.1	3432	6	AX322398	AX322398 Sequence
c 286	8	2.1	1719	6	AX653531	AX653531 Sequence	c 359	8	2.1	3458	3	AY118518	AY118518 Drosophil
c 287	8	2.1	1771	6	AX780664	AX780664 Sequence	c 360	8	2.1	3486	6	CQ806568	CQ806568 Sequence
288	8	2.1	1776	3	U35251	U35251 Onchocerca	c 361	8	2.1	3486	6	AX598680	AX598680 Sequence
289	8	2.1	1790	9	AR055020	AR055020 Homo sapi	c 362	8	2.1	3486	6	AX767370	AX767370 Sequence
c 290	8	2.1	1828	6	AX056411	AX056411 Sequence	c 363	8	2.1	3486	6	AX795676	AX795676 Sequence
c 291	8	2.1	1857	8	D84408	D84408 Maize mRNA	c 364	8	2.1	3486	6	AX822125	AX822125 Sequence
292	8	2.1	1890	3	CEU35250	U35250 Caenorhabdi	c 365	8	2.1	3486	6	AX825765	AX825765 Sequence
293	8	2.1	1901	3	AY061150	AY061150 Drosophil	c 366	8	2.1	3560	10	AF016180	AF016180 Rattus no
c 294	8	2.1	1905	3	AX427440S3	AX427442 Leishmani	c 367	8	2.1	3568	6	AR148500	AR148500 Sequence
295	8	2.1	1907	6	BD260776	BD260776 50 human	c 368	8	2.1	3568	6	E26053	E26053 Human P27K1
296	8	2.1	1917	5	CR386254	CR386254 Gallus ga	c 369	8	2.1	3568	6	AR258001	AR258001 Sequence

370	8	2.1	3568	6	AR282895	Sequence	443	8	2.1	12342	9	AL592544	AL592544 Human DNA
371	8	2.1	3568	6	AR401352	Sequence	c 444	8	2.1	12759	1	AB011518	AB011518 Leptospir
372	8	2.1	3568	6	BD012114	Vitamin D	c 445	8	2.1	14559	1	AJ608775	AJ608775 Homo sapi
373	8	2.1	3571	9	AB003688	Homo sapi	c 446	8	2.1	14634	9	AJ608774	AJ608774 Homo sapi
374	8	2.1	3578	6	BD193189	Novel fam	c 447	8	2.1	14945	1	AE008240	AE008240 Agrobacte
375	8	2.1	3597	5	BC081135	Xenopus l	c 448	8	2.1	17000	6	AR560893	AR560893 Sequence
376	8	2.1	3688	14	AB064600	TT Virus	c 449	8	2.1	17000	6	AX685138	AX685138 Sequence
377	8	2.1	3706	6	C0587633	Sequence	c 450	8	2.1	17626	3	CEY43CSA	CEY43CSA Caenorhab
378	8	2.1	3706	9	AF339153	Homo sapi	c 451	8	2.1	17731	8	SC9877	SC9877 S. cerevisia
379	8	2.1	3730	9	AF339152	Homo sapi	c 452	8	2.1	17934	6	AX346620	AX346620 Sequence
380	8	2.1	3776	8	SCYOR113W	S. cerevisia	c 453	8	2.1	20089	8	SC8142B	SC8142B S. cerevisia
381	8	2.1	3819	6	BD160636	Primer fo	c 454	8	2.1	20741	1	AF372703	AF372703 Pseudomon
382	8	2.1	3819	6	AX883967	Sequence	c 455	8	2.1	21025	2	AC136162	AC136162 Rattus no
383	8	2.1	3819	9	AK024370	Homo sapi	c 456	8	2.1	21631	10	AB070523	AB070523 Mus muscu
384	8	2.1	3826	9	AF339154	Homo sapi	c 457	8	2.1	22143	5	AC151464	AC151464 Xenopus t
385	8	2.1	3875	3	DFU22357	Drosophila	c 458	8	2.1	22199	8	AB028619	AB028619 Arabidops
386	8	2.1	4080	1	CTU47637	Comamonas t	c 459	8	2.1	22923	2	AC020133	AC020133 Drosophil
387	8	2.1	4216	8	SCAZF1	S. cerevisia	c 460	8	2.1	23065	9	HUMATPSG	HUMATPSG Homo sapien
388	8	2.1	4284	6	C0849905	Sequence	c 461	8	2.1	23366	1	AE002311	AE002311 Chlamydia
389	8	2.1	4284	9	AK126972	Homo sapi	c 462	8	2.1	24681	2	AC149936	AC149936 Strongylo
390	8	2.1	4286	6	AR447980	Homo sapi	c 463	8	2.1	27037	9	AB009666	AB009666 Homo sapi
391	8	2.1	4407	5	AY072908	Gallus ga	c 464	8	2.1	27251	9	AX284661	AX284661 Human DNA
392	8	2.1	4641	1	AF378369	Staphyloc	c 465	8	2.1	30350	3	AF000194	AF000194 Caenorhab
393	8	2.1	4750	6	AX336647	Sequence	c 466	8	2.1	31587	2	AC149374	AC149374 Phakopsor
394	8	2.1	4750	9	H5U67092	Human ataxi	c 467	8	2.1	32110	3	CEFA0G12	CEFA0G12 Caenorhabdi
395	8	2.1	4832	7	AF212847	Lactococc	c 468	8	2.1	32126	3	CEY23F11	CEY23F11 Trypanoso
396	8	2.1	4902	6	C0600011	Sequence	c 469	8	2.1	32129	3	CEY23F11	CEY23F11 Caenorhabdi
397	8	2.1	5091	6	CQ580059	Sequence	c 470	8	2.1	32172	7	AF242738	AF242738 Bacteriop
398	8	2.1	5091	6	CQ847812	Sequence	c 471	8	2.1	32436	1	AB101202	AB101202 Acinetoba
399	8	2.1	5114	3	AY051698	Drosophil	c 472	8	2.1	32829	6	CQ870408	CQ870408 Sequence
400	8	2.1	5127	3	AF029395	Drosophil	c 473	8	2.1	34727	9	AL356586	AL356586 Human DNA
401	8	2.1	5261	9	AB058772	Homo sapi	c 474	8	2.1	35089	2	AC149323	AC149323 Phakopsor
402	8	2.1	5317	3	AB018796	Halocynth	c 475	8	2.1	35089	2	AC149323	AC149323 Phakopsor
403	8	2.1	5335	5	AY648832	Danio rer	c 476	8	2.1	35121	3	CEY10G8	CEY10G8 Caenorhabdi
404	8	2.1	5395	10	RATDRP	L20319 Rattus norv	c 477	8	2.1	35257	2	AC149339	AC149339 Phakopsor
405	8	2.1	5577	6	CQ720807	Sequence	c 478	8	2.1	35710	2	AC100510	AC100510 Mus muscu
406	8	2.1	5957	10	AB098163	Mus muscu	c 479	8	2.1	36000	3	DMC11F6	DMC11F6 Drosophil
407	8	2.1	6043	8	YGACDC25A	M94160 Candida alb	c 480	8	2.1	36075	3	AF025468	AF025468 Caenorhab
408	8	2.1	6201	6	C0590528	Sequence	c 481	8	2.1	36116	2	AC149332	AC149332 Phakopsor
409	8	2.1	6216	9	AB007936	Homo sapi	c 482	8	2.1	36808	2	CEH36F17	CEH36F17 Caenorhabdi
410	8	2.1	6343	10	MWBOX35	X63507 M. musculus	c 483	8	2.1	36972	6	AX059504	AX059504 Sequence
411	8	2.1	6669	6	AR453029	Sequence	c 484	8	2.1	37059	6	AX059523	AX059523 Sequence
412	8	2.1	6669	6	AX281141	Sequence	c 485	8	2.1	37247	9	AP000545	AP000545 Homo sapi
413	8	2.1	6669	6	AX345095	Sequence	c 486	8	2.1	37350	9	AC126392	AC126392 Homo sapi
414	8	2.1	6669	6	AX356372	Sequence	c 487	8	2.1	37445	3	U51998	U51998 Caenorhabdi
415	8	2.1	6858	3	AF243382	Drosophil	c 488	8	2.1	37938	5	AF110982	AF110982 Gallus ga
416	8	2.1	6883	7	INIKE	X02139 Bacterioph	c 489	8	2.1	38941	2	AC149346	AC149346 Phakopsor
417	8	2.1	6941	9	HS118D241	ALI62331 Novel hum	c 490	8	2.1	39000	2	HSN86D4	HSN86D4 Human DNA s
418	8	2.1	7286	1	AY077638	AY077638 Moraxella	c 491	8	2.1	39011	2	AC036140	AC036140 Homo sapi
419	8	2.1	8066	7	AF212846	AF212846 Lactococc	c 492	8	2.1	39490	3	LMFL2954	LMFL2954 Leishmani
420	8	2.1	8285	6	AR217828	Sequence	c 493	8	2.1	39651	2	AC014131	AC014131 Drosophil
421	8	2.1	8285	6	AX787071	Sequence	c 494	8	2.1	39827	8	SC8142A	SC8142A S. cerevisia
422	8	2.1	8541	6	CQ580058	Sequence	c 495	8	2.1	40181	9	AL645699	AL645699 Human DNA
423	8	2.1	8552	1	AF212844	AF212844 Lactococc	c 496	8	2.1	42416	9	AC005551	AC005551 Homo sapi
424	8	2.1	8850	8	AB026637	AB026637 Arabidops	c 497	8	2.1	44028	2	AC107035	AC107035 Pan trogl
425	8	2.1	9224	3	DNALD	X60064 D. melanogas	c 498	8	2.1	44059	9	AL669815	AL669815 Human DNA
426	8	2.1	9299	6	AX346626	Sequence	c 499	8	2.1	46120	9	AL691473	AL691473 Human DNA
427	8	2.1	9352	6	AX345005	Sequence	c 500	8	2.1	48265	9	AC000388	AC000388 Genomic s
428	8	2.1	9905	6	CQ612461	Sequence	c 501	8	2.1	49507	2	AC129982	AC129982 Mus muscu
429	8	2.1	9922	7	AF208055	AF208055 Bacteriop	c 502	8	2.1	50587	3	DMBH48C10	DMBH48C10 Drosophil
430	8	2.1	10038	14	AF414119	AF414119 Pineapple	c 503	8	2.1	50984	8	SCXVORFS	SCXVORFS S. cerevisia
431	8	2.1	10224	1	AX112722	AX112722 Bifidobac	c 504	8	2.1	51253	9	BX005132	BX005132 Human DNA
432	8	2.1	10274	6	CQ579254	Sequence	c 505	8	2.1	52498	2	AC104583	AC104583 Homo sapi
433	8	2.1	10393	1	AE011957	AE011957 Xanthomon	c 506	8	2.1	54016	5	AL845303	AL845303 Zebrafish
434	8	2.1	10853	1	AE005749	AE005749 Caulobact	c 507	8	2.1	54762	2	AC130294	AC130294 Homo sapi
435	8	2.1	10920	6	AX406005	Sequence	c 508	8	2.1	55996	6	AX695632	AX695632 Sequence
436	8	2.1	10942	6	CQ613889	Sequence	c 509	8	2.1	56943	9	AL391063	AL391063 Human DNA
437	8	2.1	10969	9	AB007922	Homo sapi	c 510	8	2.1	57199	2	AC135985	AC135985 Homo sapi
438	8	2.1	11043	1	AE007739	Clostridi	c 511	8	2.1	57839	2	AC106021	AC106021 Homo sapi
439	8	2.1	11164	1	AE009374	Agrobacte	c 512	8	2.1	57930	9	AL445705	AL445705 Human DNA
440	8	2.1	11259	1	AE014666	Bifidobac	c 513	8	2.1	58063	2	AP005496	AP005496 Continuation (9 of
441	8	2.1	11827	6	AX709316	Sequence	c 514	8	2.1	58071	5	AC147818	AC147818 Xenopus t
442	8	2.1	12099	6	CQ594818	Sequence	c 515	8	2.1	58949	2	BX649482	Continuation (4 of

516	8	2.1	5369	2	AC115765	AC115765 Mus muscu	C 589	8	2.1	88736	9	AC010420	AC010420 Homo sapi
517	8	2.1	5920	2	AC014068	AC014068 Drosophi	C 590	8	2.1	88848	8	T24H24	AF007598 Arabidops
518	8	2.1	5920	10	AL929107	AL929107 Mouse DNA	C 591	8	2.1	89134	2	AP004162	AF004162 Oryza sat
519	8	2.1	59888	2	AC011588	AC011588 Homo sapi	C 592	8	2.1	89652	5	BX324196	BX324196 Zebrafish
520	8	2.1	60014	2	AC131267	AC131267 Homo sapi	C 593	8	2.1	89677	9	AC026704	AC026704 Homo sapi
521	8	2.1	60573	2	AC018267	AC018267 Drosophi	C 594	8	2.1	90551	10	AL928543	AL928543 Mouse DNA
522	8	2.1	60661	2	AC120009	AC120009 Mus muscu	C 595	8	2.1	90601	9	AC087308	AC087308 Homo sapi
523	8	2.1	61712	10	AL929227	AL929227 Mouse DNA	C 596	8	2.1	91433	3	AC087074	AC087074 Caenorhab
524	8	2.1	61923	9	AC108139	AC108139 Homo sapi	C 597	8	2.1	91506	9	AL354761	AL354761 Human DNA
525	8	2.1	62067	2	AC120018	AC120018 Mus muscu	C 598	8	2.1	92118	9	AC074384	AC074384 Homo sapi
526	8	2.1	62067	2	AC120018	AC120018 Mus muscu	C 599	8	2.1	92154	5	BX248320	BX248320 Zebrafish
527	8	2.1	62309	8	NCB11C21	BX294022 Neurospor	C 600	8	2.1	92675	8	AP006402	AP006402 Lotus cor
528	8	2.1	62536	9	AC005692	AC005692 Homo sapi	C 601	8	2.1	93724	8	AC007592	AC007592 Genomic s
529	8	2.1	62768	2	AC017293	AC017293 Drosophi	C 602	8	2.1	94000	9	AP000562	AP000562 Homo sapi
530	8	2.1	63726	9	AC002071	AC002071 Human PAC	C 603	8	2.1	94696	2	AC142647	AC142647 Macaca mu
531	8	2.1	63748	8	AP000604	AP000604 Arabidops	C 604	8	2.1	96592	6	AX695713	AX695713 Sequence
532	8	2.1	63788	2	AC136707	AC136707 Mus muscu	C 605	8	2.1	98209	9	HS26079	HS26079 Human DNA
533	8	2.1	63788	2	AC136707	AC136707 Mus muscu	C 606	8	2.1	98232	9	AC012271	AC012271 Homo sapi
534	8	2.1	63788	2	AC136707	AC136707 Mus muscu	C 607	8	2.1	98532	8	AP006120	AP006120 Lotus cor
535	8	2.1	63788	2	AC136707	AC136707 Mus muscu	C 608	8	2.1	98864	9	HS460D19	HS460D19 Human DNA
536	8	2.1	63788	2	AC136707	AC136707 Mus muscu	C 609	8	2.1	99241	9	AC079030	AC079030 Homo sapi
537	8	2.1	63788	2	AC136707	AC136707 Mus muscu	C 610	8	2.1	99497	9	HS2931L6	HS2931L6 Human DNA
538	8	2.1	63788	2	AC136707	AC136707 Mus muscu	C 611	8	2.1	100000	9	AP000201	AP000201 Homo sapi
539	8	2.1	63788	2	AC136707	AC136707 Mus muscu	C 612	8	2.1	100102	10	AL954135	AL954135 Mouse DNA
540	8	2.1	63788	2	AC136707	AC136707 Mus muscu	C 613	8	2.1	100678	8	ATT18D12	ATT18D12 Arabidops
541	8	2.1	63788	2	AC136707	AC136707 Mus muscu	C 614	8	2.1	101230	9	HSBA517H2	HSBA517H2 Human DNA
542	8	2.1	63788	2	AC136707	AC136707 Mus muscu	C 615	8	2.1	101728	9	HS1090E8	HS1090E8 Human DNA
543	8	2.1	63788	2	AC136707	AC136707 Mus muscu	C 616	8	2.1	102138	5	BX510351	BX510351 Zebrafish
544	8	2.1	63788	2	AC136707	AC136707 Mus muscu	C 617	8	2.1	102205	2	AC141074	AC141074 Homo sapi
545	8	2.1	63788	2	AC136707	AC136707 Mus muscu	C 618	8	2.1	103129	2	AC136286	AC136286 Medicago
546	8	2.1	63788	2	AC136707	AC136707 Mus muscu	C 619	8	2.1	103260	10	AL713995	AL713995 Mouse DNA
547	8	2.1	63788	2	AC136707	AC136707 Mus muscu	C 620	8	2.1	104269	9	AC016596	AC016596 Homo sapi
548	8	2.1	63788	2	AC136707	AC136707 Mus muscu	C 621	8	2.1	104762	2	AC108086	AC108086 Homo sapi
549	8	2.1	63788	2	AC136707	AC136707 Mus muscu	C 622	8	2.1	104889	2	AC141292	AC141292 Homo sapi
550	8	2.1	63788	2	AC136707	AC136707 Mus muscu	C 623	8	2.1	105410	9	AC118650	AC118650 Homo sapi
551	8	2.1	63788	2	AC136707	AC136707 Mus muscu	C 624	8	2.1	105692	2	AP003953	AP003953 Oryza sat
552	8	2.1	63788	2	AC136707	AC136707 Mus muscu	C 625	8	2.1	105866	2	AC021602	AC021602 Homo sapi
553	8	2.1	63788	2	AC136707	AC136707 Mus muscu	C 626	8	2.1	105960	9	HS209A6	HS209A6 Human DNA
554	8	2.1	63788	2	AC136707	AC136707 Mus muscu	C 627	8	2.1	105962	9	AP000439	AP000439 Homo sapi
555	8	2.1	63788	2	AC136707	AC136707 Mus muscu	C 628	8	2.1	106115	2	AC114879	AC114879 Rattus no
556	8	2.1	63788	2	AC136707	AC136707 Mus muscu	C 629	8	2.1	106449	9	AC096949	AC096949 Homo sapi
557	8	2.1	63788	2	AC136707	AC136707 Mus muscu	C 630	8	2.1	106716	8	AC006413	AC006413 Arabidops
558	8	2.1	63788	2	AC136707	AC136707 Mus muscu	C 631	8	2.1	107135	9	HS145B12	HS145B12 Human DNA
559	8	2.1	63788	2	AC136707	AC136707 Mus muscu	C 632	8	2.1	107318	9	AC105226	AC105226 Homo sapi
560	8	2.1	63788	2	AC136707	AC136707 Mus muscu	C 633	8	2.1	107898	9	AF124731	AF124731 Homo sapi
561	8	2.1	63788	2	AC136707	AC136707 Mus muscu	C 634	8	2.1	108022	9	AC008857	AC008857 Homo sapi
562	8	2.1	63788	2	AC136707	AC136707 Mus muscu	C 635	8	2.1	108531	2	AC145164	AC145164 Medicago
563	8	2.1	63788	2	AC136707	AC136707 Mus muscu	C 636	8	2.1	108644	2	AC135320	AC135320 Medicago
564	8	2.1	63788	2	AC136707	AC136707 Mus muscu	C 637	8	2.1	108834	3	AC130389	AC130389 Drosophi
565	8	2.1	63788	2	AC136707	AC136707 Mus muscu	C 638	8	2.1	109149	2	AP000681	AP000681 Homo sapi
566	8	2.1	63788	2	AC136707	AC136707 Mus muscu	C 639	8	2.1	109431	8	AC035249	AC035249 Arabidops
567	8	2.1	63788	2	AC136707	AC136707 Mus muscu	C 640	8	2.1	109485	9	AC008395	AC008395 Homo sapi
568	8	2.1	63788	2	AC136707	AC136707 Mus muscu	C 641	8	2.1	110000	1	AE017180	AE017180 Rattus no
569	8	2.1	63788	2	AC136707	AC136707 Mus muscu	C 642	8	2.1	110000	1	AE017225	AE017225 Oryza sat
570	8	2.1	63788	2	AC136707	AC136707 Mus muscu	C 643	8	2.1	110000	1	AE017261	AE017261 Oryza sat
571	8	2.1	63788	2	AC136707	AC136707 Mus muscu	C 644	8	2.1	110000	1	AE017333	AE017333 Oryza sat
572	8	2.1	63788	2	AC136707	AC136707 Mus muscu	C 645	8	2.1	110000	1	AE017334	AE017334 Oryza sat
573	8	2.1	63788	2	AC136707	AC136707 Mus muscu	C 646	8	2.1	110000	1	AE017355	AE017355 Oryza sat
574	8	2.1	63788	2	AC136707	AC136707 Mus muscu	C 647	8	2.1	110000	1	AP006618	AP006618 Medicago
575	8	2.1	63788	2	AC136707	AC136707 Mus muscu	C 648	8	2.1	110000	1	BS571856	BS571856 Arabidops
576	8	2.1	63788	2	AC136707	AC136707 Mus muscu	C 649	8	2.1	110000	1	BS571857	BS571857 Arabidops
577	8	2.1	63788	2	AC136707	AC136707 Mus muscu	C 650	8	2.1	110000	1	BS571966	BS571966 Arabidops
578	8	2.1	63788	2	AC136707	AC136707 Mus muscu	C 651	8	2.1	110000	1	CP000001	CP000001 Arabidops
579	8	2.1	63788	2	AC136707	AC136707 Mus muscu	C 652	8	2.1	110000	1	CP000002	CP000002 Arabidops
580	8	2.1	63788	2	AC136707	AC136707 Mus muscu	C 653	8	2.1	110000	1	CP000003	CP000003 Arabidops
581	8	2.1	63788	2	AC136707	AC136707 Mus muscu	C 654	8	2.1	110000	1	CP000004	CP000004 Arabidops
582	8	2.1	63788	2	AC136707	AC136707 Mus muscu	C 655	8	2.1	110000	1	CP000005	CP000005 Arabidops
583	8	2.1	63788	2	AC136707	AC136707 Mus muscu	C 656	8	2.1	110000	1	CR543861	CR543861 Arabidops
584	8	2.1	63788	2	AC136707	AC136707 Mus muscu	C 657	8	2.1	110000	2	AC091343	AC091343 Homo sapi
585	8	2.1	63788	2	AC136707	AC136707 Mus muscu	C 658	8	2.1	110000	2	AC091361	AC091361 Homo sapi
586	8	2.1	63788	2	AC136707	AC136707 Mus muscu	C 659	8	2.1	110000	2	AC094578	AC094578 Rattus no
587	8	2.1	63788	2	AC136707	AC136707 Mus muscu	C 660	8	2.1	110000	2	AC094578	AC094578 Rattus no
588	8	2.1	63788	2	AC136707	AC136707 Mus muscu	C 661	8	2.1	110000	2	AC095084	AC095084 Rattus no

808	8	2.1	137991	10	AL627073	Mouse DNA	881	8	2.1	145844	9	AC004931	AC004931 Homo sapi
809	8	2.1	138033	2	AP002339	Homo sapi	882	8	2.1	145885	9	AC139427	AC139427 Homo sapi
810	8	2.1	138062	9	AL161938	Human DNA	883	8	2.1	146191	1	D50453	D50453 Bacillus su
811	8	2.1	138155	2	AC151564	Dasyapus n	884	8	2.1	146350	9	HS225L15	HS225L15 Homo sapi
812	8	2.1	138176	5	AC145791	Xenopus t	885	8	2.1	146362	2	BX294174	BX294174 Mus muscu
813	8	2.1	138203	10	AC110221	Mus muscu	886	8	2.1	146679	2	AC115713	AC115713 Mus muscu
814	8	2.1	138329	2	AC093226	Homo sapi	887	8	2.1	146783	2	AC131590	AC131590 Homo sapi
815	8	2.1	138434	2	AC150120	Gallus ga	888	8	2.1	146851	2	AC027697	AC027697 Homo sapi
816	8	2.1	138563	2	AC140575	Macaca mu	889	8	2.1	147118	9	AC007513	AC007513 Homo sapi
817	8	2.1	138582	10	AL844864	Mouse DNA	890	8	2.1	147166	10	AC132272	AC132272 Mus muscu
818	8	2.1	138688	9	AC118553	Homo sapi	891	8	2.1	147179	5	CR384061	CR384061 Zebrafish
819	8	2.1	138926	8	AP005246	Oryza sat	892	8	2.1	147179	5	CR384061	CR384061 Zebrafish
820	8	2.1	138999	9	AC090426	Homo sapi	893	8	2.1	147387	5	AL954326	AL954326 Zebrafish
821	8	2.1	139217	8	AP006481	Oryza sat	894	8	2.1	147456	5	EX950856	EX950856 Zebrafish
822	8	2.1	139226	8	OSUN00274	Human DNA	895	8	2.1	147585	10	AC126457	AC126457 Mus muscu
823	8	2.1	139267	2	AC135174	Oryza sat	896	8	2.1	147640	5	EX323035	EX323035 Zebrafish
824	8	2.1	139480	2	AC012837	Drosophil	897	8	2.1	147664	4	AC144403	AC144403 Felis cat
825	8	2.1	139480	9	HUAC002331	Homo sapi	898	8	2.1	147836	8	AP003983	AP003983 Oryza sat
826	8	2.1	139591	2	CR388227	Danio rer	899	8	2.1	147859	2	AC015692	AC015692 Homo sapi
827	8	2.1	139868	8	AP004161	Oryza sat	900	8	2.1	147952	9	AC008712	AC008712 Homo sapi
828	8	2.1	139917	2	AC141246	Homo sapi	901	8	2.1	147999	2	AL161635	AL161635 Homo sapi
829	8	2.1	140596	2	CR75815	Rattus no	902	8	2.1	148263	9	AC091988	AC091988 Homo sapi
830	8	2.1	140686	2	AC137773	Homo sapi	903	8	2.1	148275	5	EX005016	EX005016 Zebrafish
831	8	2.1	140714	2	RN374E16	Rattus no	904	8	2.1	148487	2	AC011583	AC011583 Homo sapi
832	8	2.1	140769	8	AP003508	Oryza sat	905	8	2.1	148540	9	HS212P9	HS212P9 Human DNA
833	8	2.1	140917	10	AL929380	Mouse DNA	906	8	2.1	148588	2	AC073827	AC073827 Mus muscu
834	8	2.1	141154	9	AC026442	Homo sapi	907	8	2.1	148693	2	AC137789	AC137789 Homo sapi
835	8	2.1	141319	8	AP004457	Oryza sat	908	8	2.1	148732	10	BSX13330	BSX13330 Mouse DNA
836	8	2.1	141447	9	AC016204	Homo sapi	909	8	2.1	148732	10	BSX13330	BSX13330 Mouse DNA
837	8	2.1	141868	9	AC109338	Homo sapi	910	8	2.1	148737	2	AC026702	AC026702 Homo sapi
838	8	2.1	141881	4	AC087421	Felis cat	911	8	2.1	148835	2	AC128002	AC128002 Rattus no
839	8	2.1	141894	9	AC093211	Homo sapi	912	8	2.1	148897	9	AL139034	AL139034 Human DNA
840	8	2.1	141895	9	AL356269	Human DNA	913	8	2.1	148976	2	AC130201	AC130201 Mus muscu
841	8	2.1	141944	9	AC122108	Homo sapi	914	8	2.1	149030	2	AC005375	AC005375 Homo sapi
842	8	2.1	142018	9	HS1033H22	Human DNA	915	8	2.1	149037	9	AC138511	AC138511 Homo sapi
843	8	2.1	142056	2	AC150441	Medicago	916	8	2.1	149287	2	AC079017	AC079017 Homo sapi
844	8	2.1	142056	9	AC010491	Homo sapi	917	8	2.1	149746	2	AC068534	AC068534 Homo sapi
845	8	2.1	142182	8	AP004399	Oryza sat	918	8	2.1	150136	9	BS000056	BS000056 Pan trogl
846	8	2.1	142227	2	AL162492	Homo sapi	919	8	2.1	150224	9	HSJ1059L7	HSJ1059L7 Human DNA
847	8	2.1	142235	2	AP005973	Oryza sat	920	8	2.1	150300	2	AC145019	AC145019 Felis cat
848	8	2.1	142350	5	BP664625	Zebrafish	921	8	2.1	150339	2	AC141750	AC141750 Apis mell
849	8	2.1	142420	2	AC102709	Mus muscu	922	8	2.1	150442	2	AC022782	AC022782 Mus muscu
850	8	2.1	142555	9	AL139214	Human DNA	923	8	2.1	150485	2	AY360387	AY360387 Oryza sat
851	8	2.1	142715	9	AC008387	Homo sapi	924	8	2.1	150489	2	AC069491	AC069491 Homo sapi
852	8	2.1	142726	9	AC104836	Homo sapi	925	8	2.1	150530	2	AC151658	AC151658 Dasyapus n
853	8	2.1	142728	9	HSJ792G4	Human DNA	926	8	2.1	150638	2	AC129994	AC129994 Rattus no
854	8	2.1	142764	2	AC026119	Homo sapi	927	8	2.1	150872	2	AC148037	AC148037 Rattus no
855	8	2.1	142776	2	AP005109	Oryza sat	928	8	2.1	150996	2	AC118264	AC118264 Mus muscu
856	8	2.1	143160	2	AP004796	Oryza sat	929	8	2.1	151327	2	AC135487	AC135487 Rattus no
857	8	2.1	143180	2	AC120596	Rattus no	930	8	2.1	151414	2	AC115523	AC115523 Rattus no
858	8	2.1	143280	10	AL845285	Mouse DNA	931	8	2.1	151505	2	AC021875	AC021875 Homo sapi
859	8	2.1	143444	9	AC007541	Homo sapi	932	8	2.1	151783	4	AC150593	AC150593 Bos tauru
860	8	2.1	143509	2	AC068683	Homo sapi	933	8	2.1	151813	2	AC026737	AC026737 Homo sapi
861	8	2.1	143575	2	AC092370	Homo sapi	934	8	2.1	151930	2	AC151171	AC151171 Bos tauru
862	8	2.1	143712	9	AP004395	Oryza sat	935	8	2.1	152005	9	AC100834	AC100834 Homo sapi
863	8	2.1	143715	9	AL589947	Human DNA	936	8	2.1	152186	2	AC084284	AC084284 Homo sapi
864	8	2.1	143988	2	AC129500	Homo sapi	937	8	2.1	152186	2	CR354581	CR354581 Danio rer
865	8	2.1	144084	8	CNS08CCB	Human DNA	938	8	2.1	152224	2	AC007933	AC007933 Homo sapi
866	8	2.1	144191	8	AC079874	Oryza sat	939	8	2.1	152334	9	AL356299	AL356299 Human DNA
867	8	2.1	144202	2	AC110179	Mus muscu	940	8	2.1	152350	2	AC107322	AC107322 Felis cat
868	8	2.1	144244	9	AC025219	Homo sapi	941	8	2.1	152438	9	AL139809	AL139809 Human DNA
869	8	2.1	144552	9	AP001577	Homo sapi	942	8	2.1	152620	10	AC132081	AC132081 Mus muscu
870	8	2.1	144644	8	AP002818	Oryza sat	943	8	2.1	152654	9	AC134882	AC134882 Homo sapi
871	8	2.1	144666	9	AL160287	Human DNA	944	8	2.1	152937	9	AC007157	AC007157 Homo sapi
872	8	2.1	144739	2	AC130299	Homo sapi	945	8	2.1	152952	9	AC074143	AC074143 Homo sapi
873	8	2.1	144741	8	AP004574	Oryza sat	946	8	2.1	153056	10	AL607090	AL607090 Mouse DNA
874	8	2.1	144792	8	AY555143	Zea may B	947	8	2.1	153133	9	AC091980	AC091980 Homo sapi
875	8	2.1	144828	9	AP001577	Homo sapi	948	8	2.1	153139	5	BSX571971	BSX571971 Zebrafish
876	8	2.1	145016	9	AC123980	Pan trogl	949	8	2.1	153324	2	AC124260	AC124260 Homo sapi
877	8	2.1	145066	2	AP002418	Homo sapi	950	8	2.1	153624	9	HS1018K9	HS1018K9 Human DNA
878	8	2.1	145314	8	AC146852	Medicago	951	8	2.1	153705	9	AL445650	AL445650 Human DNA
879	8	2.1	145546	2	AC120216	Mus muscu	952	8	2.1	153904	2	BSX510650	BSX510650 Homo sapi
880	8	2.1	145739	8	OSUN00157	Oryza sat	953	8	2.1	154228	2	AC124261	AC124261 Homo sapi

954	8	2.1	154474	8	AP006048	Oryza sat	AP006048	Oryza sat	Score: 377.00	Matches: 377
c 955	8	2.1	154633	10	AC145427	Rattus no	AC145427	Rattus no	Percent Similarity: 100.00%	Conservative: 0
c 956	8	2.1	154679	2	AC022019	Homo sapi	AC022019	Homo sapi	Best Local Similarity: 100.00%	Mismatches: 0
957	8	2.1	154704	9	AC092660	Homo sapi	AC092660	Homo sapi	Query Match: 100.00%	Indels: 0
958	8	2.1	154841	2	AC109793	Bos tauru	AC109793	Bos tauru	DB: 6	Gaps: 0
c 959	8	2.1	154890	3	AC008136	Drosophi	AC008136	Drosophi	US-09-736-250-1 (1-377) x AR145734 (1-1133)	
960	8	2.1	154912	2	AC141604	Homo sapi	AC141604	Homo sapi	Qy	1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle 20
961	8	2.1	155103	10	AL645666	Mouse DNA	AL645666	Mouse DNA	Db	1 ATGAGTTTCAGGGCCCTTTGGAAAACACAGAGATTGCTTCTTCCTGTTGGAAAAGCCAAATC 60
c 962	8	2.1	155168	8	AP005848	Oryza sat	AP005848	Oryza sat	Qy	21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
c 963	8	2.1	155191	2	AC149618	Papio anu	AC149618	Papio anu	Db	61 ACTAGGGAAGCACAGATGTGGAAAGTGAATGTGCGGAAATGCCTTCAATCAGAAATGTT 120
c 964	8	2.1	155254	2	AC129952	Mus muscu	AC129952	Mus muscu	Qy	41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysLysTrpGlnPheAsn 60
965	8	2.1	155609	2	BX927284	Danio rer	BX927284	Danio rer	Db	121 TCTCCATCCAGAGAGATGAAGTAATTAATTCATGGCTGCCAACTCAAGTAGTACCAATTCAC 180
966	8	2.1	155612	5	AL935044	Zebrafish	AL935044	Zebrafish	Qy	61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuLeuAspArgPheLeuAlaThrVal 80
967	8	2.1	155666	9	AC008696	Homo sapi	AC008696	Homo sapi	Db	181 CTTTACCAGAGAAATTTGCTCTGGCTAGCAGCTTTTGGATAGATTGTTTGTAGCTACCGTA 240
968	8	2.1	155757	2	AC118548	Homo sapi	AC118548	Homo sapi	Qy	81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaAlaLys 100
c 969	8	2.1	156079	5	BX088716	Zebrafish	BX088716	Zebrafish	Db	241 AAGGCTCATCAAAATACTTTGAGTTGTATTGCAATCAGCTGTTTTTCTTAGCTGCCAAG 300
c 970	8	2.1	156273	9	AC009091	Homo sapi	AC009091	Homo sapi	Qy	101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
971	8	2.1	156292	9	CNS057D6	Human chr	AL356016	Human chr	Db	301 ACTGTTGAGGAAGATGAGAAATTCAGTACTAAGGATATTGGCAAGACAGATTTCTGT 360
972	8	2.1	156300	9	AC005919	Homo sapi	AL772286	Homo sapi	Qy	121 GlyCysSerSerSerGluLeuLeuArgMetGluArgIleLeuLeuAspLysLeuAsnTrp 140
c 973	8	2.1	156408	2	AL772286	Homo sapi	AL772286	Homo sapi	Db	361 GGATGTTCTCACTGAAATTTTGAGATGGAGAGATATTCTGGATTAAGTTGAAATGG 420
c 974	8	2.1	156479	2	AC101833	Mus muscu	AC101833	Mus muscu	Qy	141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
c 975	8	2.1	156504	2	AC148250	Otolemur	AC148250	Otolemur	Db	421 GATCTTCACACAGCACACACATTTGATTTCTTCATATTTTCCATGTCATTCAGAGTCA 480
c 976	8	2.1	156592	9	AC093523	Homo sapi	AC093523	Homo sapi	Qy	161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
c 977	8	2.1	156741	2	AC131312	Homo sapi	AC131312	Homo sapi	Db	481 ACTAGGCTCAGTTACTTTTTCAGTTTCCCAAAATGAGCCCATCTCAACATTTGGCAGTC 540
c 978	8	2.1	156795	2	AC135389	Rattus no	AC135389	Rattus no	Qy	181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
c 979	8	2.1	156830	2	AC027693	Homo sapi	CR847511	Danio rer	Db	541 CTTACCAAGCAACTACTTCTACTGTATGGCTGCAACCACTTCTGCAATTCAGAGATCC 600
c 980	8	2.1	156981	2	CR847511	Danio rer	CR847511	Danio rer	Qy	201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
c 981	8	2.1	157118	9	AC069286	Homo sapi	AC069286	Homo sapi	Db	601 ATGCTTCTCTGGCCATGGTTAGTCTGGAATGAGAAACTCATTTCTGATTGCTTTCT 660
c 982	8	2.1	157145	2	AC146323	Pan trogl	AC146323	Pan trogl	Qy	221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
c 983	8	2.1	157201	8	AP003048	Oryza sat	CR790377	Danio rer	Db	661 CTTACAATTAAGCTGCTTCAGAAAGCACAGATGGATAGCTCCCGATGATCCATTTGTCGG 720
c 984	8	2.1	157405	2	CR790377	Danio rer	AC11071	Mus muscu	Qy	241 GluLeuValAlaHisHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
c 985	8	2.1	157493	2	AC111071	Mus muscu	AC111071	Mus muscu	Db	721 GAGCTTGTGGCACATCATCTTTTCTACTCTGAGCTCTTCCCTGCTCTCGAATTCGGTTAT 780
c 986	8	2.1	157493	9	AC044836	Homo sapi	AC044836	Homo sapi	Qy	261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
c 987	8	2.1	157502	5	AC144486	Gasterost	AC144486	Gasterost	Db	781 GTCTACCGTCCCTCAAGCACACCCCTGGTGCCTGTGACAAAGGAGTGTTCAGATTACAT 840
c 988	8	2.1	157509	2	AC141988	Rattus no	AC141988	Rattus no	Qy	281 ProSerSerValProGlyProAspPheSerLysAsnSerLysProGluValProVal 300
c 989	8	2.1	157574	9	AL592293	Human DNA	AL592293	Human DNA	Db	841 CCCTCTCTGTCCAGGCCCCAGACTTCTCCAGGACCAACAGCAGCCAGAGTCCAGTC 900
c 990	8	2.1	157606	2	AC069172	Homo sapi	AC069172	Homo sapi	Qy	301 ArgGlyThrAlaAlaPheTyrHisHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
c 991	8	2.1	157851	2	AC020509	Drosophi	AC020509	Drosophi	Db	901 AGAGGTACAGACGCTTTTACCATCATCTCCAGCTCCAGTGGTGGTCCAGACGACCTCT 960
c 992	8	2.1	157857	2	AC072032	Homo sapi	AC072032	Homo sapi	Qy	321 ThrLysArgLysValGluGluMetGluValAspAspPheTyrAspGlyIleLysArgLeu 340
c 993	8	2.1	157892	9	AC008115	Homo sapi	AC008115	Homo sapi	Db	
c 994	8	2.1	157929	10	AC124407	Mus muscu	AC124407	Mus muscu	Qy	
c 995	8	2.1	157974	8	AP003755	Oryza sat	AP003755	Oryza sat	Db	
c 996	8	2.1	158241	2	AC021804	Homo sapi	AC021804	Homo sapi	Qy	
c 997	8	2.1	158365	2	AC150811	Callithri	AC150811	Callithri	Db	
c 998	8	2.1	158408	2	BX927402	Danio rer	BX927402	Danio rer	Qy	
c 999	8	2.1	158676	2	AC133921	Homo sapi	AC133921	Homo sapi	Db	
1000	8	2.1	158766	2	AC015851	Homo sapi	AC015851	Homo sapi	Qy	

ALIGNMENTS

RESULT 1	AR145734	AR145734	linear	PAT 08-AUG-2001
LOCUS	Sequence 2 from patent US 6218115.	1133 bp	DNA	
DEFINITION	Sequence 2 from patent US 6218115.			
ACCESSION	AR145734			
VERSION	AR145734.1	GI:15108923		
KEYWORDS	Unknown.			
SOURCE	Unknown.			
ORGANISM	Unclassified.			
REFERENCE	1 (bases 1 to 1133)			
AUTHORS	Nakamura,T.			
TITLE	Human cyclin I and genes encoding same			
JOURNAL	Patent: US 6218115-A 2 17-APR-2001;			
FEATURES	Location/Qualifiers			
source	1..1133			
	/organism="unknown"			
	/mol_type="unassigned DNA"			
ORIGIN				
Alignment Scores:				
Pred. No.:	0			1133

```
Db 961 ACTAAACCAAGTAGAGAAATGGAAGTGATGACCTTCTATGATGGAAATCAAAACGGCTC 1020
Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
Db 1021 TATAATGAAGATAATGCTCAGAAAATGTGGTCTGTGTGGCACTGATTTATCAAGA 1080
Qy 361 GlnGluGlyHisAlaSerProCysProGluProLeuGlnProValSerValMet 377
Db 1081 CAAGAGGACATGCTTCCCTTGTCCACCTTTGCAGCGCTGTTCTGTGCATG 1131

RESULT 2
AR087353 LOCUS 1260 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 5 from patent US 5986055.
ACCESSION AR087353
VERSION AR087353.1 GI:10014116
KEYWORDS
SOURCE
ORGANISM
REFERENCE
  1 (bases 1 to 1260)
  Yang, M., Nandabalan, K. and Schultz, V. Peter.
  CDK2 interactions
  TITLE
  Patent: US 5986055-A 5 16-NOV-1999;
  JOURNAL
  FEATURES
    Location/Qualifiers
      1..1260
      /organism="unknown"
      /mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.: 0 Length: 1260
Score: 377.00 Matches: 377
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-736-250-1 (1-377) x AR087353 (1-1260)
Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuGluLysAlaIle 20
Db 1 ATGAAGTTTCAGGGCCCTTGGAAACCCAGAGATGCTTTCCTGTGGAAAAGCCAAATC 60
Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 61 ACTAGGGAAGCACAGATGTGGAAGTGAATGTGGGAAATGCCCTTCAAAATCAGAAATGTT 120
Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTrpGlnPheAsn 60
Db 121 TCTCCATCCAGAGAGATGAAGTAATTCATATGGCTGGCCAAACTCAAGTACCAATTCAC 180
Qy 61 LeuTrpProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 181 CTTTACCAGAAAACATTTGCTGTGGCTAGCAGTCTTTTGGATAGTTTTTGTAGTACCGTA 240
Qy 81 LysAlaHisProLysTrpLeuSerCysIleAlaIleSerCysPhePheLeuAlaAlaLys 100
Db 241 AAGGCTCATCCAAATACTTGAATGTTATTCATTCATCAGCTGTTTTCCTAGCTGCCAAG 300
Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 301 ACTGTGTGGAAGATGAGAGAAATTCAGTACTAAAGGTATTGGCAAGAGACAGATTTCTGT 360
Qy 121 GlyCysSerSerGluIleLeuArgMetGluArgIleIleLeuAspLysLeuAsnTrp 140
Db 361 GGATGTTCTCATCTGAAATTTTGAAATGAGAGAAATTTCTGGATAAGTTGAATGG 420
Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 421 GATCTTCACAGCCACACCATGGATTTTCTTCATATTTTCCATGTCATGCGAGTGTC 480
```

```
Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 481 ACTAGGCGCTCAGTTACTTTTTTTCAGTTTCCCAAAATGAGCCCATCTCAACATTTTGGCAGTC 540
Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
Db 541 CTTACCAAGCACTACTTCTACTGTATGGCTGCAACCAACTTCTGCAATTCAGAGGATCC 600
Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
Db 601 ATGCTTCTCTGGCCATGGTTAGTCTGGAATGAGAAACTCATTTCTGATGGCTTTCT 660
Qy 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
Db 661 CTTACAATTAAGCTGCTTCAGAAAGCACAGATGATAGTCCCAAGTTCATTCATGTGG 720
Qy 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTrp 260
Db 721 GAGCTTGTGGCACAATCACCTTTCTACTCTGCAGTCTTCCCTGCTCTGAATTCGGTTAT 780
Qy 261 ValTrpArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db 781 GTCTACCGTCCCTCAAGCACACCTGCTGACCTGTGCAAAAGAGTGTTCAGATTACAT 840
Qy 281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
Db 841 CCTCTCTCTGTCAGGCCCCAGACTTCTCCAAGGACACACAGCAAGCCAGAGTCCCAAGTC 900
Qy 301 ArgGlyThrAlaAlaPheTrpHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
Db 901 AGAGTTACAGCAGCTTTTACCATCATCTCCAGCTGCCAGTGGTGGTGCACAGCACCTCT 960
Qy 321 ThrLysArgLysValGluGluMetGluValAspPheTrpAspGlyIleLysArgLeu 340
Db 961 ACTAAACGCAAGTAGAGGAAATGGAAGTGGATGACTTCTATGATGGAATCAAAACGGCTC 1020
Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
Db 1021 TATAATGAAGATAATGCTCAGAAAATGTGGTCTGTGTGGCACTGATTTATCAAGA 1080
Qy 361 GlnGluGlyHisAlaSerProCysProLeuGlnProValSerValMet 377
Db 1081 CAAGAGGACATGCTTCCCTTGTCCACCTTTGCAGCGCTGTTCTGTGCATG 1131

RESULT 3
LOCUS CQ812312 1260 bp DNA linear PAT 24-MAY-2004
DEFINITION Sequence 64 from Patent WO2004038020.
ACCESSION CQ812312
VERSION CQ812312.1 GI:47601932
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE
  1
  Wittig, R., Poustka, A., Mollenhauer, J. and Schadenbord, D.
  Target genes for the diagnosis and treatment of cancer
  TITLE
  Patent: WO 2004038020-A 64 06-MAY-2004;
  JOURNAL
  Deutsches Krebsforschungszentrum Stiftung des oeffentlichen n Rechts
  (DE)
FEATURES
  source
    1..1260
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"
  misc_feature
    1..1260
    /note="D50310"
ORIGIN
Alignment Scores:
Pred. No.: 0 Length: 1260
Score: 377.00 Matches: 377
```

```
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-736-250-1 (1-377) x CQ812312 (1-1260)

Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuGluLysAlaIle 20
Db 1 ATGAAGTTTCAGGGCCCTTGAAACCGAGATTGCTTCTTCTGGTGGAAAGGCAATC 60

Qy 21 ThrArgGluAlaGlnMetTyrLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 61 ACTAGGGAAGCACAGATCGGAAGTGAATGTGGGAAATGCCTTCAAATCAGATGTT 120

Qy 41 SerProSerGlnArgAspGluValIleGlnTyrPheAlaLysLeuLysTyrGlnPheAsn 60
Db 121 TCTCCATCCAGAGAGATGAAGTAAATCAATGGCTGGCCAAACTCAAGTACCAATTCAAC 180

Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 191 CTTTACCCAGAAACATTTGCTCTGGCTAGCAGTCTTTTGGATAGTTTGTAGCTACCGTA 240

Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaAlaLys 100
Db 241 AAGGCTCATCCAAATACTTGCAGTTGATTGCAATCAGCTGTTTCTTCTAGCTGCCAAG 300

Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 301 ACTGTGTAGGAAGATGAGAGAAATCCAGTACTAAAGGTATTTGGCAAGACAGATTTCTGT 360

Qy 121 GlyCysSerSerGluIleLeuArgMetGluArgIleLeuAspLysLeuAsnTyr 140
Db 361 GGATGTTCTCATCTGAAATTTTGGAAATGAGAGAAATATTTGGATAGTTTGTAGTTGG 420

Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 421 GATCTTCACAGCCACACCATGATGTTTCTTATATTTTCCATGCTTCAATGCAAGTGTCA 480

Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 481 ACTAGGCTCATGTTACTTCTTCAATGTTGCCAAATGAGCCCATCTCAACATTTGGCAGTC 540

Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
Db 541 CTTACCAAGCACTACTTCTGATGATGCTTGCACCACTTCTGCAATTCAGAGGATCC 600

Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTyrLeuSer 220
Db 601 ATGCTTGTCTGGCCATGGTGTAGTCTGGAATGGAGAAACTCATTTCTGATTTGGCTTTCT 660

Qy 221 LeuThrIleGluLeuGlnLysAlaGlnMetAspSerSerGlnLeuLysIleHisCysArg 240
Db 661 CTTCAATTTGAATGCTCTTCAAGAACGACAGATGGATGCTCCAGTTGATTCATTTGTCGG 720

Qy 241 GluLeuValAlaHisIleSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
Db 721 GAGCTTGTGGACATCACTTCTTACTCTGAGTCTTCCCTGCTCTGAAATCCGTTTAT 780

Qy 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db 781 GTCTACCGTCCCTCAAGCACACCTGCTGACCTGTGACAAAGGAGTCTTCAAGATTACAT 840

Qy 281 ProSerValProGlyProAspPheSerLysAspAsnSerLeuProGluValProVal 300
Db 841 CCTCTCTGTCTCCAGGCCACACTTCTCCAAAGAACAGCAAGCCAGAGTGGCCAGTC 900

Qy 301 ArgGlyThrAlaAlaPheTyrHisIleLeuProAlaAlaSerGlyCysLysGlnThrSer 320
Db 901 AGAGGTACAGCAGCCTTTTACCATCATCTCCAGCTGCCAGTGGGTGGCAAGCAGACCTCT 960

Qy 321 ThrLysArgLysValGluGluMetGluValAspAspPheTyrAspGlyIleLysArgLeu 340
Db 1081 CAAGAGGACATGCTTCCCTTGTCCACCTTTGCAGCTTGTCTTGTGTGTCATG 1131

Db 961 ACTAAACGCAAGTAGAGGAATGGAAGTGGATGACCTTCTATGATGGAATCAAACGGCTC 1020
Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
Db 1021 TATAATGAAGATAATGCTCAGAAATGTGGTCTTGTGTGGCACTGATTTATCAAGA 1080
Qy 361 GlnGluGlyHisAlaSerProCysProProLeuGlnProValSerValMet 377
Db 1081 CAAGAGGACATGCTTCCCTTGTCCACCTTTGCAGCTTGTCTTGTGTGTCATG 1131

RESULT 4
LOCUS AR281918 1260 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 5 from patent US 6521412.
ACCESSION AR281918
VERSION AR281918.1 GI:29717848
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1260)
AUTHORS Yang M., Nandabalan, K. and Schulz, V. P.
TITLE Hsreq1 and hsqreq2 proteins and use thereof to detect CDK2
JOURNAL Patent: US 6521412-A 5 18-FEB-2003;
FEATURES
    Location/Qualifiers
    1..1260
    /organism="unknown"
    /mol_type="genomic DNA"

ORIGIN
Alignment Scores:
Pred. No.: 0 Length: 1260
Score: 377.00 Matches: 377
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-736-250-1 (1-377) x AR281918 (1-1260)

Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuGluLysAlaIle 20
Db 1 ATGAAGTTTCAGGGCCCTTTGGAAACCGAGATTGCTTCTTCTGGTGGAAAGGCAATC 60

Qy 21 ThrArgGluAlaGlnMetTyrLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 61 ACTAGGGAAGCACAGATGTTGGAAAGTGAATGTGGGAAATGCCTTCAAATCAGATGTT 120

Qy 41 SerProSerGlnArgAspGluValIleGlnTyrPheAlaLysLeuLysTyrGlnPheAsn 60
Db 121 TCTCCATCCAGAGAGATGAAGTAAATCAATGGCTGGCCAAACTCAAGTACCAATTCAAC 180

Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 181 CTTTACCCAGAAACATTTGCTCTGGCTAGCAGTCTTTTGGATAGTTTGTAGCTACCGTA 240

Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaAlaLys 100
Db 241 AAGGCTCATCCAAATACTTGCAGTTGATTGCAATCAGCTGTTTCTTCTAGCTGCCAAG 300

Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 301 ACTGTGTAGGAAGATGAGAGAAATCCAGTACTAAAGGTATTTGGCAAGACAGATTTCTGT 360

Qy 121 GlyCysSerSerGluIleLeuArgMetGluArgIleLeuAspLysLeuAsnTyr 140
Db 361 GGATGTTCTCATCTGAAATTTTGGAAATGAGAGAAATATTTGGATAGTTTGTAGTTGG 420

Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 421 GATCTTCACAGCCACACCATGATGTTTCTTATATTTTCCATGCTTCAATGCAAGTGTCA 480

Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
```

```
Db 481 ACTAGGCTCAGTTACTTTTTCAGTTTGCCAAATGAGCCCATCTCAACATTTGGCAGTC 540
Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgLysSer 200
Db 541 CTTACCAAGCAACTACTTCACTGTATGCGCTGCAACCAACTTCTGCAATTCAGAGGATCC 600
Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuLeuProAspTrpLeuSer 220
Db 601 ATGCTGTCTCTGGCCATGGTATGCTGGAATGGAGAACTCAITTCCTGATTTGGCTTCT 660
Qy 221 LeuThrLysGlnLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuLeuHisCysArg 240
Db 661 CTTACCAATGAACTGCTTCAGAACACAGATGATAGCTCCAGTTGATCCATTTGTCGG 720
Qy 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
Db 721 GAGCTTGTGGCACATCACTTCTACTCTGCAGTCTTCCCTGCCTCGATTCGATTTAT 780
Qy 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLysHis 280
Db 781 GTCTACCGTCCCTCAACACACACCTGCTGACCTGTGACAAAGGAGTGTTCAGATTACAT 840
Qy 281 ProSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
Db 841 CCTCTCTGTGCCAGGCCAGACTTCTCCAGGACAAACAGCAAGCCAGAGTGGCCAGTC 900
Qy 301 ArgGlyThrAlaAlaPheTyrHisLeuProAlaLeuSerGlyCysLysGlnThrSer 320
Db 901 AGAGGTACAGCAGCCTTTTACCATCATCTCCAGCTGCCAGTGGGTGCAAGCACCTCT 960
Qy 321 ThrLysArgLysValGluMetGluValAspPhePheTyrAspGlyLysLysArgLys 340
Db 961 ACTAAACCAAGATAGAGAAATGAACTGATGATGATGATGATGATGATGATGATGATGAT 1020
Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLysSerArg 360
Db 1021 TATAATGAAGATAATGCTTCAGAAATGTTGGTCTGTGTGGCAGCTGTTTGTGTCATG 1080

RESULT 5
AR380354
LOCUS AR380354 1260 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 899 from patent US 6607879.
ACCESSION AR380354
VERSION AR380354.1 GI:40087988
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1260)
AUTHORS Cocks,B.G., Stuart,S.G. and Seilhamer,J.J.
TITLE Compositions for the detection of blood cell and immunological response gene expression
JOURNAL Patent: US 6607879-A 899 19-AUG=2003;-
FEATURES
source Location/Qualifiers
1..1260
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Alignment Scores:
Pred. No.: 0 Length: 1260
Score: 377.00 Matches: 377
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-736-250-1 (1-377) x AR380354 (1-1260)
```

```
Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaLys 20
Db 1 ATGAAGTTTCCAGGGCTTTTGGAAACACAGAGATTGTCTTCTCTGTGTGAAAGGCAATC 60
Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 61 ACTAGGGAAGCACAGATGTGGAAAGTGAATGTGCGGAAATGCGCTTCAAAATCAGATGTT 120
Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysLeuLysTrpGlnPheAsn 60
Db 121 TCTCCATCCAGAGAGATGAAGTAATTCATGGCTGGCCAAACTCAAGTACCAATTCAC 180
Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 181 CTTTACCAGCAAAACATTTGCTCTGGCTAGCAGTCTTTTGGATAGGTTTTAGTACCCTGA 240
Qy 81 LysAlaHisProLysTyrLeuSerCysLysLeuAlaLysSerCysPhePheLeuAlaLys 100
Db 241 AAGGCTCATCCAAATATCTTGAAGTTGATTGCAATCAGCTGTTTTTCTAGCTGCCAAG 300
Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 301 ACTGTTGAGGAGATGAGAGATTCAGTACTAAGGTATTGGCAAGGACAGATTTCTGT 360
Qy 121 GlyCysSerSerSerGluLeuLeuArgMetGluArgIleLeuLeuAspLysLeuAsnTrp 140
Db 361 GGATGTTTCTCATCTGAAATTTTGAAGATGGAGAGAATTATCTCGATAAGTTGAATTGG 420
Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaLysAlaValSer 160
Db 421 GATCTTCACACAGCACACCATTTGATTTTCTCATATTTTCCATGTCATTTGCAAGTGTCA 480
Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 481 ACTAGGCTCAGTTACTTTTTCAGTTTCCCAAAATGAGCCCATCTCAACATTTGGCAGTC 540
Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgLys 200
Db 541 CTTACCAAGCAACTACTTCACTGTATGCGCTGCAACCAACTTCTGCAATTCAGAGGATCC 600
Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuLeuProAspTrpLeuSer 220
Db 601 ATGCTGTCTCTGGCCATGGTGTAGTCTGGAATGGAGAACTCAITTCCTGATTTGGCTTCT 660
Qy 221 LeuThrLysGlnLeuLeuLysAlaGlnMetAspSerSerGlnLeuLeuHisCysArg 240
Db 661 CTTACCAATGAACTGCTTCAGAACACAGATGATAGCTCCAGTGTGATCCATTTGTCGG 720
Qy 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
Db 721 GAGCTTGTGGCACATCACTTCTACTCTGCAGTCTTCCCTGCCTCGATTCGATTTAT 780
Qy 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLysHis 280
Db 781 GTCTACCGTCCCTCAAGCACACCTGCTGACCTGTGCAAAAGGAGTGTTCAGATTACAT 840
Qy 281 ProSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
Db 841 CCTCTCTGTGCCAGGCCAGACTTCTTCAAGGACAAACAGCAAGCCAGAGTGGCCAGTC 900
Qy 301 ArgGlyThrAlaAlaPheTyrHisLeuProAlaLeuSerGlyCysLysGlnThrSer 320
Db 901 AGAGGTACAGCAGCCTTTTACCATCATCTCCAGCTGCCAGTGGGTGCAAGCACCTCT 960
Qy 321 ThrLysArgLysValGluMetGluValAspPhePheTyrAspGlyLysLysArgLys 340
Db 961 ACTAAACCAAGATAGAGAAATGAACTGATGATGATGATGATGATGATGATGATGATGAT 1020
Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLysSerArg 360
Db 1021 TATAATGAAGATAATGCTTCAGAAATGTTGGTCTGTGTGGCAGCTGTTTGTGTCAGAA 1080
```

```
Qy 361 GlnGluGlyHisAlaSerProCysProLeuGlnProValSerValMet 377
|||||
Db 1081 CAAGAGGACATGCTTCCCTTGTCACCTTGAGCCCTGTTCTGTCATG 1131

RESULT 6
HUMCYI
LOCUS Human mRNA for cyclin I, complete cds.
DEFINITION D50310.1 GI:1183161
ACCESSION D50310.1
VERSION cyclin I.
KEYWORDS Homo sapiens
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (sites)
AUTHORS Nakamura, T., Sanokawa, R., Sasaki, Y.F., Ayusawa, D., Oishi, M. and
Mori, N.
TITLE Cyclin I: a new cyclin encoded by a gene isolated from human brain
JOURNAL Exp. Cell Res. 221 (2), 534-542 (1995)
MEDLINE 96086276
PUBMED 7493655
REFERENCE 2 (bases 1 to 1260)
AUTHORS Nakamura, T.
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 1260)
AUTHORS Nakamura, T.
JOURNAL Direct Submission
TITLE Submitted (17-APR-1995) Takeshi Nakamura, Sumitomo Electric
JOURNAL Industries, Biomedical R&D Department; 1, Taya-cho, Sakae-ku,
Yokohama, Kanagawa 244, Japan (E-mail:tnakamr@pele.sumiden.co.jp,
Tel:045-853-7275, Fax:045-853-3528)
FEATURES
Location/Qualifiers
1..1260
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="F06"
/tissue_type="Brain"
1..1133
/codon_start=1
/product="cyclin I"
/protein_id="BAA08849.1"
/db_xref="GI:1183162"
/translation="MKPGPLENORLSFLEKAITREAOQMKVNRKMPNSQNVSPSQ
RDEVOMLAKLYONFLYPETFALASILLDRFLATVKHPKYLSCIALSCFFLAQKV
BEDERI PVKVLARDSCFCSSSEILRMERIIIDKLNDLHTATPLPLHIFHAIAS
TRPQLLPSLXSLPSQHLAVLTQLLHMCACNQLQFQSGMLAMVSENEKLIPIW
LSLTTELKQAMDSSQLIHRELVHHLSTLQSSLPLNSVYVYRPLKHTLVTCDKGV
FRLHPSSVPGPDFGKDNKSPVVRGTAAFYHLPLAASGCKQSTKRVEMEVDDFY
DGIKRLYNEDNVSENVSGVCGTDLRQEGHASPCPPLQPVSM"

CDS
1..1260
/product="cyclin I"
/protein_id="BAA08849.1"
/db_xref="GI:1183162"
/translation="MKPGPLENORLSFLEKAITREAOQMKVNRKMPNSQNVSPSQ
RDEVOMLAKLYONFLYPETFALASILLDRFLATVKHPKYLSCIALSCFFLAQKV
BEDERI PVKVLARDSCFCSSSEILRMERIIIDKLNDLHTATPLPLHIFHAIAS
TRPQLLPSLXSLPSQHLAVLTQLLHMCACNQLQFQSGMLAMVSENEKLIPIW
LSLTTELKQAMDSSQLIHRELVHHLSTLQSSLPLNSVYVYRPLKHTLVTCDKGV
FRLHPSSVPGPDFGKDNKSPVVRGTAAFYHLPLAASGCKQSTKRVEMEVDDFY
DGIKRLYNEDNVSENVSGVCGTDLRQEGHASPCPPLQPVSM"

ORIGIN
Alignment Scores:
Pred. No.: 0 Length: 1260
Score: 377.00 Matches: 377
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-736-250-1 (1-377) x HUMCYI (1-1260)
Qy 1 MetLysPheProGlyProLeuGlnAsnGlnArgLeuSerPheLeuLeuGluLysAlaTle 20
Db 1 ATGAAGTTTCAGGGCCCTTGGAAACACAGAGATTGCTTTCTCTCTGGAAAGCAATC 60

Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 61 ACTAGGGAAGCACACATGTGGAAGTGAATGTGCGGAAATAGCCCTTCAATCAGAAATGTT 120

Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn 60
|||||
```

```
Db 121 TCTCCATCCAGAGAGATGAAGTAATTAATGCTGGCCAAACTCAAGTACCAATCAAC 180
Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
|||||
Db 181 CTTTACCAGAAACATTTGCTCTGGCTAGCAGCTTTTGGATAGGTTTGTAGCTACCGTA 240
|||||
Qy 81 LysAlaHisProLysTyrLeuSerCysAlaAlaLysSerCysPhePheLeuAlaAlaLys 100
|||||
Db 241 AAGGCTCATCCAAATACTTTGAGTTGATTCGAATCAGCTGTTTCTTCTAGCTGCCAAG 300
|||||
Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgSerPheCys 120
|||||
Db 301 ACTGTTGAGGAAGATGAGAGAAATTCAGTACTAAGGATATTGGCAAGACAGATTCTGT 360
|||||
Qy 121 GlyCysSerSerSerGluLeuLeuArgMetGluArgIleLeuLeuAspLysLeuAsnTrp 140
|||||
Db 361 GGAATGTTCTCACTCACTGAAATTTTGAGAAATGGAGAGAAATATTCTGGATAGATTGG 420
|||||
Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
|||||
Db 421 GATCTTCACACAGCCACACCATTTGATTTCTTCATATTTCCATGCAATTCAGTGTCA 480
|||||
Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
|||||
Db 481 ACTAGGCTCAGTTACTTTTTCAGTTTCCCAAAATGAGCCCATCTCAACATTTGGCAGTC 540
|||||
Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgLysSer 200
|||||
Db 541 CTTACCAAGCACTACTCTTCTGTAAGCTGCAACCACTTCTGCAATTCAGAGGATCC 600
|||||
Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
|||||
Db 601 ATGCTGCTCTGGCCATGTTAGTCTGGAATGAGAAACTCATTTCTCTGATGCTGCTTCT 660
|||||
Qy 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
|||||
Db 661 CTTACAAATGAACGTCTTCAGAAAGCACAGATGATAGCTCCAGTGTGATCCATTTGTCGG 720
|||||
Qy 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
|||||
Db 721 GAGCTTGTGGCACATCACTTTCTACTCTGAGTCTTCCCTGCTCTGAATTCGTTAT 780
|||||
Qy 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
|||||
Db 781 GTCTACCGTCCCTCAAGCACACCTGCTGACCTGTGCACAAAGGAGTGTTCAGATTACAT 840
|||||
Qy 281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
|||||
Db 841 CCTCTCTGTGCCAGGCCAGACTTCTCCAAGGACACAGCAAGCCAGAAAGTCCAGTC 900
|||||
Qy 301 ArgGlyThrAlaAlaPheTyrHisHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
|||||
Db 901 AGAGGTACAGCAGCCTTTTACCATCATCTCCAGCTGCCAGTGGGTGCAAGCAGCTCT 960
|||||
Qy 321 ThrLysArgLysValGluGluMetGluValAspAspPheTyrAspGlyIleLysArgLeu 340
|||||
Db 961 ACTAAACGCAAAAGTAGAGGAAATGGAAGTGGATGACTTCTATGATGGAATCAAAAGGCTC 1020
|||||
Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
|||||
Db 1021 TATAATGAAGATAATGCTCTCAGAAATGTGGTGTCTGTGTGGCAGCTGATTTATCAAGA 1080
|||||
Qy 361 GlnGluGlyHisAlaSerProCysProLeuGlnProValSerValMet 377
|||||
Db 1081 CAAGAGGACATGCTTCCCTTGTCACCTTTGAGCCCTGTTCTGTCATG 1131

RESULT 7
AF135162
LOCUS Homo sapiens cyclin I (CYC1) mRNA, complete cds.
DEFINITION AF135162
ACCESSION AF135162
VERSION AF135162.1
KEYWORDS GI:7259481
```


Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
 Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
 Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,
 Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
 Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
 Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
 Buterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
 Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.,
 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 12477932
 2 (bases 1 to 1817)
 Strausberg, R.
 Direct Submission
 Submitted (15-NOV-2000) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 On Nov 6, 2003 this sequence version replaced gi:12653302.
 Contact: MGC help desk
 Email: cgapbs@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
 DNA Sequencing by: National Institutes of Health Intramural
 Sequencing Center (NISC),
 Gaithersburg, Maryland;
 Web site: <http://www.nisc.nih.gov/>
 Contact: nisc_mgc@hgrl.nih.gov
 Akhter, N., Avele, K., Beckerstrom-Sternberg, S.M., Benjamin, B.,
 Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
 Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghigini, P.,
 Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,
 Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
 McDowell, J., Pearson, R., Stanitrop, S., Thomas, P.J., Touchman, J.W.,
 Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
 Young, A., Zhang, L.-H. and Green, E.D.
 Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/ILNL at: <http://image.llnl.gov>
 Series: IRAL plate: 1 Row: 0 Column: 8
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA gi: 17738314.
 Location/Qualifiers
 1. .1817
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="MGC:8665 IMAGE:2964432"
 /tissue_type="Muscle, rhabdomyosarcoma"
 /clone_lib="NIH_MGC_17"
 /lab_host="DH10B-R"
 /note="Vector: pOTB7"
 1. .1817
 /gene="CCNI"
 /note="synonyms: CYC1, CYI"
 /db_xref="LocusID:10983"
 544. .1677
 /gene="CCNI"
 /codon_start=1
 /product="cyclin I"
 /protein_id="AAH00420.1"
 /db_xref="GI:12653303"
 /db_xref="LocusID:10983"
 /translation="MKFPGPLENQRSLFLEKAITREQMKNVVRKMPNSQNVSPSQ
 RDEVQWLAKYQFNLYPETPALASLLDRFLATVKAHPKYLSCIALSCFFLAQTV
 BEDRIPLVKLARDSCGSSSEILRMERITLDKLNLDLHTATPLDIFIHFAIYVS
 TEPQLLSPLKSPSLAVLTQKLLHGMAGNQLQPRGMLALAMLEMEKLIIPDW
 LSLTLELQKQMSQLHCELVHHLSTLQSLPLNSVYVYRPLKHTLVTCDKGV
 FKLHPSPFGPDSKDNKPEVPVGRGTAAFPYHLLPAASGCKQTSTKRVEMEDVDFY
 DGIKRLYNEDNVSENVSGVCGTDLRQEGHASPCPPLOPVSVM"

ORIGIN
 Alignment Scores:
 Pred. No.: 0 Length: 1817
 Score: 377.00 Matches: 377
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0
 US-09-736-250-1 (1-377) x BC000420 (1-1817)
 Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuGluLysAlaIle 20
 Db 544 ATGAAGTTTCAGGGCCCTTTGGAAACACAGAGATTGCTTCTCTGTTGGAAAGGCAATC 603
 Qy 21 ThrArgGluAlaGlnMetTyrLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
 Db 604 ACTAGGGAAGCACAGATGTGGAAGTGAATGTGCGGAAAAATGCCCTTCAGAAATCGAATGTT 663
 Qy 41 SerProSerGlnArgAspGluValIleGlnTyrLeuAlaLysLeuLysTyrGlnPheAsn 60
 Db 664 TCTCCATCCAGAGAGATGAAGTAATTAATGGCTGCCAAACTCAAGTACCAATTCAAC 723
 Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
 Db 724 CTTTACCAGAAACATTTGCTCTGGCTAGCAGTCTTTTGGATAGTGTTTTGTAGCTACCGTA 783
 Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaAlaLys 100
 Db 784 AAGGCTCATCCAAATACTTGAGTTGTAATGCAATCAGCTGTTTTCCTAGCTGCCAAG 843
 Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
 Db 844 ACTGTTGAGGAGATGAGAGATTCAGTACTAAGATATTGCAAGACAGACAGATTTCTGT 903
 Qy 121 GlyCysSerSerGluIleLeuArgMetGluArgIleLeuAspLysLeuAsnTyr 140
 Db 904 GGATGTTCTCATCTGAAATTTTGAGAAATGAGAGAAATATTCTGGATAAGATTGAAATGG 963
 Qy 141 AspleuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
 Db 964 GATCTTCACACAGCACCATTTGATTTCTTCATATTTTCCATGCAATTCAGTGTGCA 1023
 Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
 Db 1024 ACTAGGCTCTAGTTACTTTTCAGTTTGCCTCCAAATGAGCCCATCTCAACATTGCGAGTC 1083
 Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuGlnPheArgGlySer 200
 Db 1084 CTTACCAAGCAACTACTTCTACTGTATGGCTTGCACCACTTCTGCAATTCAGAGGATCC 1143
 Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTyrLeuSer 220
 Db 1144 ATGCTTGTCTTGGCCATGGTTAGTCTGGAATGAGAAACTCATCTCTGATGCTTTCT 1203
 Qy 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
 Db 1204 CTTACATTTGACTGCTTCAGAAAGCACAGATGATAGTCTCCAGTTGATTCATTGTCGG 1263
 Qy 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
 Db 1264 GAGCTTGTGGCACATCATCTTTCTACTGTGAGTCTTCCCTCGCTCTGAAATTCGGTTTAT 1323
 Qy 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
 Db 1324 GTTACCTGCTCCCTCAGCACACCTCTGTGTGACCTGTGCAAGAGAGTTCAGATTACAT 1383
 Qy 281 ProSerSerValProGlyProAspPheSerLysPheAsnSerLysProGluValProVal 300
 Db 1384 CCCTCTCTGTCCAGGGCCAGAGATCTTCTCAAGGACAAACAGCAAGCCAGAGAGTGCAGTC 1443
 Qy 301 ArgGlyThrAlaAlaPheTyrHisIleuProAlaAlaSerGlyCysLysGlnThrSer 320

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

REMARK

COMMENT

FEATURES

source

gene

CDS

```

Db      1444 AGAGGTACAGCAGCCTTTTACCATCATCTCCAGCTGCCAGTGGGTGCAAGCAGACCTCT 1503
Qy      321 ThrLysArgLysValGluGluMetGluValAspAspPheTyrAspGlyIleLysArgLeu 340
Db      1504 ACTAAACGCAAGTAGAGAAATGGAAGTGGATGATCTTATGATGGAATCAAAACGGCTC 1563
Qy      341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
Db      1564 TATAATGAAGATTAATGTCTCAGAAATGTGGTCTCTGTGTGGCACTGATTTATCAAGA 1623
Qy      361 GlnGluGlyHisAlaSerProCysProLeuGlnProValSerValMet 377
Db      1624 CAAGAGGAGACATGCTTCCCTTGTCCACCTTTGCGACCTGTTCTGTCTATG 1674

RESULT 9
LOCUS      CQ468129                1889 bp      DNA      linear      PAT 30-JAN-2004
DEFINITION Sequence 10907 from Patent WO0192581.
ACCESSION  CQ468129
VERSION    CQ468129.1   GI:41433748
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS   Algate,P.A., Harlocker,S.L. and Jones,R.
TITLE     Compositions and methods for the therapy and diagnosis of
          ovariancancer
JOURNAL   Patent: WO 0192581-A 10907 06-DEC-2001
FEATURES   Location/Qualifiers
           source
           1..1889
           /organism="Homo sapiens"
           /mol_type="unassigned DNA"
           /db_xref="taxon:9606"

ORIGIN
Alignment Scores:
Pred. No.:      0      Length:      1889
Score:          377.00  Matches:      377
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match:      100.00%  Indels: 0
DB:               6      Gaps: 0

US-09-736-250-1 (1-377) x CQ468129 (1-1889)

Qy      1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle 20
Db      544 ATGAAGTTTCCAGGGCCCTTGGAAACCCAGAGATTGTCTTCTCTGTTGGAAAGGCAATC 603
Qy      21 ThrArgGluAlaGlnMetTyrLysValAsnValArgLysMetProSerAsnGluAsnVal 40
Db      604 ACTAGGGAAGCACAGATGTGGAAAGTGAATGTGCGGAAATGCCCTTCAAAATCAGAAATGTT 663
Qy      41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn 60
Db      664 TCTCCATCCAGAGATGAAGTAAATCAATGGCTGGCCAAACTCAAGTACCAATTCAC 723
Qy      61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db      724 CTTTACCAGAAACATTTGCTCTGGCTAGCAGTCTTTTGGATAGGTTTTAGTACCCTA 783
Qy      81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaLys 100
Db      784 AAGGCTCATCCAAATACTTGTAGTTGTATGTGAATCAGCTGTTTCTTCTAGCTGCCAAG 843
Qy      101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db      844 ACTGTTGAGGAAGATGAGAGAAATCCAGTACTAAAGGTATTGGCAAGAGACAGTTTCTGT 903

```

```

Qy      121 GlyCysSerSerSerGluIleLeuArgMetGluArgIleIleLeuAspLysLeuAsnTrp 140
Db      904 GGATGTTCTCTCATCTGAAATTTTGAAGATGAGAGAATATTCTGGATTAAGTTGAATGG 963
Qy      141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db      964 GATCTTCACACAGCACACCATTTGGATTTCTTATATTTTCCATGCCATTCAGTGTCA 1023
Qy      161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db      1024 ACTAGGCCCTCAGTTACTTTTTCAGTTTGCCTTGGCCAAATTTAGGCCCATCTCAACATTTGGCAGTC 1083
Qy      181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
Db      1084 CTTTACCAGCAACTACTTCACTGTATGCGCTGCACCAACCAACTTCTGCAATTCAGAGGATCC 1143
Qy      201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTyrLeuSer 220
Db      1144 ATGCTTGTCTTGGCCATGTTAGTCTGGAAATGGAGAAACCTCATCTCTGATTTGGTTTCT 1203
Qy      221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
Db      1204 CTTTCAATTTGAATGCTTTCAGAAAGCACAGATGATAGTCTCCAGTTGATCCATTTGTCGG 1263
Qy      241 GluLeuValAlaHisHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
Db      1264 GAGCTTGTGGCACATCACCTTTTACTGTGCAGTCTTCCCTGCGCTCTCGAATTCGGTTTAT 1323
Qy      261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db      1324 GTCTACCGTCCCTTCAAGCACACCTTGGTGACCTGTGACAAAGGAGTGTTCAGATTACAT 1383
Qy      281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
Db      1384 CCTCTCTGTCTCCAGGCCAGACTTCTTCCAAAGCACAAACAGACCAAGAGTGCAGTC 1443
Qy      301 ArgGlyThrAlaAlaPheTyrHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
Db      1444 AGAGGTACAGCAGCCTTTTACCATCATCTCCAGCTGCCAGTGGGTGCAAGCAGACCTCT 1503
Qy      321 ThrLysArgLysValGluGluMetGluValAspAspPheTyrAspGlyIleLysArgLeu 340
Db      1504 ACTAAACGCAAGTAGAGAAATGGAAGTGAATGATCTTATGATGGAATCAACGGCTC 1563
Qy      341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
Db      1564 TATAATGAAGATAATGTCTCAGAAATGTGGTCTGTGTGTGGCACTGATTTATCAAGA 1623
Qy      361 GlnGluGlyHisAlaSerProCysProLeuGlnProValSerValMet 377
Db      1624 CAAGAGGAGACATGCTTCCCTTGTCCACCTTTGCGACCTGTTCTGTCTATG 1674

RESULT 10
LOCUS      BC004975                1889 bp      mRNA      linear      PRI 29-JUN-2004
DEFINITION Homo sapiens cyclin I, mRNA (cdna clone MGC:3795 IMAGE:2957878),
          complete cds.
ACCESSION  BC004975
VERSION    BC004975.1   GI:13436391
KEYWORDS   MGC.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  1 (bases 1 to 1889)
AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
          Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
          Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
          Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Heieh,F.,
          Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
          Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
          Scheetz,T.E., Brownstein,M.J., Uudin,T.B., Toshiyuki,S.,
          Carninci,P., Prange,C., Rana,S.S., Loquellano,N.A., Peters,G.J.,

```

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzyzinski, M.I., Skalska, U., Smailus, D.E.,
Schnerker, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 1889)
Strausberg, R.
Direct Submission
Submitted (21-MAR-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgapsb-remail.nih.gov
Tissue procurement: DCTD/BTP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,
Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth
Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,
Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin,
Teika Olson, Diana Palquist, Anca Petrescu, Anna Liisa Prabh, Parvaneh Saeedi, JR Santos, Angeliue Schnerch, Ursula Skalska,
Duane Smailus, Jeff Stott, Miranda Tsai, George Yang, Jacquie
Schein, Asim Siddiqui, Rob Holt, Marco Marra.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAL Plate: 9 Row: b Column: 16.

FEATURES
source

```
1..1889
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="MGC:3795 IMAGE:2957878"
/tissue_type="Kidney, renal cell adenocarcinoma"
/clone_lib="NIH MGC 14"
/lab_host="DH10B-R"
/notes="Vector: pOTB7"
```

gene

```
1..1889
/gene="CCNI"
/notes="synonyms: CYC1, CVI"
/db_xref="LocusID:10983"
```

CDS

```
544..1677
/gene="CCNI"
/codon_start=1
/product="cyclin I"
/protein_id="AAH04975.1"
/db_xref="GI:13436392"
/db_xref="LocusID:10983"
/translation="MKFPGPLENORLSFLLEKATITREAOVMKVNVRKMPNSQNSVPSQ  
RDEVIOWLAKLYOENLYPEYFALASLIDRFLATVKAHPKVLSCIALSCFPAKTV  
EDERIPVLKVLARDSFCGSSSEILRMERILDKLWDLHTATPLDFLHIFALIVS  
TRPQLFLSLKLSQSSQSLIHRELVAHLSTLQSSLPNLSVYVYRPLHLEKLPDW  
LSLTLELQKQMSQSLIHRELVAHLSTLQSSLPNLSVYVYRPLHLEKLPDW  
FLHPSVYVGPDPFSDKNSKPEVPVGRGTAAFYHILPAAAGCGQTSTKRVEMVEDDFY  
DGIRKLYNEDNVSENVGVCVGTDLRSQEGHASPCLPLQPSVM"
```

ORIGIN

```
Alignment Scores:
1444 AGAGGTACAGCAGCCTTTTACCATCACTCCAGCTGCAGTGGGTGCAAGCAGACCTCT 1503
```

```
Pred. No.: 0 Length: 1889
Score: 377.00 Matches: 377
Percent Similarity: 100.00% Conservat: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
```

US-09-736-250-1 (1-377) x BC004975 (1-1889)

```
QY 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuGluLysAlaLalle 20
Db 544 ATGAAGTTTCAGGGCCTTTGGAAAACAGAGATTCTTCTCTGTTGGAAAAGCGCAATC 603
QY 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 604 ACTAGGGAAGCACAGATGTGGAAAGTGAATGTGGGAAAATGCCTTCAATCAGAAATGTT 663
QY 41 SerProSerGlnArgAspGluValLleGlnTrpLeuAlaLysLeuLysTrpGlnPheAsn 60
Db 664 TCTCCATCCCAGAGAGATGAAGTAATTCATATGGCTGGCCAAACTCAAGTACCAATTCAC 723
QY 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 724 CTTTACCCAGAAACATTTGCTCTGGCTAGCAGTCTTTTGGATAGTCTTTTACGTACCGTA 783
QY 81 LysAlaHisProLysTyrLeuSerCysAlaLalleSerCysPhePheLeuAlaLalle 100
Db 784 AAGGCTCATCCAAATACTTGGATTGTATTGCAATCAGCTGTTTCTTCTAGCTGCCAAG 843
QY 101 ThrValGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 844 ACTCTTGAGGAAGATGAGAGAAATTCAGTAGTAAAGGTATTGGCAAGACAGATTTCTGT 903
QY 121 GlyCysSerSerGluLeuLeuArgMetGluArgIleLeuLeuAspLysLeuAsnTrp 140
Db 904 GGATGTTCTCACTGAAATTTTGGAAATGGAGAGAAATATTCTGGATTAAGTTGATGG 963
QY 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaLalleAlaValSer 160
Db 964 GATCTTCACAGCAGCCACACCATTTGATTTCTTTCATATTTCCATGTCATTCAGTGTCA 1023
QY 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 1024 ACTAGGCTCAGTTACTTTTTCAGTTTCCCAAAATGGAGCCCATCTCAACATTTGGCAGTC 1083
QY 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgLysSer 200
Db 1084 CTTTACCAAGCACTACTTCTACTGTATGGCTGGCAACCAACTTCTGCAATTCAGAGGATCC 1143
QY 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
Db 1144 ATGCTTGCTCTGGCCATGGTTAGTCTGAAATGGAGAAACTCAATTCCTGATTTGGCTTCT 1203
QY 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuLysHisCysArg 240
Db 1204 CTTTCAAAATGAATGCTTTCAGAAAGCACAGATGATAGTCTCCAGTTCATTCATTTGTCGG 1263
QY 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
Db 1264 GAGCTTGTGGACACATCACCCTTTCTACTCTGAGTCTTCCCTGCTCTGAATTCGGTTAT 1323
QY 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db 1324 GTCTACCGCTCCCTCAAGCACACCCCTGGTACCTGTGACAAAGGAGTGTTCAGATTACAT 1383
QY 281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
Db 1384 CCCTCTCTGTGCCAGGCCAGAGTCTTCCAAAGGACACACAGCAAGCCAGAGAGTGCAGTC 1443
QY 301 ArgGlyThrAlaAlaPheTyrHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
Db 1444 AGAGGTACAGCAGCCTTTTACCATCACTCCAGCTGCAGTGGGTGCAAGCAGACCTCT 1503
```

```
Qy 321 ThrLysArgLysValGluMetGluValAspAspPheTyrAspGlyIleLysArgLeu 340
Db 1504 ACTAAACCAAGTAGAGGAAATGGAAGTGGATGACCTTCTATGATGGAAATCAAAACGGCTC 1563

Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
Db 1564 TATATGGAAGATATGCTTCAGAAATGTGGTCTCTGTGTGGCACTGATTTATCAAGA 1623

Qy 361 GlnGluGlyHisAlaSerProCysProProLeuGlnProValSerValMet 377
Db 1624 CAAGAGGGACATGCTTCCCTTGTCCACCTTTGCGACGCTGTCTTCTGTCTCATG 1674

RESULT 11
LOCUS CQ414515 2755 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 21586 from Patent WO0170979.
ACCESSION CQ414515
VERSION CQ414515.1 GI:41322296
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Lee, J. and Lillie, J.
TITLE Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
JOURNAL Patent: WO 0170979-A 21586 29/SEP/2001
FEATURES
source
Location/Qualifiers
1..2755
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Alignment Scores:
Pred. No.: 2.98e-281 Length: 2755
Score: 266.00 Matches: 266
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 70.56% Indels: 0
DB: 6 Gaps: 0

US-09-736-250-1 (1-377) x CQ414515 (1-2755)

Qy 103 GluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCysGlyCys 122
Db 1099 GAGGAGATGAGAGATTCAGTACTAAAGTATTTGGCAAGACAGATTTCTGTGGATGT 1158

Qy 123 SerSerGluIleLeuArgMetGluArgIleLeuAspLysLeuAsnTrpAspLeu 142
Db 1159 TCCTCATCTGAAATTTTCAGAAATGAGAGAAATTTCTGGATAAGTTGAAATGGGATCTT 1218

Qy 143 HisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSerThrArg 162
Db 1219 CACACAGCCACACCATTTGATTTCTTCATATTTTCCATGTCATTTGCACTGCACTAGG 1278

Qy 163 ProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaValLeuThr 182
Db 1279 CCTAGTTACTTTTCAGTTTCCCAAAATGAGCCATCTCAACATTTGGCAGTCTCTTACC 1338

Qy 183 LysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgLysMetLeu 202
Db 1339 AAGCAACTACTTCACTGTATGCGCTGCAACCAACTTCTGCAATTCAGAGGATCCATGCTT 1398

Qy 203 AlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSerLeuThr 222
Db 1399 GCTCTGGCCATGTTAGTCTGAAATGGAGAAACTCATCTCTGATTTGCTTCTCTTACA 1458

Qy 223 IleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArgGluLeu 242
Db 1459 ATTGAATGCTTTCAGAAAGACAGATGGATAGTCCCAAGTTCATTCATTCGCGGAGCTT 1518
```

```
Qy 243 ValAlaHisHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyrValTyr 262
Db 1519 GTGGCACATCACCTTTCTACTCTGCAGTCTTCCCTGCTCTGAATTCGTTTATGTCTAC 1578

Qy 263 ArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHisProSer 282
Db 1579 CGTCCCTCAAGCACACCTGTGACCTGTGACAAAGAGAGTTCAGATTTACATCCCTCC 1638

Qy 283 SerValProGlyProAspPheSerLysAspAsnSerLysProGluValProValArgGly 302
Db 1639 TCTGTCCAGGCCAGACTTCTCCAGGACAAACAGCAGCCAGAAAGTGCAGAGGT 1698

Qy 303 ThrAlaAlaPheTyrHisHisLeuProAlaAlaSerGlyCysLysGlnThrSerThrLys 322
Db 1699 ACAGCAGCCTTTTACCATCATCTCCAGCTGCCAGTGGGTGCAAGCAGACCTCTACTAAA 1758

Qy 323 ArgLysValGluGluMetGluValAspAspPheTyrAspGlyIleLysArgLeuTyrAsn 342
Db 1759 CGCAAGTAGAGGAAATGGAGTGGATCTTCTATGATGGAATCAAAACGGCTCTATTAAT 1818

Qy 343 GluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArgGlnGlu 362
Db 1819 GAAGATATATCTCTCAGAAATGTGGTCTGTGTGTGGCACTGATTTATCAAGACAGAG 1878

Qy 363 GlyHisAlaSerProCys 368
Db 1879 GGACATGCTTCCCTTGT 1896

RESULT 12
LOCUS CR541783 1131 bp mRNA linear PRI 29-JUN-2004
DEFINITION Homo sapiens full open reading frame cDNA clone RZPD0834E0730D for
gene CCNI, cyclin I; complete cds, without stopcodon.
ACCESSION CR541783
VERSION CR541783.1 GI:49456522
KEYWORDS Full ORF shuttle clone, Gateway(TM), complete cds.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Halleck, A., Ebert, L., Mkoundinya, M., Schick, M., Eisenstein, S.,
Neubert, P., Kstrang, K., Schatten, R., Shen, B., Henze, S., Mar, W.,
Korn, B., Zuo, D., Hu, Y. and LaBaer, J.
TITLE Cloning of human full open reading frames in Gateway(TM) system
entry vector (pDONR201)
JOURNAL Unpublished
REFERENCE 2
AUTHORS Halleck, A., Ebert, L., Mkoundinya, M., Schick, M., Eisenstein, S.,
Neubert, P., Kstrang, K., Schatten, R., Shen, B., Henze, S., Mar, W.,
Korn, B., Zuo, D., Hu, Y. and LaBaer, J.
TITLE Direct Submission
JOURNAL Submitted (28-JUN-2004) RZPD Deutsches Ressourcenzentrum fuer
Genomforschung GmbH, Im Neuenheimer Feld 580, D-69120 Heidelberg,
Germany
COMMENT RZPD; RZPD0834E0730D, ORFNo 3592
www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=RZPD0834E0730D RZPDLIB;
Human Full ORF Clones Gateway(TM) - RZPD (kan-resist.) RZPD LIB No.
834
www.rzpd.de/cgi-bin/products/showLib.pl.cgi/response?libNo=834
www.rzpd.de/products/orfclones/
Contact: Inge Arlart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH,
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 100
Fax: +49 30 32639 111
www.rzpd.de
This clone is available from RZPD;
Contact RZPD (customer.service@rzpd.de) for further information.
Clone name at Harvard Institute of Proteomics
(www.hip.harvard.edu): FLH131015.01L
This CDS clone is part of a collection of human full ORF clones
```

jointly established and verified by the Harvard Institute of Proteomics (HIP) and RZPD.
 This CDS has been cloned without stopcodon.
 The CDS has been inserted into pDONR201 via a BP Clonase(TM) reaction. Additional sequence has been added in front of the start codon: att. .AAAAA GCA GGC TCC ACC (ATG).
 The last codon is followed by the 3' att site: GACCCAGCTTCTT. .att
 The clone is validated by full sequence check.
 Compared to the reference sequence NM_006835 (GI:1738314) we found
 AA exchange(s) at position (first base of changed triplet):
 223 (arg->gly) 409 (lys->arg)
 Clone distribution: http://www.rzpd.de/products/orfclones/.

FEATURES

source

Location/Qualifiers
 1. .1131
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone_lib="RZPD0834E0730D"
 /lab_host="Human Full ORF Clones Gateway (TM) - RZPD"
 /note="Vector: pDONR201, Site_1: attP1, Site_2: attP2"
 1. .1131
 /gene="CCNI"
 1. .>1131
 /gene="CCNI"
 /codon_start=1
 /protein_id="CAG46582.1"
 /db_xref="GI:49454523"
 /translation="MKFPGPLENQRLSFLLEKAITREAOQMKVNRKMPNSQNVSPSQ
 RDEIOWIAKQYQNPETPFASSLDGLFATVKAHPKYLSCIAISCFPLAAKT
 BEDERIPVLKARDSCGSSSEILRMERIIIDRLNWLHTATPLDPLHIFHAIAYS
 TRPQLFSLKPLSPSHLAVLTQKLLHMACNQLOPRGSMALAMTSLMEKILPDW
 LSLTTELLQKQMSDQLHCKELVAHLSLTQSSLPNSVVVRLPKHTATVCKDGV
 FRLHPSSVGPDPFSDKNSKPEVVRGTAFPHLPAAGCGCKQTSTKRKVEENEVDFFI
 DGIRKLYNEDNVSENVGSGTDLRSQGHASPCFPLQFVSM"

gene

CDS

Alignment Scores:
 Pred. No.: 4,776-253 Length: 1131
 Score: 240.00 Matches: 375
 Percent Similarity: 98.94% Conservative: 0
 Best Local Similarity: 98.94% Mismatches: 2
 Query Match: 63.66% Indels: 4
 DB: 9 Gaps: 0

ORIGIN

US-09-736-250-1 (1-377) x CR541783 (1-1131)
 QY 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle 20
 DB 1 ATGAAGTTTCCAGGGCCCTTGGAAACCCAGAGATTGCTTTCTCTGTTGGAAAGGCAATC 60
 QY 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGluAsnVal 40
 DB 61 ACTAGGGAAGACAGATGTGGAAGTGAATGTGGGAAATGCCCTTCAATCAGAAATGTT 120
 QY 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyTrGlnPheAsn 60
 DB 121 TCTCATCCAGAGAGATGAAGTAATTCAATGGCTGGCCAAACTCAAGTACCAATTCAAC 180
 QY 61 LeuTyTrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArg-PheLeuAlaThrVa 80
 DB 181 CTTTACCAGAAACATTTGCTGCTGCTAGCAGTCTTTTGGATGG-GTTTATTAGTACCGT 239
 QY 80 LysAlaHisProLysTyTrLeuSerCysIleAlaIleSerCysPhePheLeuAlaAlaLy 100
 DB 240 AAAGGCTCATCCAAATACTTGGATTGATTGCAATCAGCTGTTTCTTAGTGCGAA 299
 QY 100 sthrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCy 120
 DB 300 GACTGTTGAGGAATGAGAGAAATTCAGTACTAAAGTATTGGCAAGAGACAGATTCTG 359
 QY 120 sGlyCysSerSerGluLeuLeuArgMetGluArgIleLeuLeuAspLys-LeuAsnT 140

DB 350 TGGATGTTCTCATCTCAATCTGAAATTTTTCAGATCGAGAGAAATTTCTGGATAG-GTTGAATT 418
 QY 140 rpAspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValS 160
 DB 419 GGGATCTTCACACAGCCACACCATTTGGATTCTTCATATTTTCCATGTCAGTGT 478
 QY 160 erThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaV 180
 DB 479 CAATAGGCCCTCAGTTACTTTTCAGTTTGGCCAAATTTGAGCCCATCTCAACATTTGGCAG 538
 QY 180 alLeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgLys 200
 DB 539 TCCATTACCAAGCAACTACTTCACTGTATGGCTGCACCAACTTCTGCAATTCAGAGAT 598
 QY 200 erMetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuS 220
 DB 599 CCATGCTTGTCTGCGCCATGTTAGTCTGGAAATGGAGAAATCACTTCTCTGATTGGCTTT 658
 QY 220 erLeuThrIleGluLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysA 240
 DB 659 CTCTTACAATGAACCTGCTTCAGAAAGCACAGATGGATAGCTCCAGTTGATCATTTGTC 718
 QY 240 rgGluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValT 260
 DB 719 GGGAGCTTGTGGCACATCACTTTCTACTCTGCACTCTTCCCTGCTCTGAAATTCGGTTT 778
 QY 260 yrValTyArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuH 280
 DB 779 ATGTCTACCGTCCCTCAAGCACACCCCTGGTGTGCTGTGCAAGAGAGTGTTCAGATTAC 838
 QY 280 isProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProV 300
 DB 839 ATCCCTCTCTGTCCAGGCCAGACTTCTCCAGGCAACAGCAAGCAAGTGGCCAG 898
 QY 300 alArgGlyThrAlaAlaPheTyRHisLeuProAlaAlaSerGlyCysLysGlnThrS 320
 DB 899 TCAGAGGTACAGCAGCCTTTTACCATCATCTCCAGCTGCCAGTGGGTGCAAGCAGACCT 958
 QY 320 erThrLysArgLysValGluGluMetGluValAspAspPheTyRAspGlyLysArgL 340
 DB 959 CTACTAAACGCAAGTAGAGGAAATGGAAGTGGATGACTTCTATGATGGAAATCAACAGGC 1018
 QY 340 euTyRAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerA 360
 DB 1019 TCTATAATGAAGATAATGTCTCAGAAATGTGGGTCTGTGTGGCAGCTGATTATCAA 1078
 QY 360 rgGlnGluGlyHisAlaSerProCysProProLeuGlnProValSerValMet 377
 DB 1079 GACAAGAGGAGACATGCTTCCCTTGTCCACCTTTGAGCCCTGTTTCTGTCTCATG 1131
 RESULT 13
 QY21727
 LOCUS
 DEFINITION
 Sequence 7661 from Patent WO02068579.
 QY21727
 ACCESSION
 QY21727.1 GI:42282584
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1
 Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
 'Kits, such as nucleic acid arrays, comprising a majority of
 humanexons or transcripts, for detecting expression and other uses
 thereof'
 Patent: WO 02068579-A 7661 06-SEP-2002;
 PE Corporation (NY) (US)
 JOURNAL
 Location/Qualifiers
 FEATURES
 1. .690
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN

Alignment Scores:

Pred. No.: 2,926-242 Length: 690
Score: 230.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 61.01% Indels: 0
DB: 6 Gaps: 0

US-09-736-250-1 (1-377) x CQ721727 (1-690)

Qy 1 MetLysPheProGluPheLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle 20
Db 1 ATGAAGTTTCAGGGCCCTTGGAAACACAGAGATTGCTTTCCTGTTGGAAAGGCAATC 60
Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 61 ACTAGGGAAGCACAGATGTGGAAGTGAATGTGCGGAATGCTTCAATCAGATGTT 120
Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyTrGlnPheAsn 60
Db 121 TCTCCATCCACAGAGATGAATTCATGGCTGGCCAAACTCAAGTACCAATTCAC 180
Qy 61 LeuTyProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 181 CTTTACCAGAAACATTTGCTCTGCTAGCAGTCTTTTGGATAGGTTTTAGCTACCGTA 240
Qy 81 LysAlaHisProLysTyLeuSerCysIleAlaIleSerCysPhePheLeuAlaAlaLys 100
Db 241 AAGGCTCATCCAAATATCTGAGTTGATTTGCAATCAGCTGTTTTCTAGTGGCAAG 300
Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 301 ACTGTTGAGGAAGATGAGAGAATTCAGTACTAAAGGTATTGGCAAGAGACAGTTTCTGT 360
Qy 121 GlyCysSerSerSerGluLeuLeuArgMetGluArgIleLeuLeuAspLysLeuAsnTrp 140
Db 361 GGATGTTCTCATCTGAAATTTTGAAGATGGAGAGAATTTATCTGGATPAAGTTGAATGG 420
Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 421 GATCTTCACAGCCACACCAATTTGATTTTCTCATATTTTCCATGCCATTCAGTGCA 480
Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 481 ACTAGGCTCAGTTACTTTTTCAGTTTGCCTGCAATTTAGCCCATCTCAACATTTGGCAGTC 540
Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
Db 541 CTTACCAAGCAACTACTTCTGATGCTGCTGCAACCAACTTCTGCAATTCAGAGGATCC 600
Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
Db 601 ATGCTTGCTCTGGCCATGGTAGTCTGGAATGGAGAACTCATTTCTGATGGCTTCT 660
Qy 221 LeuThrIleGluLeuLeuGlnLysAlaGln 230
Db 661 CTTACAATGAATGCTCTCAGAAAGCACAC 690

RESULT 14

AY207372 29867 bp DNA linear PRI 05-JAN-2003
LOCUS
DEFINITION Homo sapiens cyclin I (CCNI) gene, complete cds.
ACCESSION AY207372
VERSION AY207372.1 GI:27501933
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 29867)
AUTHORS Rieder,M.J., Livingston,R.J., Daniels,M.R., Montoya,M.A.,

Chung,M.-W., Miyamoto,K.E., Nguyen,C.P., Nguyen,D.A., Poel,C.L.,
Robertson,P.D., Schackwitz,W.S., Sherwood,J.K., Witrak,L.A. and
Nickerson,D.A.
Submitted<(26-DEC-2002)>Genome Sciences, University of Washington,
1705 NE Pacific, Seattle, WA 98195, USA
To cite this work please use: NIEHS-SNPs, Environmental Genome
Project, NIEHS ES15478, Department of Genome Sciences, Seattle, WA
(URL: <http://egp.gs.washington.edu>).
Location/Qualifiers
1..29867
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
256
/frequency="0.01"
/replace="a"
328
/frequency="0.01"
/replace="c"
351
/frequency="0.04"
/replace="c"
460
/frequency="0.01"
/replace="a"
494
/frequency="0.01"
/replace="a"
538
/frequency="0.13"
/replace="c"
568
/frequency="0.02"
/replace="a"
623
/frequency="0.02"
/replace="a"
646
/frequency="0.02"
/replace="a"
737
/frequency="0.01"
/replace="a"
770
/frequency="0.01"
/replace="c"
784
/frequency="0.01"
/replace="g"
832
/frequency="0.01"
/replace="g"
884..28840
/gene="CCNI"
Join(884..1384,10453..10609,18229..18357,20541..20615,
20762..20902,21484..21714,28204..28840)
/gene="CCNI"
/product="cyclin I"
1126
/gene="CCNI"
/frequency="0.01"
/replace="t"
1178
/gene="CCNI"
/frequency="0.01"
/replace="t"
1208..1213
/gene="CCNI"
/frequency="0.18"
/replace="n"
1269
/gene="CCNI"

FEATURES

source

variation

variation

variation

variation

variation

variation

variation

variation

variation

variation

variation

variation

variation

gene

mRNA

variation

variation

variation

variation

[illegible]


```

Oy 329 GluValAspAspPheTyAspGlyIleLysArgLeuTyAenGluAAsnValSerGlu 348
Db 28498 GAATGGATGACTTCTATGATGAATCAACGGCTCTATAATGAAGATAATGCTCAGAA 28557
Oy 349 AenValGlySerValCveGlyThrAspLeuSerArgGlnGluGlyHisAlaSerProCys 368
Db 28558 AATGGGTGCTGTGTGTGGCACTGATTTATCAAGACAAGAGGACATGCTTCCCTTGT 28617
Oy 369 ProProLeuGlnProValSerValMet 377
Db 28618 CCACCTTTGCAGCCTGTTCTGTCAAG 28644

RESULT 15
AC111196/c
LOCUS AC111196 Homo sapiens BAC clone RP11-585K17 from 4, complete sequence.
DEFINITION AC111196
ACCESSION AC111196
VERSION AC111196.4 GI:20069715
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 35191)
Toward a complete human genome sequence
JOURNAL Genome Res. 8 (11), 1097-1108 (1998)
MEDLINE 99063792
PUBMED 9847074
REFERENCE 2 (bases 1 to 35191)
AUTHORS Wang, C., Kozlowski, A., Spalding, L., Pearman, C. and Boyer, E.
TITLE The sequence of Homo sapiens BAC clone RP11-585K17
JOURNAL Unpublished (2001)
REFERENCE 3 (bases 1 to 35191)
AUTHORS Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (18-FEB-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (bases 1 to 35191)
AUTHORS Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (03-APR-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
5 (bases 1 to 35191)
AUTHORS Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (08-APR-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
6 (bases 1 to 35191)
AUTHORS Waterston, R.
TITLE Direct Submission
JOURNAL Submitted (20-APR-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Apr 8, 2002 this sequence version replaced gi:19913343.
COMMENT ----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
----- Summary Statistics
-----
Center project name: H_NH0585K17
-----

```

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:

all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

The RPI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Taten, M., Catanese, J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org> VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-123J14, 2000 bp overlap; the clone sequenced to the right is RP11-1E1, 2000 bp overlap. Actual end of this clone is at base position 27847 of RP11-1E1.

Polymorphisms exist between AC111196 and AC104687.

FEATURES

FEATURES	Location/Qualifiers
source	1..35191
	/organism="Homo sapiens"
	/mol_type="genomic DNA"
	/db_xref="taxon:9606"
	/chromosome="4"
	/map="4"
	/clone="RP11-585K17"
	/clone_lib="RPI-11"
repeat_region	366..398
	/rpt_family="(CA)n"
repeat_region	399..512
	/rpt_family="(TA)n"
repeat_region	1849..2009
	/rpt_family="MIR"
repeat_region	2359..2653
	/rpt_family="Alu"
repeat_region	3325..3408
	/rpt_family="MER103"
repeat_region	3488..3638
	/rpt_family="MER1_type"
repeat_region	4238..4531
	/rpt_family="Alu"
repeat_region	5172..5375
	/rpt_family="MIR"
repeat_region	6003..6130
	/rpt_family="MIR"
repeat_region	6432..6466
	/rpt_family="(TG)n"
repeat_region	6733..6798
	/rpt_family="CT-rich"
repeat_region	6850..6958
	/rpt_family="(TA)n"
repeat_region	7073..7340
	/rpt_family="Alu"
repeat_region	7489..7790
	/rpt_family="Alu"
repeat_region	9650..9687
	/rpt_family="(TG)n"
repeat_region	11687..11710
	/rpt_family="(TTTAA)n"
repeat_region	14176..14470
	/rpt_family="Alu"
repeat_region	19012..19077

/rpt_family=" (TTTA)n"
19135. .19445
/rpt_family="Alu"
19677. .19965
/rpt_family="Alu"
20334. .20613
/rpt_family="Alu"
20736. .20809
/rpt_family="L2"
22646. .22670
/rpt_family=" (T)n"
22909. .23185
/rpt_family="Alu"
26059. .26084
/rpt_family=" (T)n"
26206. .26226
/rpt_family="AT_rich"
26492. .26793
/rpt_family="Alu"
26978. .27172
/rpt_family="L2"
28010. .28338
/rpt_family="MER2_type"
29051. .29409
/rpt_family="L1"
31198. .31220
/rpt_family="AT_rich"
32557. .32862
/rpt_family="Alu"
33574. .33661
/rpt_family="ERV1"
33683. .33986
/rpt_family="Alu"

ORIGIN

Alignment Scores:

Pred. No.: 1,058-151 Length: 35191
Score: 149.00 Matches: 149
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 39.52% Indels: 0
DB: 9 Gaps: 0

US-09-736-250-1 (1-377) x AC111196 (1-35191)

QY	229	AlaGlnMetAspSerSerGlnLeuIleHisCysArgGluLeuValAlaAlaHisHisLeuSer	248
Db	25764	GCCACAGATGGATAGCTCCAGTTGATCCATTGTCGGAGCTTGTGGACATCACCTTCT	25705
QY	249	ThrLeuGlnSerSerLeuProLeuAsnSerValTyrValTyrArgProLeuLysHisThr	268
Db	25704	ACTCTGCAGTCTTCCTGCCTCTGAATTCCGTTTATGTCTACCGTCCCTCAAGCACACC	25645
QY	269	LeuValThrCysAspLysGlyValPheArgLeuHisProSerSerValProGlyProAsp	288
Db	25644	CTGGTGACTGTGACAAAGGAGTGTTCAGATTACATCCCTCTCTCCAGGCCACAG	25585
QY	289	PheSerLysAspAsnSerLysProGluValProValArgGlyThrAlaAlaPheTyrHis	308
Db	25584	TTCTCCAAGGACACACAGCCAGAGTCCAGTCCAGGTACAGCAGCCCTTTTACCAT	25525
QY	309	HisLeuProAlaAlaSerGlyCysLysGlnThrSerThrLysArgLysValGluGluMet	328
Db	25524	CATCTCCAGCTGCCAGTGGGTGCAAGCAGACCTCTACTAAACGCAAGTAGAGAAATG	25465
QY	329	GluValAspAppPheTyrAspGlyIleLysArgLeuTyrAsnGluAspAsnValSerGlu	348
Db	25464	GAAGTGGATGACTTCTATGATGGATCAACGGCTCTATATGAATATATGCTCAGAA	25405
QY	349	AsnValGlySerValCysGlyThrAspLeuSerArgGlnGluGlyHisAlaSerProCys	368
Db	25404	AATGTGGTCTCTGTGTGGCACTGATTTATCAAGACAAAGAGGACATGCTTCCCTTGT	25345

QY 369 ProProLeuGlnProValSerValMet 377
Db 25344 CCACCTTTGCAGCCTGTTTCTGTCTCATG 25318

Search completed: February 11, 2005, 14:33:40
Job time : 7807.45 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 11, 2005, 02:58:09 ; Search time 3.97442 Seconds
(without alignments)
1362.372 Million cell updates/sec

Title: US-09-736-250-5

Perfect score: 74

Sequence: 1 EDVNSVNGVCGT 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	74	100.0	14	AAW21966	Aaw21966 Human cys
2	74	100.0	300	ADN01131	Adn01131 Human cel
3	74	100.0	334	AAE37938	Aae37938 Human CGD
4	74	100.0	377	AAW21965	Aaw21965 Human cys
5	74	100.0	377	AAV52185	Aav52185 Human cyc
6	74	100.0	377	ABR39934	Abr39934 Human pro
7	74	100.0	377	ADP12615	Adp12615 Protein e
8	74	100.0	377	ABM80569	Abm80569 Tumour-as
9	44	59.5	464	ABP66192	Abp66192 Bifidobac
10	43	58.1	469	ADN23705	Adn23705 Bacterial
11	43	58.1	762	ABR61598	Abr61598 Z. mays v
12	43	58.1	764	ADN20925	Adn20925 Beta vulg
13	43	58.1	770	ABR91014	Abr91014 Herbicida
14	43	58.1	1849	ABB61023	Abb61023 Drosophil
15	42	56.8	672	ABJ25449	Abj25449 Aspergill
16	42	56.8	672	ABJ26049	Abj26049 Aspergill
17	42	56.8	720	ADE08519	Ade08519 Novel pro
18	41	55.4	345	ABB67087	Abb67087 Drosophil
19	41	55.4	544	AAR90298	Aar90298 Maize pro
20	41	55.4	544	AAW25748	Aaw25748 Maize pro
21	41	55.4	544	AAW41606	Aaw41606 Maize pro
22	41	55.4	544	AAW51256	Aaw51256 Maize pro
23	41	55.4	544	AAE08751	Aae08751 Maize pro
24	41	55.4	544	AAE14662	Aae14662 Maize pro
25	41	55.4	544	AAE10223	Aae10223 Maize pro

26	41	55.4	544	4	AAE13204	Aae13204 Maize pro
27	41	55.4	544	4	AAW2904	Aaw2904 Maize pro
28	41	55.4	544	5	AAW78537	Aaw78537 Maize pro
29	41	55.4	544	5	AAE26008	Aae26008 Maize pro
30	40	54.1	135	5	ABB89159	Abb89159 Human pol
31	40	54.1	177	7	ADJ70525	Adj70525 Human hea
32	40	54.1	200	1	AAW80436	Aaw80436 Recombina
33	40	54.1	201	1	AAW80918	Aaw80918 Sequence
34	40	54.1	201	1	AAW80917	Aaw80917 Sequence
35	40	54.1	201	1	AAW2077	Aap2077 Mouse glu
36	40	54.1	201	7	ADJ68233	Adj68233 Human hea
37	40	54.1	201	8	ADO77886	Ado77886 Glutathio
38	40	54.1	205	1	AAW80916	Aaw80916 Sequence
39	40	54.1	293	4	AAW87773	Aaw87773 Human T2R
40	40	54.1	293	8	ADR29130	Adr29130 Taste rec
41	40	54.1	300	6	ABU04666	Abu04666 Human exp
42	40	54.1	356	4	ABG07458	Abg07458 Novel hum
43	40	54.1	470	8	ADN47440	Adn47440 Thermococ
44	39	52.7	110	4	ABBI5314	Abbi5314 Human ner
45	39	52.7	259	5	ABU51611	Abu51611 Helicobac

ALIGNMENTS

RESULT 1

AAW21966
ID AAW21966 standard; protein; 14 AA.

XX AC AAW21966;

XX DT 02-DEC-1997 (first entry)

XX DE Human cyclin I peptide fragment.

XX KW human; cyclin I; antisense; probe; neurone; cancer; antibody.

XX OS Homo sapiens.

XX PN WO9712973-A1.

XX PD 10-APR-1997.

XX PF 07-OCT-1996; 96WO-JP002905.

XX PR 05-OCT-1995; 95JP-00284663.

XX PA (SUME) SUMITOMO ELECTRIC IND CO.

XX PI Nakamura T;

XX DR WPI; 1997-226217/20.

XX PT Human cyclin I protein and related (anti:sense) DNA - used for neuron

XX PT labelling method and cancer cell detection.

XX CC Claim 7; Page 30; 45pp; Japanese.

XX CC This peptide is a fragment of human cyclin I which can be specifically
XX CC recognised by antibodies of the invention. The antibodies are used to
XX CC detect the presence of cyclin I. Antisense cyclin I polynucleotides are
XX CC useful for as probes and can be labelled and used for detection of
XX CC neurones by hybridisation with mRNA for cyclin I (contained in the
XX CC neurones and arising by the expression of the cyclin I gene in these
XX CC cells). The gene can be used for detection of cancer cells by detecting
XX CC the expression of the cyclin I gene in these cells.

XX SQ Sequence 14 AA;

Query Match 100.0%; Score 74; DB 2; Length 14;

Best Local Similarity 100.0%; Pred. No. 1.1e-05;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX	Sequence 300 AA;	Query Match 100.0%; Score 74; DB 8; Length 300;	
SQ		Best Local Similarity 100.0%; Pred. No. 0.00026;	
		Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 EDNVSENVGVCVT 14		
DB	266 EDNVSENVGVCVT 279		
AAE37938			
AAE37938			
06-NOV-2003	(first entry)		
Human CGDD-27 protein.			
Human; cell growth, differentiation and death protein; CGDD; leukaemia; neurodegenerative disorder; Parkinson's disease; Alzheimer's disease; muscular disorder; myotonic dystrophy; catatonia; endocrine disorder; diabetes; Grave's disease; cancer; immunological disorder; scleroderma; systemic lupus erythematosus; allergy; Crohn's disease; renal disorder; gastrointestinal disorder; Goodpasture's syndrome; infection; cirrhosis; cardiovascular disorder; atherosclerosis; hepatic disease; transgenic; transgenic animal; gene therapy; neuroprotective; relaxant; cytotstatic; dermatological; immunosuppressive; cerebroprotective; anticonvulsant; antitubercular; antiparasitic; fungicide; virucide; uropathic; cardiant; protozoacide; nootropic.			
Homo sapiens.			
WO2003050253-A2.			
19-JUN-2003.			
04-DEC-2002; 2002WO-US039133.			
07-DEC-2001; 2001US-0340747P.			
20-DEC-2001; 2001US-0342761P.			
15-JAN-2002; 2002US-0349705P.			
06-FEB-2002; 2002US-0354764P.			
12-FEB-2002; 2002US-0356216P.			
(INCY-) INCYTE GENOMICS INC.			
Griffin JA, Ramkumar J, Emerling BM, Kable AE, Elliott VS; Marquis JP, Baughn MR, Gorvad AE, Yue H, Lee EA, Becha SD, Tran UK, Swarnakar A, Lee S, Ison CH, Hafalia AJA, Tran B; Sprague WW, Lee SY, Khare R, Gandhi AK, Gietzen KJ, Bhatia U; Burrill JD, Blake JJ, Ho A, Zheng W;			
WPI; 2003-532903/50.			
N-PSDB; AAD57247.			
New CGDD polypeptides, useful for diagnosing, preventing, and treating disorders associated with an abnormal expression or activity of CGDD, e.g. neuromuscular, immunological, cardiovascular disorders, cancer and/or infections.			
Claim 1; Page 250; 299pp; English.			
The present invention relates to novel cell growth, differentiation and death (CGDD) proteins and polynucleotides encoding them. The sequences of the invention are useful in diagnosing, preventing and treating disorders associated with an abnormal expression or activity of CGDD such as neurodegenerative disorders (e.g. Parkinson's disease, Alzheimer's disease), muscular disorders (e.g. myotonic dystrophy, catatonia), endocrine disorders (e.g. diabetes, Grave's disease), cancers (e.g.			

CC leukaemia, cervical or breast cancers), immunological disorders (e.g.
 CC scleroderma, systemic lupus erythematosus, allergies), gastrointestinal
 CC disorders (e.g. Crohn's disease), renal disorders (e.g. Goodpasture's
 CC syndrome), infections (e.g. viral, bacterial, fungal, parasitic,
 CC protozoal, helminthic), cardiovascular disorders (e.g. atherosclerosis)
 CC and hepatic diseases (e.g. cirrhosis). The polynucleotides can be used to
 CC create humanised animals or transgenic animals to model human diseases.
 CC The invention is also used in gene therapy. The present sequence is human
 CC CGDD-27 protein
 XX
 SQ Sequence 334 AA;

Query Match 100.0%; Score 74; DB 7; Length 334;
 Best Local Similarity 100.0%; Pred. No. 0.00029; Mismatches 0; Indels 0; Gaps 0;
 Matches 14; Conservative 0;

Qy 1 EDNVSENVGVCVT 14
 |||||
 Db 300 EDNVSENVGVCVT 313

RESULT 4
 AAW21965
 ID AAW21965 standard; protein; 377 AA.

XX AAW21965;
 DT 02-DEC-1997 (first entry)
 XX Human cyclin I.
 DE human; cyclin I; antisense; probe; neurone; cancer; antibody.
 KW Homo sapiens.

OS
 XX WO9712973-A1.
 PN 10-APR-1997.
 PD 07-OCT-1996; 96WO-JP002905.
 XX 05-OCT-1995; 95JP-00284663.
 PR (SUME) SUMITOMO ELECTRIC IND CO.
 PA Nakamura T;
 PI WPI; 1997-226217/20.
 DR N-PSDB; AAT73937.

XX Human cyclin I protein and related (anti:sense) DNA - used for neuron
 PT labelling method and cancer cell detection.

PS Claim 1; Fig 1; 45pp; Japanese.

CC This sequence is human cyclin I. Antisense polynucleotides are useful for
 CC as probes and can be labelled and used for detection of neurones by
 CC hybridisation with mRNA for cyclin I (contained in the neurones and
 CC arising by the expression of the cyclin I gene in these cells). The gene
 CC can be used for detection of cancer cells by detecting the expression of
 CC the cyclin I gene in these cells. Also antibodies specific for the
 CC fragments of the protein (especially AAW21966) can be used for detection
 XX

SQ Sequence 377 AA;
 Query Match 100.0%; Score 74; DB 2; Length 377;
 Best Local Similarity 100.0%; Pred. No. 0.00032; Mismatches 0; Indels 0; Gaps 0;
 Matches 14; Conservative 0;

Qy 1 EDNVSENVGVCVT 14
 |||||
 Db 343 EDNVSENVGVCVT 356

RESULT 5
 AAY52185
 ID AAY52185 standard; protein; 377 AA.

XX AAY52185;
 AC
 DT 09-FEB-2000 (first entry)
 XX Human cyclin I amino acid sequence.

XX Cyclin-dependent kinase 2; CDK2; hsReq; hsReq*-1; hsReq*-2; cyclin I;
 KW ERH; cell cycle; proliferation; cancer; hyperproliferative disorder;
 KW atherosclerosis; tumour.

OS Homo sapiens.
 XX WO9925829-A2.
 PN 27-MAY-1999.

XX 12-NOV-1998; 98WO-US024095.
 XX 13-NOV-1997; 97US-00969106.
 PR (CURA-) CURAGEN CORP.

PA Yang M, Nandabalan K, Schulz VP;
 XX WPI; 2000-061923/05.
 DR N-PSDB; AAZ37836.

XX New complexes of the cyclin-dependent kinase 2 protein with its
 PT interacting proteins, used to treat, e.g. atherosclerosis.

PS Example; Fig 2; 90pp; English.

XX This is the human Cyclin I amino acid sequence. Cyclin I is expressed at
 CC almost constant levels throughout the cell cycle, and is implicated in
 CC controlling cell cycle progression and transcriptional control. Cyclins
 CC form complexes with cyclin-dependent kinases. CDK2, cyclin-dependent
 CC kinase 2, is used in the invention which relates to complexes of the CDK2
 CC protein with other proteins, selected from cyclin I, ERH, hsReq, hsReq*-1
 CC and hsReq*-2 (AAY52185-Y52188). CDK2 is expressed late in G1 or early in
 CC S phase of the cell cycle, and is pivotal for G1/S transition.

CC Compositions containing a CDK2 complex, an antibody targeting the
 CC complex, and nucleotide sequences encoding CDK2 or its derivatives can be
 CC used therapeutically. The complexes and their nucleotide sequences can be
 CC used to treat diseases or disorders associated with increased or
 CC decreased levels of the complex. Screening the complex, or a derivative
 CC or a modulator of the complex for neoplastic activity by measuring the
 CC survival or proliferation of cells from a malignant cell line when in
 CC contact with the complex can be used to indicate if the the complex has
 CC anti-neoplastic activity. Screening for molecules that modulate the
 CC formation of the complexes can be used for treating or preventing
 CC atherosclerosis or atherosclerosis-associated disease by contacting cells
 CC or using a test animal, in which tumour growth or regression is measured
 CC to test whether anti-neoplastic activity is displayed. Diseases which can
 CC be treated or prevented by molecule/s which modulate the function of the
 CC complex include cancer, hyperproliferative disorders and atherosclerosis
 XX

SQ Sequence 377 AA;

Query Match 100.0%; Score 74; DB 3; Length 377;
 Best Local Similarity 100.0%; Pred. No. 0.00032; Mismatches 0; Indels 0; Gaps 0;
 Matches 14; Conservative 0;

Qy 1 EDNVSENVGVCVT 14
 |||||
 Db 343 EDNVSENVGVCVT 356

RESULT 6

```

ABR39934
ID  ABR39934 standard; protein; 377 AA.
AC  ABR39934;
XX
DT  11-AUG-2003 (first entry)
DE  Human prostate selective polypeptide Pr325.
XX
KW  Prostate; molecular marker; cancer; cytostatic; gene therapy; human.
XX
OS  Homo sapiens.
XX
PN  WO2003014298-A2.
XX
PD  20-FEB-2003.
XX
PF  02-AUG-2002; 2002WO-US024431.
XX
PR  03-AUG-2001; 2001US-0309470P.
XX
PR  30-OCT-2001; 2001US-0330747P.
XX
PA  (ORIG-) ORIGENE TECHNOLOGIES INC.
XX
PI  Sun Z, Li X, Jay G, Kovacs KF, Shu Y, Fan W;
XX
WPI; 2003-256562/25.
XX
DR  N-PSDB; ACC47339.
XX
XX  New polynucleotide, useful for preparing a composition for treating
PT  prostate disease, e.g., cancer.
XX
XX  Claim 5; Page 147-149; 212pp; English.
PS
XX  The invention relates to prostate selective polynucleotides and
CC  polypeptides. The polynucleotides are expressed in prostate and are
CC  useful as molecular markers, as drug targets, and for detecting,
CC  monitoring, preventing or treating diseases and conditions related to
CC  prostate, such as prostate cancers. The present sequence represents a
CC  prostate specific polypeptide
XX
SQ  Sequence 377 AA;

Query Match      100.0%; Score 74; DB 6; Length 377;
Best Local Similarity 100.0%; Pred. No. 0.00032;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1 EDNVSENVGVCVGT 14
Db  343 EDNVSENVGVCVGT 356

RESULT 7
ADP12615
ID  ADP12615 standard; protein; 377 AA.
XX
AC  ADP12615;
XX
DT  12-AUG-2004 (first entry)
XX
DE  Protein encoded by mRNA of the invention #225.
XX
KW  transplant rejection; immune system; rheumatoid arthritis; lupus;
XX  inflammatory bowel disease; multiple sclerosis; HIV; AIDS.
XX
OS  Homo sapiens.
XX
PN  WO2004042346-A2.
XX
XX  21-MAY-2004.
XX
PF  24-APR-2003; 2003WO-US012946.
XX

Query Match      100.0%; Score 74; DB 8; Length 377;
Best Local Similarity 100.0%; Pred. No. 0.00032;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1 EDNVSENVGVCVGT 14
Db  343 EDNVSENVGVCVGT 356

RESULT 8
ABM80569
ID  ABM80569 standard; protein; 377 AA.
XX
AC  ABM80569;
XX
DT  18-NOV-2004 (first entry)
XX
DE  Tumour-associated antigenic target (TAT) polypeptide PRO4605, SEQ:1450.
XX
KW  Tumour-associated antigenic target; TAT; human; overexpression; cancer;
XX  tumour; diagnosis; cell proliferative disorder; breast cancer;
XX  colorectal cancer; lung cancer; ovarian cancer; liver cancer;
XX  central nervous system cancer; bladder cancer; pancreatic cancer;
XX  cervical cancer; melanoma; leukaemia; hybridisation probe;
XX  chromosome identification; chromosome mapping; gene mapping;
XX  gene therapy; cytostatic.
XX
OS  Homo sapiens.
XX
PN  WO2004030615-A2.
XX
XX  15-APR-2004.
XX
PF  29-SEP-2003; 2003WO-US028547.
XX
PR  02-OCT-2002; 2002US-0414971P.
XX
PA  (GETH ) GENENTECH INC.
XX
PI  Wu TD, Zhang Z, Zhou Y;

```

```

PR  24-APR-2002; 2002US-00131831.
PR  20-DEC-2002; 2002US-00325899.
XX
PA  (EXPR-) EXPRESSION DIAGNOSTICS INC.
XX
PI  Wohlgenuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;
PI  Rosenberg S;
XX
DR  WPI; 2004-400724/37.
XX
XX  Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,
PT  pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
PT  rejection, in an individual, comprises detecting the expression level of
PT  the genes.
XX
XX  Claim 65; SEQ ID NO 2624; 1762pp; English.
PS
XX  The present invention relates to diagnosing or monitoring transplant
CC  rejection, e.g. cardiac or kidney transplant rejection, in an individual
CC  comprises detecting the expression level of one or more genes. The
CC  methods, system and kits are useful in diagnosing or monitoring
CC  transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
CC  islet, lung, bone marrow or stem cell transplant rejection.
CC  xenotransplant rejection or mechanical organ replacement rejection, in an
CC  individual. The method is also useful in assessing the immune status of
CC  an individual. The methods are also useful in diagnosing and monitoring
CC  diseases that involve the immune system, e.g. rheumatoid arthritis,
CC  lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
CC  viral, bacterial or fungal infection. The present sequence represents a
CC  protein that is encoded by the mRNA of the invention.
XX
XX  Sequence 377 AA;

Query Match      100.0%; Score 74; DB 8; Length 377;
Best Local Similarity 100.0%; Pred. No. 0.00032;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1 EDNVSENVGVCVGT 14
Db  343 EDNVSENVGVCVGT 356

RESULT 8
ABM80569
ID  ABM80569 standard; protein; 377 AA.
XX
AC  ABM80569;
XX
DT  18-NOV-2004 (first entry)
XX
DE  Tumour-associated antigenic target (TAT) polypeptide PRO4605, SEQ:1450.
XX
KW  Tumour-associated antigenic target; TAT; human; overexpression; cancer;
XX  tumour; diagnosis; cell proliferative disorder; breast cancer;
XX  colorectal cancer; lung cancer; ovarian cancer; liver cancer;
XX  central nervous system cancer; bladder cancer; pancreatic cancer;
XX  cervical cancer; melanoma; leukaemia; hybridisation probe;
XX  chromosome identification; chromosome mapping; gene mapping;
XX  gene therapy; cytostatic.
XX
OS  Homo sapiens.
XX
PN  WO2004030615-A2.
XX
XX  15-APR-2004.
XX
PF  29-SEP-2003; 2003WO-US028547.
XX
PR  02-OCT-2002; 2002US-0414971P.
XX
PA  (GETH ) GENENTECH INC.
XX
PI  Wu TD, Zhang Z, Zhou Y;

```


PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 XX
 PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
 XX
 DR WPI; 2004-061375/06.
 XX
 XX New recombinant DNA construct comprising a promoter positioned to provide
 PT for expression of a polynucleotide encoding a polypeptide from a
 PT microbial source, useful for producing plants with improved properties.
 XX
 PS Claim 1; SEQ ID NO 6358; 122pp; English.
 XX
 CC The invention relates to a recombinant DNA construct comprising a
 CC promoter functional in a plant cell, where the promoter is positioned to
 CC provide for expression of a polynucleotide encoding a polypeptide from a
 CC microbial source. The invention also relates to a transformed plant
 CC comprising the recombinant DNA construct and a method of producing a
 CC transformed plant having an improved property. The plant is a crop plant
 CC such as maize or soybean. The method of producing a transformed plant
 CC having an improved property comprises transforming a plant with the
 CC recombinant DNA construct and growing the transformed plant, where the
 CC polynucleotide or polypeptide is useful for improving plant properties.
 CC The recombinant DNA construct is useful for producing plants with
 CC improved plant properties, e.g. improved cold, heat or drought tolerance,
 CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
 CC increased resistance to plant disease, better growth rate by modification
 CC of the cell cycle pathway with plant growth regulators, increased rate of
 CC homologous recombination, modified seed oil or protein yield and/or
 CC content, improved yield by modification of carbohydrate, nitrogen or
 CC phosphorus use and/or uptake, by modification of photosynthesis or by
 CC providing improved plant growth and development under at least one stress
 CC condition, improved lignin production or improved galactomannan
 CC production. This sequence represents a bacterial polypeptide used in the
 CC scope of the invention. Note: The sequence data for this patent did not
 CC form part of the printed specification but was obtained in electronic
 CC format from USPTO at seqdata.uspto.gov/sequence.html.
 XX
 SQ Sequence 469 AA;
 Query Match 58.1%; Score 43; DB 8; Length 469;
 Best Local Similarity 58.3%; Pred. No. 91;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 Qy 3 NVSENVGSVCCT 14
 |||:|:|
 Db 330 NQSEIGNACCT 341
 RESULT 11
 ABR61598
 ID ABR61598 standard; protein; 762 AA.
 XX
 AC ABR61598;
 XX
 DT 15-JAN-2004 (first entry)
 XX
 DE Z. mays vacuolar pyrophosphatase.
 XX
 KW Silk exsersion; plant; transformation; transgenic; gl2; cell expansion;
 KW vacuolar pyrophosphatase; enzyme.
 XX
 OS Zea mays.
 XX
 XX WO2003087313-A2.
 XX
 PD 23-OCT-2003.
 XX
 PF 08-APR-2003; 2003WO-US010544.
 XX
 PR 08-APR-2002; 2002US-0370796P.
 XX

PA (PION-) PIONEER HI-BRED INT INC.
 XX
 PI Zinselmeier C, Helentjaris TG;
 XX
 DR WPI; 2003-845315/78.
 DR N-PSDB; ACF58166.
 XX
 PT Enhancing silk exsersion in a Zea mays plant under stress, relative to a
 PT non-transformed Zea mays plant under stress by transforming the plant or
 PT its ancestor with a construct comprising a silk-specific or silk-
 PT preferred promoter.
 XX
 PS Example; Page 94-98; Opp; English.
 XX
 CC The invention relates to enhancing silk exsersion in a Zea mays plant
 CC under stress, relative to a non-transformed Zea mays plant under stress.
 CC The method involves transforming the plant or its ancestor with a
 CC construct comprising a silk-specific or silk-preferred promoter operably
 CC linked to a polynucleotide encoding a polypeptide that increases cell
 CC division. The present sequence represents a Z. mays vacuolar
 CC pyrophosphatase, a polypeptide which increases the rate of cell expansion
 XX
 SQ Sequence 762 AA;
 Query Match 58.1%; Score 43; DB 7; Length 762;
 Best Local Similarity 58.3%; Pred. No. 1.5e+02;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 Qy 2 DNVSENVGSVCCT 13
 |||:|:|:|
 Db 275 DNVGDNVGDIAG 286
 RESULT 12
 ADS20925
 ID ADS20925 standard; protein; 764 AA.
 XX
 AC ADS20925;
 XX
 DT 16-DEC-2004 (first entry)
 XX
 DE Beta vulgaris vacuolar beta pyrophosphatase (Bvpl) protein SeqID 5.
 XX
 KW beta pyrophosphatase; bvp1; enzyme; transgenic; sugar beet; plant;
 KW vacuolar pyrophosphatase; V-Pase; cytosolic pyrophosphatase;
 KW nuclear localised pyrophosphatase; C-Pase.
 XX
 OS Beta vulgaris.
 XX
 PN WO2004083440-A1.
 XX
 PD 30-SEP-2004.
 XX
 PF 14-FEB-2004; 2004WO-EP001405.
 XX
 PR 20-MAR-2003; 2003DE-01013795.
 XX
 XX (SUED-) SUEBZUCKER AG MANNHEIM/OCHSENFURT.
 PA
 PI Greiner S, Harms K, Kunz M, Munir M, Rausch T, Schirmer M;
 XX
 DR WPI; 2004-691058/67.
 DR N-PSDB; ADS20924.
 XX
 XX Preparation of transgenic sugar beet with increased sucrose content, by
 PT transformation with genes encoding both vacuolar and cytosolic/nuclear
 PT pyrophosphatase.
 XX
 PS Claim 2; SEQ ID NO 5; 89pp; German.
 XX
 CC This invention relates to a novel method for preparing a transgenic sugar
 CC beet plant. Specifically, it refers to the introduction into cells of at
 CC least two transgenes, one encoding vacuolar pyrophosphatase (V-Ppase) and

CC a second encoding a cytosolic and/or nuclear localised pyrophosphatase (C
 CC -Pase). The present invention describes producing transgenic plants with
 CC an increased sucrose content in the root, increased or prolonged meristem
 CC activity and/or reduced sucrose degradation during storage. The
 CC transgenes isolated from Beta vulgaris (B. vulgaris) are under the
 CC control of the cauliflower mosaic virus 35S promoter in separate vectors
 CC that were subsequently used to transform the sugar beet plant. This
 CC polypeptide sequence is the B. vulgaris vacuolar beta pyrophosphatase
 CC (bvpl) protein (V-Pase) of the invention.
 CC
 XX SQ Sequence 764 AA;

Query Match 58.1%; Score 43; DB 8; Length 764;
 Best Local Similarity 58.3%; Pred. No. 1.5e+02;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DNSENVSVCVCG 13
 ||| : ||| : |
 Db 277 DNVDNVDIAG 288

RESULT 13
 ABB91014
 ID ABB91014 standard; protein; 770 AA.
 XX
 AC ABB91014;
 XX
 DT 31-MAY-2002 (first entry)
 XX
 DE Herbicidally active polypeptide SEQ ID NO 225.
 XX
 KW Herbicidal; plant; agriculture; herbicide.
 XX
 OS Arabidopsis thaliana.
 XX
 PN WO200210210-A2.
 XX
 PD 07-FEB-2002.

XX
 XX 28-AUG-2001; 2001WO-EP009892.
 XX
 XX 28-AUG-2001; 2001WO-EP009892.
 XX
 XX (FARB) BAYER AG.
 XX
 XX Tietjen K, Weidler M;
 XX
 XX WPI; 2002-269010/31.
 XX
 XX Identifying plant target proteins for herbicidally active compounds,
 PT comprising aligning and comparing nucleic acid or amino acid sequences
 PT from plant with nucleic acid or amino acid sequences from non-plant
 PT organisms.
 XX

PS Claim 5; SEQ ID NO 225; 261pp + Sequence Listing; English.

XX
 XX The invention relates to identifying target proteins (ABB90790-ABB94016)
 CC for herbicidally active compounds, comprising aligning and comparing
 CC nucleic acid or amino acid sequences from plant with nucleic acid or
 CC amino acid sequences from non-plant organisms using suitable search
 CC parameters, where plant sequences having an E-value greater by a factor
 CC of 3 than the E-value of most similar non-plant sequences are selected.
 CC The polypeptides or nucleic acids encoding them are useful for
 CC identifying modulators. The identified modulators are useful as
 CC herbicides
 XX

XX SQ Sequence 770 AA;

Query Match 58.1%; Score 43; DB 5; Length 770;
 Best Local Similarity 58.3%; Pred. No. 1.5e+02;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DNSENVSVCVCG 13

Db 283 DNVDNVDIAG 294
 ||| : ||| : |

RESULT 14
 ABB61023
 ID ABB61023 standard; protein; 1849 AA.
 XX
 AC ABB61023;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster polypeptide SEQ ID NO 9861.
 XX
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.
 XX
 OS Drosophila melanogaster.
 XX
 PN WO200171042-A2.
 XX
 PD 27-SEP-2001.

XX 23-MAR-2001; 2001WO-US009231.

XX 23-MAR-2000; 2000US-0191637P.

XX 11-JUL-2000; 2000US-00614150.

XX (PEKE) PE CORP NY.

XX Venter JC, Adams M, Li PWD, Myers EW;

XX WPI; 2001-656860/75.

XX DR N-PSDB; ABL05126.

XX
 XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signaling and cell-cell
 PT interactions.

XX Disclosure; SEQ ID NO 9861; 21pp + Sequence Listing; English.

XX
 XX The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
 CC ABB72072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 1849 AA;

Query Match 58.1%; Score 43; DB 4; Length 1849;

Best Local Similarity 63.6%; Pred. No. 3.8e+02;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 NVSENVSVCVCG 13
 ||| : ||| : |

Db 1148 NVQMNIGVCG 1158

RESULT 15
 ABB25449
 ID ABB25449 standard; protein; 672 AA.
 XX
 AC ABB25449;

XX
 XX 16-APR-2003 (first entry)
 XX
 XX Aspergillus fumigatus essential gene protein #107.
 XX

KW Fungicide; cytostatic; essential gene; Aspergillus fumigatus; infection;
KW cancer; contamination; biofilm; antibody; immune response.

XX Aspergillus fumigatus.

XX WO200286090-A2.

PN

XX

PD

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

PI Jiang B, Tishkoff D, Zamudio C, Eroshkin AM, Hu W, Lemieux SM;

XX WPI; 2003-093124/08.

XX New purified or isolated nucleic acids of essential genes of Aspergillus
PT fumigatus, useful for treating or preventing infections by A. fumigatus,
PT or for treating a non-infectious disease in a subject e.g. cancer.

PS Disclosure; Page; 175pp; English.

XX The invention relates to novel purified or isolated nucleic acids of
CC essential genes of Aspergillus fumigatus. The isolated nucleic acids of
CC the invention are used to treat or prevent infections by a pathogenic
CC organism such as A. fumigatus, to treat a non-infectious disease in a
CC subject (e.g. cancer), to prevent or contain contamination of an object
CC by A. fumigatus, or to prevent or inhibit formation on a surface of a
CC biofilm comprising A. fumigatus. The polynucleotides are useful for
CC expressing recombinant protein for characterisation, screening or
CC therapeutic use, as markers for host tissues in which the pathogenic
CC organisms invade or reside, for comparing with the DNA sequence of A.
CC fumigatus to identify duplicated genes or paralogues having the same or
CC similar biochemical activity and/or function, for comparing with DNA
CC sequences of other related or distant pathogenic organisms to identify
CC potential orthologous essential or virulence genes, for selecting and
CC making oligomers for attachment to a nucleic acid array for examination
CC of expression patterns, for raising anti-protein antibodies, as an
CC antigen to raise anti-DNA antibodies or to elicit another immune
CC response, and for identifying polynucleotides encoding the other protein,
CC with which binding occurs or to identify inhibitors of the binding
CC interaction. The polypeptides may be used to raise antibodies or to
CC elicit immune response, as a reagent in assays designed to quantitatively
CC determine levels of the protein in biological fluids, as a marker for
CC host tissues in which pathogenic organism invade or reside, and to
CC isolate correlative receptors or ligands in the case of virulence
CC factors. This sequence represents a protein of one of the essential genes
CC of Aspergillus fumigatus of the invention

XX Sequence 672 AA;

Query Match 56.8%; Score 42; DB 6; Length 672;

Best Local Similarity 61.5%; Pred. No. 2e+02;

Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EDNVSENVGVCG 13

Db 41 EDSVQENYGVIG 53

Search completed: February 11, 2005, 03:03:28

Job time : 6.97442 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 11, 2005, 03:00:19 ; Search time 1.18159 Seconds
(without alignments)
884.478 Million cell updates/sec

Title: US-09-736-250-5
Perfect score: 74
Sequence: 1 EDNVSENVGVCGT 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pap.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pap.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pap.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pap.*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pap.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	74	100.0	14	3	US-09-054-492B-5
2	74	100.0	377	2	Sequence 5, Appli
3	74	100.0	377	3	Sequence 6, Appli
4	74	100.0	377	4	Sequence 1, Appli
5	41	55.4	544	1	Sequence 6, Appli
6	41	55.4	544	2	Sequence 8, Appli
7	41	55.4	544	3	Sequence 8, Appli
8	41	55.4	544	3	Sequence 8, Appli
9	41	55.4	544	3	Sequence 8, Appli
10	41	55.4	544	3	Sequence 8, Appli
11	41	55.4	544	3	Sequence 8, Appli
12	41	55.4	544	3	Sequence 8, Appli
13	41	55.4	544	3	Sequence 8, Appli
14	41	55.4	544	3	Sequence 8, Appli
15	41	55.4	544	4	Sequence 8, Appli
16	40	54.1	122	4	Sequence 912, App
17	40	54.1	201	4	Sequence 865, App
18	40	54.1	226	3	Sequence 8, Appli
19	39	52.7	1095	4	Sequence 6594, Ap
20	38	51.4	91	4	Sequence 3719, Ap
21	38	51.4	114	4	Sequence 4846, Ap
22	38	51.4	190	4	Sequence 954, App
23	38	51.4	316	4	Sequence 11232, A
24	37	50.0	91	4	Sequence 60251, A
25	37	50.0	132	4	Sequence 11744, A
26	37	50.0	157	4	Sequence 33175, A
27	37	50.0	157	4	Sequence 48392, A

28	37	50.0	332	4	US-09-270-767-44788	Sequence 44788, A
29	37	50.0	346	4	US-09-170-496D-254	Sequence 254, App
30	37	50.0	346	4	US-09-170-496D-274	Sequence 274, App
31	37	50.0	358	4	US-09-809-665A-155	Sequence 155, App
32	37	50.0	380	3	US-08-468-846-2	Sequence 2, Appli
33	37	50.0	380	3	US-08-915-096A-2	Sequence 2, Appli
34	37	50.0	384	4	US-09-949-016-9661	Sequence 9661, Ap
35	37	50.0	401	2	US-08-820-521-2	Sequence 2, Appli
36	37	50.0	401	3	US-09-248-715-2	Sequence 2, Appli
37	37	50.0	401	3	US-09-248-715-2	Sequence 2, Appli
38	37	50.0	488	4	US-09-809-665A-44	Sequence 44, Appli
39	37	50.0	568	4	US-09-198-452A-1073	Sequence 1073, Ap
40	37	50.0	684	4	US-09-809-665A-109	Sequence 109, App
41	37	50.0	697	4	US-09-252-391A-2783	Sequence 2783, A
42	37	50.0	698	4	US-09-438-185A-1000	Sequence 1000, Ap
43	37	50.0	699	4	US-09-540-236-2259	Sequence 2259, Ap
44	37	50.0	705	4	US-09-328-352-8112	Sequence 8112, Ap
45	37	50.0	716	4	US-09-809-665A-171	Sequence 171, App

ALIGNMENTS

RESULT 1
US-09-054-492B-5
; Sequence 5, Application US/09054492B
; Patent No. 6218115
; GENERAL INFORMATION:
; APPLICANT: TAKESHI NAKAMURA
; TITLE OF INVENTION: HUMAN CYCLIN I AND GENES ENCODING SAME
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY, MADISON & SUTRO
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/054,492B
; FILING DATE: APRIL 3, 1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: PAUL E. WHITE, JR.
; REGISTRATION NUMBER: 32,011
; REFERENCE/DOCKET NUMBER: 7898/252159
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; TELEX: 6714627CUSH
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-054-492B-5

Query Match 100.0%; Score 74; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 EDNVSENVGVCGT 14
Db 1 EDNVSENVGVCGT 14

RESULT 2

```
US-08-969-106-6
; Filing Date: APRIL 3, 1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: PAUL E. WHITE, JR.
; REGISTRATION NUMBER: 32,011
; REFERENCE/DOCKET NUMBER: 7898/252159
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; TELEX: 6714627CUSH
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 377
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-054-492B-1
Query Match 100.0%; Score 74; DB 3; Length 377;
Best Local Similarity 100.0%; Pred. No. 0.00042;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EDNVSENVGVCVT 14
Db 343 EDNVSENVGVCVT 356

RESULT 4
US-09-338-125-6
; Sequence 6, Application US/09338125
; Patent No. 6521412
; GENERAL INFORMATION:
; APPLICANT: Yang, M.
; APPLICANT: Nandabalan, K.
; APPLICANT: Schulz, V.
; TITLE OF INVENTION: CDK2 INTERACTIONS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER: US/09/338,125
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/969,106
; FILING DATE: 13-NOV-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7934-057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 377 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-969-106-6
Query Match 100.0%; Score 74; DB 2; Length 377;
Best Local Similarity 100.0%; Pred. No. 0.00042;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EDNVSENVGVCVT 14
Db 343 EDNVSENVGVCVT 356

RESULT 3
US-09-054-492B-1
; Sequence 1, Application US/09054492B
; Patent No. 6218115
; GENERAL INFORMATION:
; APPLICANT: TAKESHI NAKAMURA
; TITLE OF INVENTION: HUMAN CYCLIN I AND GENES ENCODING SAME
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY, MADISON & SUTRO
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/054,492B
```

```
Query Match      100.0%; Score 74; DB 4; Length 377;
Best Local Similarity 100.0%; Pred. No. 0.00042;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 EDNVSENVGSGCT 14
Db      343 EDNVSENVGSGCT 356

RESULT 5
US-08-472-028A-8
; Sequence 8, Application US/08472028A
; Patent No. 5767373
; GENERAL INFORMATION:
; APPLICANT: Ward, Eric R
; APPLICANT: Volrath, Sandra
; TITLE OF INVENTION: Manipulation of Protoporphyrinogen
; TITLE OF INVENTION: Oxidase Enzyme Activity in Eukaryotic Organisms
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba-Geigy Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472.028A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: CGC 1748/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8614
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 544 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-472-028A-8

Query Match      55.4%; Score 41; DB 1; Length 544;
Best Local Similarity 58.3%; Pred. No. 1.2e+02;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy      1 EDNVSENVGSGC 12
Db      182 EEHLSVSGSFC 193

RESULT 6
US-08-808-931-8
; Sequence 8, Application US/08808931
; Patent No. 5939602
; GENERAL INFORMATION:
; APPLICANT: Volrath, Sandra
; APPLICANT: Johnson, Marie
; APPLICANT: Potter, Sharon
; APPLICANT: Ward, Eric
; APPLICANT: Heifetz, Peter
; TITLE OF INVENTION: DNA Molecules Encoding Plant
; TITLE OF INVENTION: Protoporphyrinogen Oxidase and Inhibitor-Resistant Mutants
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 35
```

```
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5939602artis Corporation
; STREET: 520 White Plains Road, P.O. Box 2005
; CITY: Tarrytown
; STATE: NY
; COUNTRY: USA
; ZIP: 10591-9005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/808,931
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/012,705
; FILING DATE: 28-FEB-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,612
; FILING DATE: 28-FEB-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/020,003
; FILING DATE: 21-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: CGC 1847
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8587
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 544 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-808-931-8

Query Match      55.4%; Score 41; DB 2; Length 544;
Best Local Similarity 58.3%; Pred. No. 1.2e+02;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy      1 EDNVSENVGSGC 12
Db      182 EEHLSVSGSFC 193

RESULT 7
US-08-808-323-8
; Sequence 8, Application US/08808323
; Patent No. 6018105
; GENERAL INFORMATION:
; APPLICANT: Johnson, Marie
; APPLICANT: Volrath, Sandra
; APPLICANT: Ward, Eric
; TITLE OF INVENTION: Promoters from Plant
; TITLE OF INVENTION: Protoporphyrinogen Oxidase Genes
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6018105artis Corporation
; STREET: 520 White Plains Road, P.O. Box 2005
; CITY: Tarrytown
; STATE: NY
; COUNTRY: USA
; ZIP: 10591-9005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
```

APPLICATION NUMBER: US/08/808,323
FILING DATE: 28-FEB-1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/012,705
FILING DATE: 28-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC 1846
TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 544 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-808-323-8

Query Match 55.4%; Score 41; DB 3; Length 544;
Best Local Similarity 58.3%; Pred. No. 1.2e+02;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EDNVSENVGSVC 12
Db 182 EEHLSVGSFC 193

RESULT 8

US-09-050-603A-8
Sequence 8, Application US/09050603A
Patent No. 6023012
GENERAL INFORMATION:
APPLICANT: Volrath, Sandra
APPLICANT: Johnson, Marie
APPLICANT: Potter, Sharon
APPLICANT: Ward, Eric
APPLICANT: Heifetz, Peter
TITLE OF INVENTION: DNA Molecules Encoding Plant
PROTOPORPHYRINOGEN OXIDASE
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6023012artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/050,603A
FILING DATE: 30-MAR-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/808,931
FILING DATE: 28-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/012,705
FILING DATE: 28-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,612

FILING DATE: 28-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/020,003
FILING DATE: 21-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC 1847
TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 544 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-050-603A-8

Query Match 55.4%; Score 41; DB 3; Length 544;
Best Local Similarity 58.3%; Pred. No. 1.2e+02;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EDNVSENVGSVC 12
Db 182 EEHLSVGSFC 193

RESULT 9

US-09-102-420B-8
Sequence 8, Application US/09102420B
Patent No. 6084155
GENERAL INFORMATION:
APPLICANT: Volrath, Sandra
APPLICANT: Johnson, Marie
APPLICANT: Ward, Eric
APPLICANT: Heifetz, Peter
TITLE OF INVENTION: HERBICIDE-TOLERANT PROTOPORPHYRINOGEN
OXIDASE ("PROTOX")
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6084155artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/102,420B
FILING DATE: 22-JUN-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/059,164
FILING DATE: 13-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/050,603
FILING DATE: 30-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/126,430
FILING DATE: 11-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/808,931
FILING DATE: 28-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/012,705
FILING DATE: 28-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,612

```
;; FILING DATE: 28-FEB-1996
;; PRIOR APPLICATION NUMBER: US 60/020,003
;; FILING DATE: 21-JUN-1996
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/472,028
;; FILING DATE: 06-JUN-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Weigs, J. Timothy
;; REGISTRATION NUMBER: 38,241
;; REFERENCE/DOCKET NUMBER: CGC 1847/CIP3
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (919) 541-8587
;; TELEFAX: (919) 541-8689
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 544 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-09-102-420B-8

Query Match 55.4%; Score 41; DB 3; Length 544;
Best Local Similarity 58.3%; Pred. No. 1.2e+02;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EDNVSENVGSVC 12
Db 182 EEHLSVGSVC 193

RESULT 10
US-09-071-296-8
; Sequence 8, Application US/09071296
; Patent No. 6177245
; GENERAL INFORMATION:
; APPLICANT: Ward, Eric R
; APPLICANT: Volrath, Sandra
; TITLE OF INVENTION: Manipulation of Protoporphyrinogen
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba-Geigy Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,296
; FILING DATE: 06-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/261,198
; FILING DATE: 16-JUN-94
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: CGC 1748/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8614
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 544 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

Query Match 55.4%; Score 41; DB 3; Length 544;
Best Local Similarity 58.3%; Pred. No. 1.2e+02;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EDNVSENVGSVC 12
Db 182 EEHLSVGSVC 193

RESULT 12
US-09-015-683-8
; Sequence 8, Application US/09015683
; Patent No. 6288306
; GENERAL INFORMATION:
; APPLICANT: Ward, Eric R
; APPLICANT: Volrath, Sandra
; TITLE OF INVENTION: Manipulation of Protoporphyrinogen
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba-Geigy Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,296
; FILING DATE: 06-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/261,198
; FILING DATE: 16-JUN-94
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: CGC 1748/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8614
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 544 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
```

```
US-09-071-296-8

Query Match 55.4%; Score 41; DB 3; Length 544;
Best Local Similarity 58.3%; Pred. No. 1.2e+02;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EDNVSENVGSVC 12
Db 182 EEHLSVGSVC 193

RESULT 11
US-09-196-268-8
; Sequence 8, Application US/09196268
; Patent No. 6282837
; GENERAL INFORMATION:
; APPLICANT: Ward, Eric R
; APPLICANT: Volrath, Sandra
; TITLE OF INVENTION: Manipulation of Protoporphyrinogen
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba-Geigy Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/196,268
; FILING DATE: 06-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/261,198
; FILING DATE: 16-JUN-94
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: CGC 1748/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8614
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 544 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-09-196-268-8

Query Match 55.4%; Score 41; DB 3; Length 544;
Best Local Similarity 58.3%; Pred. No. 1.2e+02;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EDNVSENVGSVC 12
Db 182 EEHLSVGSVC 193

RESULT 12
US-09-015-683-8
; Sequence 8, Application US/09015683
; Patent No. 6288306
; GENERAL INFORMATION:
; APPLICANT: Ward, Eric R
; APPLICANT: Volrath, Sandra
; TITLE OF INVENTION: Manipulation of Protoporphyrinogen
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba-Geigy Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,296
; FILING DATE: 06-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/261,198
; FILING DATE: 16-JUN-94
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: CGC 1748/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8614
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 544 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
```

NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ciba-Geigy Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: NY
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/015,683
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: CGC 1748/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8614
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 544 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-015-683-8

Query Match 55.4%; Score 41; DB 3; Length 544;
Best Local Similarity 58.3%; Pred. No. 1.2e+02;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EDNVSENVGVC 12
|:::|::|::|
Db 182 EEHLSVSGSFC 193

RESULT 13
US-09-191-998-8
Sequence 8, Application US/09191998
Patent No. 6307129
GENERAL INFORMATION:
APPLICANT: Ward, Eric R
TITLE OF INVENTION: Manipulation of Protoporphyrinogen
TITLE OF INVENTION: Oxidase Enzyme Activity in Eukaryotic Organisms
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ciba-Geigy Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: NY
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/191,998
FILING DATE: 06-JUN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/261,198
FILING DATE: 16-JUN-94
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129

REFERENCE/DOCKET NUMBER: CGC 1748/CIP.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8614
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 544 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-191-998-8

Query Match 55.4%; Score 41; DB 3; Length 544;
Best Local Similarity 58.3%; Pred. No. 1.2e+02;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EDNVSENVGVC 12
|:::|::|::|
Db 182 EEHLSVSGSFC 193

RESULT 14
US-09-497-698-8
Sequence 8, Application US/09497698
Patent No. 6308458
GENERAL INFORMATION:
APPLICANT: Volrath, Sandra
Johnson, Marie
Ward, Eric
Heifetz, Peter
TITLE OF INVENTION: HERBICIDE-TOLERANT PROTOPORPHYRINOGEN
OXIDASE ("PROTOX")
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6308458artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/497,698
FILING DATE: 03-Feb-2000
CLASSIFICATION: <Unknown>
30-MAR-1998
11-MAR-1998
28-FEB-1997
28-FEB-1996
28-FEB-1996
21-JUN-1996
06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/102,420
FILING DATE: <Unknown>
APPLICATION NUMBER: US 09/050,603
FILING DATE: 30-MAR-1998
APPLICATION NUMBER: US 60/126,430
FILING DATE: 11-MAR-1998
APPLICATION NUMBER: US 08/808,931
FILING DATE: 28-FEB-1997
APPLICATION NUMBER: US 60/012,705
FILING DATE: 28-FEB-1996
APPLICATION NUMBER: US 60/013,612
FILING DATE: 28-FEB-1996
APPLICATION NUMBER: US 60/020,003
FILING DATE: 21-JUN-1996
APPLICATION NUMBER: US 08/472,028
FILING DATE: 06-JUN-1995


```
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: CGC 1847/CIP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8587
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 8:
; LENGTH: 544 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
; US-09-497-698-8
;
; Query Match 55.4%; Score 41; DB 3; Length 544;
; Best Local Similarity 58.3%; Pred. No. 1.2e+02;
; Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
;
; QY 1 EDNVSENVGSVC 12
; |::|::|::|
; Db 182 EEHLSVSGSFC 193
;
; RESULT 15
; US-09-730-525-8
; Sequence 8, Application US/09730525
; Patent No. 6808904
; GENERAL INFORMATION:
; APPLICANT: Ward, Eric
; Volrath, Sandra
; Johnson, Marie
; Potter, Sharon
; TITLE OF INVENTION: Herbicide Tolerant Protox Genes
; PRODUCED BY DNA SHUFFLING
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6808904artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/730,525
; FILING DATE: 05-Dec-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/102,419
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 09/050,603
; FILING DATE: 30-MAR-1998
; APPLICATION NUMBER: US 09/038,878
; FILING DATE: 11-MAR-1998
; APPLICATION NUMBER: US 08/808,931
; FILING DATE: 28-FEB-1997
; APPLICATION NUMBER: US 60/012,705
; FILING DATE: 28-FEB-1996
; APPLICATION NUMBER: US 60/013,612
; FILING DATE: 28-FEB-1996
; APPLICATION NUMBER: US 60/020,003
; FILING DATE: 21-JUN-1996
; APPLICATION NUMBER: US 08/472,028
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
;
; REFERENCE/DOCKET NUMBER: CGC 1847/CIP4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8587
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 8:
; LENGTH: 544 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
; US-09-730-525-8
;
; Query Match 55.4%; Score 41; DB 4; Length 544;
; Best Local Similarity 58.3%; Pred. No. 1.2e+02;
; Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
;
; QY 1 EDNVSENVGSVC 12
; |::|::|::|
; Db 182 EEHLSVSGSFC 193
;
; Search completed: February 11, 2005, 03:06:29
; Job time : 2.18159 secs
```

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 11, 2005, 03:05:24 ; Search time 3.22251 Seconds
(without alignments)
1419.543 Million cell updates/sec

Title: US-09-736-250-5

Perfect score: 74

Sequence: 1 EDNVSENVGVCVT 14

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1376875 seqs, 326749119 residues

Total number of hits satisfying chosen parameters: 1376875

Minimum DB-seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	74	100.0	14	US-09-736-250-5	Sequence 5, Appli
2	74	100.0	377	US-09-736-250-1	Sequence 1, Appli
3	44	59.5	109	US-10-424-599-246648	Sequence 246648, A
4	43	58.1	226	US-10-424-599-272932	Sequence 272932, A
5	43	58.1	469	US-10-369-493-6358	Sequence 6358, Ap
6	43	58.1	489	US-10-767-701-45549	Sequence 45549, A
7	43	58.1	504	US-10-767-701-46948	Sequence 46948, A
8	43	58.1	551	US-10-425-114-71458	Sequence 71458, A
9	43	58.1	762	US-10-409-701-25	Sequence 25, Appli
10	43	58.1	766	US-10-767-701-46989	Sequence 46989, A
11	43	58.1	767	US-10-424-599-198727	Sequence 198727, A
12	43	58.1	956	US-10-437-963-167398	Sequence 167398, A
13	43	58.1	966	US-10-437-963-134857	Sequence 134857, A

14	42	56.8	136	15	US-10-425-114-68537	Sequence 68537, A
15	42	56.8	208	15	US-10-425-114-68381	Sequence 68381, A
16	42	56.8	672	14	US-10-128-714-3107	Sequence 3107, Ap
17	42	56.8	672	14	US-10-128-714-8107	Sequence 8107, Ap
18	41	55.4	544	9	US-09-730-525-8	Sequence 8, Appli
19	41	55.4	544	9	US-09-730-917-8	Sequence 8, Appli
20	40	54.1	129	16	US-10-767-701-37922	Sequence 37922, A
21	40	54.1	135	15	US-10-264-237-1535	Sequence 1535, Ap
22	40	54.1	177	16	US-10-408-765A-2331	Sequence 2331, Ap
23	40	54.1	201	16	US-10-408-765A-39	Sequence 39, Appli
24	39	52.7	336	15	US-10-282-122A-58646	Sequence 58646, A
25	39	52.7	337	16	US-10-437-963-130322	Sequence 130322, A
26	39	52.7	345	9	US-09-815-242-11068	Sequence 11068, A
27	39	52.7	503	9	US-09-801-368-424	Sequence 424, App
28	39	52.7	503	15	US-10-369-493-1943	Sequence 1943, Ap
29	39	52.7	699	15	US-10-369-493-13011	Sequence 13011, A
30	39	52.7	729	15	US-10-282-122A-61234	Sequence 61234, A
31	39	52.7	801	14	US-10-156-761-12150	Sequence 12150, A
32	39	52.7	1037	16	US-10-437-963-170931	Sequence 170931, A
33	38	51.4	39	15	US-10-424-599-267118	Sequence 267118, A
34	38	51.4	126	16	US-10-437-963-132930	Sequence 132930, A
35	38	51.4	159	17	US-10-472-928-74	Sequence 74, Appli
36	38	51.4	309	15	US-10-424-599-238011	Sequence 238011, A
37	38	51.4	358	9	US-09-815-242-10187	Sequence 10187, A
38	38	51.4	358	15	US-10-369-493-866	Sequence 866, App
39	38	51.4	358	15	US-10-282-122A-56577	Sequence 56577, A
40	38	51.4	365	15	US-10-425-114-42890	Sequence 42890, A
41	38	51.4	371	15	US-10-424-599-207707	Sequence 207707, A
42	38	51.4	483	15	US-10-424-599-258507	Sequence 258507, A
43	38	51.4	662	16	US-10-437-963-134490	Sequence 134490, A
44	38	51.4	700	16	US-10-437-963-127893	Sequence 127893, A
45	38	51.4	709	15	US-10-282-122A-77113	Sequence 77113, A

ALIGNMENTS

RESULT 1
US-09-736-250-5
; Sequence 5, Application US/09736250
; Publication No. US20050014139A1
; GENERAL INFORMATION:
; APPLICANT: SUMITOMO ELECTRIC INDUSTRIES, LTD.
; APPLICANT: NAKAMURA, Takeshi
; TITLE OF INVENTION: HUMAN CYCLIN I AND GENES ENCODING THE SAME
; FILE REFERENCE: 050212-0278
; CURRENT APPLICATION NUMBER: US/09/736,250
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 09/054,492
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: PCT/JP96/02905
; PRIOR FILING DATE: 1996-10-07
; PRIOR APPLICATION NUMBER: 284663/1995
; PRIOR FILING DATE: 1995-10-05
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 5
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically synthesized
US-09-736-250-5

Query Match 100.0%; Score 74; DB 12; Length 14;
Best Local Similarity 100.0%; Pred. No. 3e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EDNVSENVGVCVT 14
Db 1 EDNVSENVGVCVT 14

RESULT 2
US-09-736-250-1
; Sequence 1, Application US/09736250
; Publication No. US20050014139A1
; GENERAL INFORMATION:
; APPLICANT: SUMITOMO ELECTRIC INDUSTRIES, LTD.
; APPLICANT: NAKAMURA, Takeshi
; TITLE OF INVENTION: HUMAN CYCLIN I AND GENES ENCODING THE SAME
; FILE REFERENCE: 050212-0278
; CURRENT APPLICATION NUMBER: US/09/736.250
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 09/054,492
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: PCT/JP96/02905
; PRIOR FILING DATE: 1996-10-07
; PRIOR APPLICATION NUMBER: 284663/1995
; PRIOR FILING DATE: 1995-10-05
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 1
; TYPE: PRT
; LENGTH: 377
; ORGANISM: Homo sapiens
US-09-736-250-1

Query Match 100.0%; Score 74; DB 12; Length 377;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EDNVSENVGVCCT 14
Db 343 EDNVSENVGVCCT 356

RESULT 3
US-10-424-599-246648
; Sequence 246648, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 246648
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_64754C.1.pap
US-10-424-599-246648

Query Match 59.5%; Score 44; DB 15; Length 109;
Best Local Similarity 77.8%; Pred. No. 19;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 5 SENGVGVC 13
Db 79 AENVGSICG 87

RESULT 4
US-10-424-599-272932
; Sequence 272932, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K

; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 272932
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(226)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_88480C.1.pap
US-10-424-599-272932

Query Match 58.1%; Score 43; DB 15; Length 226;
Best Local Similarity 58.3%; Pred. No. 60;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DNVSSENVGVC 13
Db 16 DNVDGNDVGIAG 27

RESULT 5
US-10-369-493-6358
; Sequence 6358, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 6358
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-6358

Query Match 58.1%; Score 43; DB 15; Length 469;
Best Local Similarity 58.3%; Pred. No. 1.3e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 3 NVSENVGVCCT 14
Db 330 NQSEENACGT 341

RESULT 6

US-10-767-701-45549
; Sequence 45549, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B

; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 45549
; LENGTH: 489
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(489)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C8573_1.pep
US-10-767-701-45549

Query Match 58.1%; Score 43; DB 16; Length 489;
Best Local Similarity 58.3%; Pred. No. 1.4e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DNSENVSVCVCG 13
||| :||| :
Db 76 DNVDNVDIAG 87

RESULT 7

US-10-767-701-46948
; Sequence 46948, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 46948
; LENGTH: 504
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(504)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C49_282.pep
US-10-767-701-46948

Query Match 58.1%; Score 43; DB 16; Length 504;
Best Local Similarity 58.3%; Pred. No. 1.4e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DNSENVSVCVCG 13
||| :||| :
Db 276 DNVDNVDIAG 287

RESULT 8

US-10-425-114-71458
; Sequence 71458, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53313)B

; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 71458
; LENGTH: 551
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700101735_FLI.pep
US-10-425-114-71458

Query Match 58.1%; Score 43; DB 15; Length 551;
Best Local Similarity 58.3%; Pred. No. 1.6e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DNSENVSVCVCG 13
||| :||| :
Db 64 DNVDNVDIAG 75

RESULT 9

US-10-409-701-25
; Sequence 25, Application US/10409701
; Publication No. US20030221224A1
; GENERAL INFORMATION:
; APPLICANT: Zinselmeier, Chris
; APPLICANT: Helentjaris, Timothy G.
; TITLE OF INVENTION: Enhanced Silk Exsersion Under Stress
; FILE REFERENCE: 1421
; CURRENT APPLICATION NUMBER: US/10/409,701
; CURRENT FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: US 60/370,796
; PRIOR FILING DATE: 2002-04-08
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 762
; TYPE: PRT
; ORGANISM: Zea mays
US-10-409-701-25

Query Match 58.1%; Score 43; DB 15; Length 762;
Best Local Similarity 58.3%; Pred. No. 2.2e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DNSENVSVCVCG 13
||| :||| :
Db 275 DNVDNVDIAG 286

RESULT 10

US-10-767-701-46989
; Sequence 46989, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 46989
; LENGTH: 766
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C49_323.pep
US-10-767-701-46989

Query Match 58.1%; Score 43; DB 16; Length 766;

Best Local Similarity 58.3%; Pred. No. 2.2e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 DNVSENVGSVC 13
|||:||||:
DB 279 DNVDNVGDIAG 290

RESULT 11
US-10-424-599-198727
; Sequence 198727, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 198727
; LENGTH: 767
; TYPE: PRT
; ORGANISM: Glycine max
; NAME/KEY: unsure
; LOCATION: (1)...(767)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_21474C.1.pep
US-10-424-599-198727

Query Match 58.1%; Score 43; DB 15; Length 767;
Best Local Similarity 58.3%; Pred. No. 2.2e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 DNVSENVGSVC 13
|||:||||:
DB 281 DNVDNVGDIAG 292

RESULT 12
US-10-437-963-167398
; Sequence 167398, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 167398
; LENGTH: 956
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_66012C.1.pep
US-10-437-963-167398

Query Match 58.1%; Score 43; DB 16; Length 956;
Best Local Similarity 66.7%; Pred. No. 2.8e+02;

Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 EDNVSENVGSVC 12
|||:||||:
DB 563 EDCISENLGSRG 574

RESULT 13
US-10-437-963-134857
; Sequence 134857, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 134857
; LENGTH: 966
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_3658C.1.pep
US-10-437-963-134857

Query Match 58.1%; Score 43; DB 16; Length 966;
Best Local Similarity 58.3%; Pred. No. 2.8e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 DNVSENVGSVC 13
|||:||||:
DB 481 DNVDNVGDIAG 492

RESULT 14
US-10-425-114-68537
; Sequence 68537, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 68537
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMROMO17114A05_FLI.pep
US-10-425-114-68537

Query Match 56.8%; Score 42; DB 15; Length 136;
Best Local Similarity 58.3%; Pred. No. 51;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 DNVSENVGSVC 13

Db 25 DNVGDNVGDIVG 36
||| :||| : |
RESULT 15
US-10-425-114-68381
; Sequence 68381, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 68381
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLMO17138G11_FLI.pep
US-10-425-114-68381
Query Match 56.8%; Score 42; DB 15; Length 208;
Best Local Similarity 58.3%; Pred. No. 80;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Qy 2 DNVSENVGSVCG 13
||| :||| : |
Db 97 DNVGDNVGDIVG 108

Search completed: February 11, 2005, 03:13:13
Job time : 4.22251 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 11, 2005, 02:59:54 ; Search time 1.07417 Seconds
(without alignments)
1254.025 Million cell updates/sec

Title: US-09-736-250-5

Perfect score: 74

Sequence: 1 EDNVSENVGSVCGT 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR.79.*

2: PIR1.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	59.5	726	2 D72409	pyrophosphatase, p
2	43	58.1	360	2 S54173	inorganic diphosph
3	43	58.1	469	2 T33963	hypothetical prote
4	43	58.1	541	2 S61425	inorganic diphosph
5	43	58.1	761	1 JCI466	inorganic diphosph
6	43	58.1	761	2 T14563	inorganic diphosph
7	43	58.1	764	2 S61422	inorganic diphosph
8	43	58.1	764	2 S42893	inorganic diphosph
9	43	58.1	765	2 S54172	inorganic diphosph
10	43	58.1	765	2 S61423	inorganic diphosph
11	43	58.1	765	2 T14564	inorganic diphosph
12	43	58.1	765	2 T10841	inorganic diphosph
13	43	58.1	766	2 S61424	inorganic diphosph
14	43	58.1	766	2 T07801	probable inorganic
15	43	58.1	767	2 S72527	inorganic diphosph
16	43	58.1	770	1 A38230	inorganic diphosph
17	43	58.1	771	2 S72526	inorganic diphosph
18	42	56.8	390	2 C84579	probable SET-domai
19	41	55.4	270	2 C97772	diaminopimelate ep
20	41	55.4	497	2 T41467	hypothetical prote
21	41	55.4	547	2 T30269	hypothetical prote
22	41	55.4	803	2 T10060	receptor-like prot
23	40	54.1	122	2 S05317	glutathione peroxi
24	40	54.1	187	2 S32968	probable membrane
25	40	54.1	190	1 A45207	glutathione peroxi
26	40	54.1	200	1 S03723	glutathione peroxi
27	40	54.1	201	1 OPMSE	glutathione peroxi
28	40	54.1	201	1 OPRTE	glutathione peroxi
29	40	54.1	202	1 OPHUE	glutathione peroxi

30	40	54.1	205	1 OPBOE	glutathione peroxi
31	40	54.1	226	2 T21380	hypothetical prote
32	40	54.1	512	2 A96695	hypothetical prote
33	40	54.1	1214	2 T21915	hypothetical prote
34	39	52.7	109	2 S64313	probable membrane
35	39	52.7	336	2 D64544	UDP-3-O-[3-hydroxy
36	39	52.7	345	2 C64082	ATP-binding protei
37	39	52.7	389	2 D64333	pyruvate synthase
38	39	52.7	503	2 S63257	probable membrane
39	39	52.7	712	2 AD2721	H+ translocating p
40	39	52.7	712	2 D87418	proton pump, proba
41	39	52.7	713	2 AE2586	polyribonucleotide
42	39	52.7	713	2 F97368	polyribonucleotide
43	39	52.7	714	2 H97502	H+ translocating p
44	39	52.7	714	2 AC3497	polyribonucleotide
45	39	52.7	775	2 AC3400	inorganic diphosph

ALIGNMENTS

RESULT 1

D72409

Pyrophosphatase, proton-translocating - Thermotoga maritima (strain MSB8)

C:Species: Thermotoga maritima

C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

C:Accession: D72409

R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
C.M.

Nature 399, 323-329, 1999

A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq

A:Reference number: A72200; MUID:99287316; PMID:10360571

A:Accession: D72409

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-726 <ARN>

A:Cross-references: UNIPROT:Q9S5X0; GB:AE001702; GB:AE000512; NID:g4980662; PIDN:AAD3526

A:Experimental source: strain MSB8

C:Genetics:

A:Gene: TM0174

C:Superfamily: H(+)-translocating inorganic pyrophosphatase

Query Match 59.5%; Score 44; DB 2; Length 726;

Best Local Similarity 66.7%; Pred. No. 11;

Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DNVSENVGSVCG 13

Db 228 DNVGDNVGDVAG 239

RESULT 2

S54173

Inorganic diphosphatase (EC 3.6.1.1) - common tobacco

C:Species: Nicotiana tabacum (common tobacco)

C:Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 03-Nov-2003

C:Accession: S54173

R:Lerchl, J.

submitted to the EMBL Data Library, January 1995

A:Reference number: S54169

A:Accession: S54173

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-360 <LER>

A:Cross-references: EMBL:X83729

C:Superfamily: H(+)-translocating inorganic pyrophosphatase

C:Keywords: hydrolase

Query Match 58.1%; Score 43; DB 2; Length 360;

Best Local Similarity 59.3%; Pred. No. 7.9;

Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DNSENVSVCVCG 13
||| :||| :
Db 279 DNVDNVGDIAG 290

RESULT 3

hypothetical protein F46E10.7 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C:Accession: T33963

R:Johnson, D.; Bradshaw, H.

submitted to the EMBL Data Library, February 1999

A:Description: The sequence of C. elegans cosmid F46E10.

A:Reference number: Z21446

A:Accession: T33963

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-469 <JOH>

A:Cross-references: EMBL:AF125955; PIDN:AAI4717.1; GSPDB:GN00023; CESP:F46E10.7

A:Experimental source: strain Bristol N2; clone F46E10

A:Genetics:

A:Gene: CESP:F46E10.7

A:Map position: 5

A:Introns: 20/3; 141/1; 181/1; 224/3; 242/3; 263/3; 384/1; 424/1

Query Match 58.1%; Score 43; DB 2; Length 469;
Best Local Similarity 58.3%; Pred. No. 10;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 3 NVSENVSVCVCGT 14
||| :||| :
Db 330 NQSEIGNACGT 341

RESULT 4

inorganic diphosphatase (EC 3.6.1.1), H⁺-translocating (clone TVP17), vacuolar membrane
C:Species: Nicotiana tabacum (common tobacco)

C>Date: 27-Apr-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004

C:Accession: S61425; S54171

R:Lerchl, J.; Koenig, S.; Zrenner, R.; Sonnwald, U.

Plant Mol. Biol. 29, 833-840, 1995

A>Title: Molecular cloning, characterization and expression analysis of isoforms encoding

A:Reference number: S61422; MUID:96128024; PMID:8541508

A:Accession: S61425

A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: mRNA

A:Residues: 1-541 <LER>

A:Cross-references: UNIPROT:Q43796; EMBL:X83728; NID:G790474; PIDN:CAA58699.1; PID:G7904

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1995

C:Superfamily: H⁺-translocating inorganic pyrophosphatase

C:Keywords: hydrolase; transmembrane protein

Query Match 58.1%; Score 43; DB 2; Length 541;
Best Local Similarity 58.3%; Pred. No. 12;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DNSENVSVCVCG 13
||| :||| :
Db 54 DNVDNVGDIAG 65

RESULT 5

JC1466

inorganic diphosphatase (EC 3.6.1.1) - barley

C:Species: Hordeum vulgare (barley)

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 27-Oct-2003

C:Accession: JC1466

R:Tanaka, Y.; Chiba, K.; Maeda, M.; Maeshima, M.

Biochem. Biophys. Res. Commun. 190, 1110-1114, 1993

A>Title: Molecular cloning of cDNA for vacuolar membrane proton-translocating inorganic

A:Reference number: JC1466; MUID:93176156; PMID:8382487

A:Accession: JC1466
A:Molecule type: mRNA
A:Residues: 1-761 <TAN>
A:Cross-references: DDBJ:D13472; NID:G285637; PIDN:BAA02717.1; PID:G285638
A:Experimental source: root

C:Superfamily: H⁺-translocating inorganic pyrophosphatase

C:Keywords: hydrolase; transmembrane protein

F:11-32/Domain: transmembrane #status predicted <TM1>

F:91-110/Domain: transmembrane #status predicted <TM2>

F:131-154/Domain: transmembrane #status predicted <TM3>

F:184-204/Domain: transmembrane #status predicted <TM4>

F:217-236/Domain: transmembrane #status predicted <TM5>

F:306-341/Domain: transmembrane #status predicted <TM6>

F:360-381/Domain: transmembrane #status predicted <TM7>

F:398-417/Domain: transmembrane #status predicted <TM8>

F:454-477/Domain: transmembrane #status predicted <TM9>

F:534-555/Domain: transmembrane #status predicted <TM10>

F:570-589/Domain: transmembrane #status predicted <TM11>

F:649-672/Domain: transmembrane #status predicted <TM12>

Query Match 58.1%; Score 43; DB 1; Length 761;
Best Local Similarity 58.3%; Pred. No. 17;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DNSENVSVCVCG 13
||| :||| :
Db 274 DNVDNVGDIAG 285

RESULT 6

Tl4563

inorganic diphosphatase (EC 3.6.1.1) - beet

C:Species: Beta vulgaris (beet)

C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 27-Oct-2003

C:Accession: Tl4563

R:Kim, Y.; Kim, E.J.; Rea, P.A.

Plant Physiol. 106, 375-382, 1994

A>Title: Isolation and characterization of cDNAs encoding the vacuolar H⁺-pyrophosphatase

A:Reference number: Z18141; MUID:95062743; PMID:7972521

A:Accession: Tl4563

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-761 <KIM>

A:Cross-references: EMBL:L32791; NID:G485741; PIDN:AAA61609.1; PID:G485742

A:Experimental source: strain Detroit dark

C:Function:

A:Description: catalyzes hydrolyzation of pyrophosphate

C:Superfamily: H⁺-translocating inorganic pyrophosphatase

C:Keywords: hydrolase

Query Match 58.1%; Score 43; DB 2; Length 761;
Best Local Similarity 58.3%; Pred. No. 17;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DNSENVSVCVCG 13
||| :||| :
Db 274 DNVDNVGDIAG 285

RESULT 7

S61422

inorganic diphosphatase (EC 3.6.1.1) (clone TVP5) - common tobacco

C:Species: Nicotiana tabacum (common tobacco)

C>Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 27-Oct-2003

C:Accession: S61422

R:Lerchl, J.; Koenig, S.; Zrenner, R.; Sonnwald, U.

Plant Mol. Biol. 29, 833-840, 1995

A>Title: Molecular cloning, characterization and expression analysis of isoforms encoding

A:Reference number: S61422; MUID:96128024; PMID:8541508

A:Accession: S61422

A>Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-764 <LER>

A;Cross-references: EMBL:X77915
A;Superfamily: H(+)-translocating inorganic pyrophosphatase
C;Keywords: hydrolase

Query Match 58.1%; Score 43; DB 2; Length 764;
Best Local Similarity 58.3%; Pred. No. 18;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DNVSNNVSVCG 13
|||:||||:|
Db 277 DNVDNVDIAG 288

RESULT 8
S42893
inorganic diphosphatase (EC 3.6.1.1) - common tobacco
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 20-May-1994 #sequence_revision 10-Nov-1995 #text_change 27-Oct-2003
C;Accession: S42893
R;Lerchl, J.
submitted to the EMBL Data Library, February 1994

A;Reference number: S42893
A;Accession: S42893
A;Molecule type: mRNA
A;Residues: 1-764 <LER>
A;Cross-references: EMBL:X77915; NID:g633598; PIDN:CAA54869.1; PID:g457744
C;Superfamily: H(+)-translocating inorganic pyrophosphatase
C;Keywords: hydrolase

Query Match 58.1%; Score 43; DB 2; Length 764;
Best Local Similarity 58.3%; Pred. No. 18;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DNVSNNVSVCG 13
|||:||||:|
Db 277 DNVDNVDIAG 288

RESULT 9
S54172
inorganic diphosphatase (EC 3.6.1.1) - common tobacco
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 27-Oct-2003
C;Accession: S54172
R;Lerchl, J.
submitted to the EMBL Data Library, January 1995

A;Reference number: S54169
A;Accession: S54172
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-765 <LER>
A;Cross-references: EMBL:X83730; NID:g790478; PIDN:CAA58701.1; PID:g790479
C;Superfamily: H(+)-translocating inorganic pyrophosphatase
C;Keywords: hydrolase

Query Match 58.1%; Score 43; DB 2; Length 765;
Best Local Similarity 58.3%; Pred. No. 18;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DNVSNNVSVCG 13
|||:||||:|
Db 278 DNVDNVDIAG 289

RESULT 10
S61423
inorganic diphosphatase (EC 3.6.1.1) (clone TVP9) - common tobacco
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 27-Oct-2003
C;Accession: S61423
R;Lerchl, J.; Koenig, S.; Zrenner, R.; Sonnwald, U.
Plant Mol. Biol. 29, 833-840, 1995
A;Title: Molecular cloning, characterization and expression analysis of isoforms encoding

A;Reference number: S61422; MUID:96128024; PMID:8541508
A;Accession: S61423
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-765 <LER>
A;Cross-references: EMBL:X83730
C;Superfamily: H(+)-translocating inorganic pyrophosphatase
C;Keywords: hydrolase

Query Match 58.1%; Score 43; DB 2; Length 765;
Best Local Similarity 58.3%; Pred. No. 18;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DNVSNNVSVCG 13
|||:||||:|
Db 278 DNVDNVDIAG 289

RESULT 11
T14564
inorganic diphosphatase (EC 3.6.1.1), vacuolar - beet
C;Species: Beta vulgaris (beet)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 27-Oct-2003
C;Accession: T14564
R;Kim, Y.; Kim, E.J.; Rea, P.A.
Plant Physiol. 106, 375-382, 1994
A;Title: Isolation and characterization of cDNAs encoding the vacuolar H(+)-pyrophosphatase
A;Reference number: Z18141; MUID:95062743; PMID:7972521
A;Accession: T14564
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-765 <KIM>
A;Cross-references: EMBL:L32792; NID:g485743; PIDN:AAA61610.1; PID:g485744
A;Experimental source: strain Detroit dark
C;Function:
A;Description: catalyzes the electrogenic translocation of H+ from the cytosol to vacuol
C;Superfamily: H(+)-translocating inorganic pyrophosphatase
C;Keywords: hydrolase

Query Match 58.1%; Score 43; DB 2; Length 765;
Best Local Similarity 58.3%; Pred. No. 18;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DNVSNNVSVCG 13
|||:||||:|
Db 277 DNVDNVDIAG 288

RESULT 12
T10841
inorganic diphosphatase (EC 3.6.1.1) - mung bean
C;Species: Vigna radiata (mung bean)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T10841
R;Hung, S.
submitted to the EMBL Data Library, July 1995

A;Reference number: Z17181
A;Accession: T10841
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-765 <HUN>
A;Cross-references: UNIPROT:P21616; EMBL:U31467; NID:g951322; PID:g951323
A;Experimental source: tissue type hypocotyl; clone VVP
C;Superfamily: H(+)-translocating inorganic pyrophosphatase
C;Keywords: hydrolase

Query Match 58.1%; Score 43; DB 2; Length 765;
Best Local Similarity 58.3%; Pred. No. 18;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DNVSNNVSVCG 13
|||:||||:|
Db 279 DNVDNVDIAG 290

C;Superfamily: H(+)-translocating inorganic pyrophosphatase
C;Keywords: hydrolase

Query Match 58.1%; Score 43; DB 2; Length 767;
Best Local Similarity 58.3%; Pred. No. 18;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 DNVSENVGVCVCG 13
|||:||||:|
DB 280 DNVDNVGDIAG 291

Search completed: February 11, 2005, 03:05:49
Job time : 2.07417 secs

RESULT 13
S61424
inorganic diphosphatase (EC 3.6.1.1) (clone TVP31) - common tobacco
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 27-Oct-2003
C;Accession: S61424
R;Lerchl, J.; Koenig, S.; Zrenner, R.; Sonnwald, U.
Plant Mol. Biol. 29, 833-840, 1995
A;Title: Molecular cloning, characterization and expression analysis of isoforms encoding
A;Reference number: S61422; MUID:96128024; PMID:8541508
A;Accession: S61424
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-766 <LER>
A;Cross-references: EMBL:X83729
C;Superfamily: H(+)-translocating inorganic pyrophosphatase
C;Keywords: hydrolase

Query Match 58.1%; Score 43; DB 2; Length 766;
Best Local Similarity 58.3%; Pred. No. 18;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 DNVSENVGVCVCG 13
|||:||||:|
DB 279 DNVDNVGDIAG 290

RESULT 14
T07801
probable inorganic diphosphatase (EC 3.6.1.1) - mung bean
C;Species: Vigna radiata (mung bean)
C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 27-Oct-2003
C;Accession: T07801
R;Nakanishi, Y.; Maeshima, M.
Plant Physiol. 116, 589-597, 1998
A;Title: Molecular cloning of vacuolar H(+)-pyrophosphatase and its developmental expres
A;Reference number: 216141; MUID:98150269; PMID:9489011
A;Accession: T07801
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-766 <NAK>
A;Cross-references: EMBL:AB009077; NID:g2653445; PIDN:BAA23649.1; PID:g2653446
A;Experimental source: strain Wilczek
C;Superfamily: H(+)-translocating inorganic pyrophosphatase
C;Keywords: hydrolase

Query Match 58.1%; Score 43; DB 2; Length 766;
Best Local Similarity 58.3%; Pred. No. 18;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 DNVSENVGVCVCG 13
|||:||||:|
DB 279 DNVDNVGDIAG 290

RESULT 15
S72527
inorganic diphosphatase (EC 3.6.1.1), H(+)-translocating, vacuolar membrane (clone OVP2)
C;Species: Oryza sativa (rice)
C;Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 09-Jul-2004
C;Accession: S72527
R;Sakakibara, Y.; Kobayashi, H.; Kasamo, K.
Plant Mol. Biol. 31, 1029-1038, 1996
A;Title: Isolation and characterization of cDNAs encoding vacuolar H(+)-pyrophosphatase
A;Reference number: S72526; MUID:97000915; PMID:8843945
A;Accession: S72527
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-767 <SAK>
A;Cross-references: UNIPROT:Q8H616; EMBL:D45384; NID:g1747295; PIDN:BAA08233.1; PID:g174
A;Note: only a part of the nucleic acid sequence is shown

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 11, 2005, 02:58:24 ; Search time 3.72379 Seconds
(without alignments)
1925.221 Million cell updates/sec

Title: US-09-736-250-5

Perfect score: 74

Sequence: 1 EDNVSENVGVCVT 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	74	100.0	377	1	CYCI_HUMAN
2	74	100.0	377	2	Q6FHH0
3	62	83.8	377	1	CYCI_MOUSE
4	62	83.8	377	2	Q8C7E2
5	62	83.8	377	2	Q99LF2
6	44	59.5	181	2	Q6UB55
7	44	59.5	196	2	Q6DUU8
8	44	59.5	464	2	Q8G446
9	44	59.5	659	2	Q67L99
10	44	59.5	671	1	HPPA_FUSNN
11	44	59.5	673	1	HPPA_CLOTE
12	44	59.5	673	2	Q7P6V4
13	44	59.5	688	2	Q6MNC1
14	44	59.5	704	1	HPPA_LEPIN
15	44	59.5	704	2	Q72Q29
16	44	59.5	721	1	HPPA_PYRAE
17	44	59.5	726	1	HPPA_THEMEA
18	44	59.5	734	1	HPPA_EACTN
19	44	59.5	734	2	Q84ZNR
20	44	59.5	751	2	Q9STC7
21	44	59.5	816	2	Q9BK08
22	44	59.5	816	2	Q9BK08
23	43	58.1	227	2	Q965V9
24	43	58.1	509	2	Q41758
25	43	58.1	541	2	Q43796
26	43	58.1	666	2	Q6SEU0
27	43	58.1	666	2	Q6SGH1
28	43	58.1	667	2	Q6SHA7
29	43	58.1	676	1	HPPI_METAC
30	43	58.1	676	1	HPPI_METNA
31	43	58.1	759	2	Q946X5

RESULT 1

ID	CYCI_HUMAN	STANDARD	PRT	377 AA
AC	Q14094			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Cyclin I.			
OS	Name=CCNI;			
GN	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Forebrain cortex;			
RX	MEDLINE=9608776; PubMed=7493655; DOI=10.1006/excr.1995.1406;			
RA	Nakamura T., Sanokawa R., Sasaki Y.F., Aysawa D., Oishi M., Mori N.;			
RT	"Cyclin I: a new cyclin encoded by a gene isolated from human brain.";			
RL	Exp. Cell Res. 221:534-542(1995).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Chen J.H., Luo W.Q., Zhou Y., Zhou H.J., Huang X.W., Yuan J.G.,			
RA	Qiang B.Q.;			
RT	"Isolating a new cDNA coding for human cyclin protein.";			
RL	Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A., AND VARIANT ILB-207.			
RA	Rieder M.J., Livingston R.J., Daniels M.R., Montoya M.A., Chung M.-W.,			
RA	Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,			
RA	Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;			
RT	"NIH-SNPs, environmental genome project, NIHES ES15478, Department			
RL	of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).";			
RN	Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Kidney, and Muscle;			
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Felling P.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Hopkins R.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Atkinson R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Maras M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,			
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Rah S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Haie S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Whiting M., Madan A., Kettaman M., Madan A.C., Rodrigues S., Sanchez A.,			
RA	Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.B.,			

ALIGNMENTS

32	43	58.1	759	2	Q9M4S1
33	43	58.1	761	2	Q42650
34	43	58.1	762	1	AVP3_HORVU
35	43	58.1	762	2	Q93Y49
36	43	58.1	762	2	Q704F4
37	43	58.1	762	2	Q75U53
38	43	58.1	762	2	Q7Y070
39	43	58.1	764	1	AVP3_PHAU
40	43	58.1	764	2	Q8LSB2
41	43	58.1	764	2	Q43801
42	43	58.1	765	2	Q42651
43	43	58.1	765	2	Q43798
44	43	58.1	766	2	Q22124
45	43	58.1	766	2	Q43797

```
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RL and mouse cDNA sequences.";   
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
[5]  
RN SEQUENCE OF 1-178 FROM N.A.  
RP TISSUE=Testis;  
RC MEDLINE=98381026; PubMed=9705831; DOI=10.1006/bbrc.1998.9052;  
RA Zhu X., Naz R.K.;  
RT Biochem. Biophys. Res. Commun. 249:56-60(1998).  
RL Expression of a novel isoform of cyclin I in human testis.";   
CC -1- TISSUE SPECIFICITY: Highest levels in adult heart, brain and  
CC skeletal muscle. Lower levels in adult placenta, lung, kidney and  
CC pancreas. Also high levels in fetal brain and lower levels in  
CC fetal lung, liver and kidney. Also abundant in testis and thyroid.  
CC -1- DEVELOPMENTAL STAGE: Expression is independent of the cell cycle  
CC in lung fibroblasts.  
CC -1- SIMILARITY: Belongs to the cyclin family.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/  
CC or send an email to license@isb-sib.ch).  
DR EMBL; D50310; BAA08849.1; -;  
DR EMBL; AY207372; AA013492.1; -;  
DR EMBL; BC000420; AAH00420.1; -;  
DR EMBL; BC004975; AAH04975.1; -;  
DR EMBL; AF135162; AAF43786.1; -;  
DR PIR; JE0264; JE0264.  
DR Genew; HGNC:1595; CCNI.  
DR H-InvdB; HIX0004313; -;  
DR GO; GO:007283; P:spermatogenesis; NAS.  
DR InterPro; IPR006670; Cyclin.  
DR InterPro; IPR011028; Cyclin like.  
DR InterPro; IPR006671; Cyclin_N.  
DR Pfam; PF00134; Cyclin_N; 1.  
DR SMART; SM00385; CYCLIN; 1.  
DR PROSITE; PS00292; CYCLINS; FALSE_NEG.  
KW Cyclin; Polymorphism.  
FT VARIANT 207 207  
FT V -> I (in dbSNP:4252903).  
FT /FTID=VAR_016312.  
FT N -> D (in Ref. 5).  
FT Q -> R (in Ref. 5).  
FT R -> G (in Ref. 5).  
SQ SEQUENCE 377 AA; 42557 MW; 2DE84EFA74698F6C CRC64;  
  
Query Match 100.0%; Score 74; DB 1; Length 377;  
Best Local Similarity 100.0%; Pred. No. 0.00022;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 EDNVSENVGVCVT 14  
Db 343 EDNVSENVGVCVT 356  
|||||  
-----  
RESULT 2  
Q6FHHO PRELIMINARY; PRT; 377 AA.  
ID Q6FHHO  
AC Q6FHHO;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE CCNI protein (Fragment).  
GN Name=CCNI;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OC NCBI_TaxID=9606;  
RN [1]
```

```
RP SEQUENCE FROM N.A.  
RA Halleck A., Ebert L., Mkundinya M., Schick M., Eisenstein S.,  
RA Neubert P., Kstrang K., Schatten R., Shen B., Henze S., Mar W.,  
RA Korn B., Zuo D., Hu Y., LaBaer J.;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: Belongs to the cyclin family.  
DR EMBL; CR541783; CAG46582.1; -;  
DR InterPro; IPR006670; Cyclin.  
DR InterPro; IPR011028; Cyclin like.  
DR InterPro; IPR006671; Cyclin_N.  
DR Pfam; PF00134; Cyclin_N; 1.  
DR SMART; SM00385; CYCLIN; 1.  
KW Cyclin.  
FT NON TER 377 377  
SQ SEQUENCE 377 AA; 42486 MW; D950A5CCF0D0F514 CRC64;  
  
Query Match 100.0%; Score 74; DB 2; Length 377;  
Best Local Similarity 100.0%; Pred. No. 0.00022;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 EDNVSENVGVCVT 14  
Db 343 EDNVSENVGVCVT 356  
|||||  
-----  
RESULT 3  
CYCI_MOUSE STANDARD; PRT; 377 AA.  
ID CYCI_MOUSE  
AC Q9Z2J9;  
DT 18-OCT-2001 (Rel. 40, Created)  
DT 18-OCT-2001 (Rel. 40, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Cyclin I.  
DE Cyclin I.  
GN Name=Ccni;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99172101; PubMed=10072591;  
RA Jensen M.R., Audolfsson T., Keck C.L., Zimonjic D.B.,  
RA Thorgeirsson S.S.;  
RT "Assignment of the cyclin I gene (Ccn1) to mouse chromosome 5E3.3-Fl.  
RT 3 by in situ hybridization.";  
RL Cytogenet. Cell Genet. 83:242-243(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20509992; PubMed=11054536; DOI=10.1016/S0378-1119(00)00361-9;  
RA Jensen M.R., Audolfsson T., Factor V.M., Thorgeirsson S.S.;  
RT "In vivo expression and genomic organization of the mouse cyclin I  
RT gene (Ccn1).";  
RL Gene 256:59-67(2000).  
CC -1- SIMILARITY: Belongs to the cyclin family.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/  
CC or send an email to license@isb-sib.ch).  
DR EMBL; AF005886; AAD01253.2; -;  
DR EMBL; AF228740; AAF43391.1; -;  
DR EMBL; AF228739; AAF43391.1; JOINED.  
DR MGD; MGI:1341077; Ccni.  
DR InterPro; IPR006670; Cyclin.  
DR InterPro; IPR011028; Cyclin like.  
DR InterPro; IPR006671; Cyclin_N.  
DR Pfam; PF00134; Cyclin_N; 1.  
DR SMART; SM00385; CYCLIN; 1.  
DR PROSITE; PS00292; CYCLINS; FALSE_NEG.
```

KW Cyclin.
SQ SEQUENCE 377 AA; 42261 MW; 4151141C6D9AE677 CRC64;
Query Match 83.8%; Score 62; DB 1; Length 377;
Best Local Similarity 85.7%; Pred. No. 0.028;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 EDNVSENVGVCCT 14
Db 343 EDNGPENVGVCCT 356
RESULT 4
Q8C7E2 PRELIMINARY; PRT; 377 AA.
AC Q8C7E2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus adult pancreas islet cells cDNA, RIKEN full-length
DE enriched library, clone: C820001G04 product: cyclin I, full insert
DE sequence.
GN Name=Ccni;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RA MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RX Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning."
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RA MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RX RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RA The FANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RA MEDLINE=2049374; PubMed=11042159; DOI=10.1101/gr.145100;
RX Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes."
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RA MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RX Shibata K., Itoh M., Aizawa K., Nagao K., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multipipillary sequencer."
RL Genome Res. 10:1757-1771(2000).
RN [6]

RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirokawa T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ono M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the cyclin family.
DR EMBL; AK050465; BAC34271.1; -.
DR MGD; MGI:1341077; Ccni.
DR GO; GO:0000074; P:regulation of cell cycle; TAS.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR011028; Cyclin_like.
DR InterPro; IPR006671; Cyclin_N.
DR Pfam; PF00134; Cyclin_N; 1.
DR SMART; SM00385; CYCLIN; 1.
KW Cyclin.
SQ SEQUENCE 377 AA; 42206 MW; A1B803EBE135B0E8 CRC64;
Query Match 83.8%; Score 62; DB 2; Length 377;
Best Local Similarity 85.7%; Pred. No. 0.028;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 EDNVSENVGVCCT 14
Db 343 EDNGPENVGVCCT 356
RESULT 5
Q99LF2 PRELIMINARY; PRT; 377 AA.
ID Q99LF2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cyclin I.
GN Name=Ccni;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Mammary tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Colling P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan B., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toehiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smalish D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]

```
RP SEQUENCE FROM N.A.
RA STRAIN=FVB/N; TISSUE=Mammary tumor;
RC Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RL -1- SIMILARITY: Belongs to the cyclin family.
CC EMBL; BC003290; AA03290.1; -.
DR MGD; MGI:1341077; Ccn1.
DR GO; GO:000074; P:regulation of cell cycle; TAS.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR011028; Cyclin like.
DR InterPro; IPR006671; Cyclin_N.
DR Pfam; PF00134; Cyclin_N; 1.
DR SMART; SM00385; CYCLIN; 1.
DR Cyclin.
KW Cyclin.
SQ SEQUENCE 377 AA; 42227 MW; FDA2D896A5366A9F CRC64;

Query Match      83.8%; Score 62; DB 2; Length 377;
Best Local Similarity 85.7%; Pred. No. 0.028;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EDNVSENVGVCVT 14
Db 343 EDNGPENVGVCVT 356

RESULT 6
Q6UB65
ID Q6UB65 PRELIMINARY; PRT; 181 AA.
AC Q6UB65;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative H+ translocating inorganic pyrophosphatase (Fragment).
OS Hyaloperonospora parasitica.
OC Eukaryota; stramenopiles; Oomycetes; Peronosporales; Peronosporaceae;
OC Hyaloperonospora.
OC Eukaryota.
OX NCBI_TaxID=123356;

[1]
RP SEQUENCE FROM N.A.
RA Bittner-Bddy P., Allen R., Rehmany A., Birch P., Bynnon J.;
RC "Use of suppression subtractive hybridization to identify downy mildew
RT genes expressed during infection of Arabidopsis thaliana.";
RL Mol. Plant Pathol. 0:0-0(2003).
DR EMBL; AY373944; AA083502.1; -.
DR InterPro; IPR004131; H_PPase.
DR Pfam; PF03030; H_PPase; 1.
DR NON_TER 1
DR NON_TER 181
FT NON_TER 181
SQ SEQUENCE 181 AA; 18752 MW; B2B134292CDE01D1 CRC64;

Query Match      59.5%; Score 44; DB 2; Length 181;
Best Local Similarity 66.7%; Pred. No. 19;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DNVSENVGVCVT 13
Db 66 DNVGDNVGDVAG 77

RESULT 7
Q6DUU8
ID Q6DUU8 PRELIMINARY; PRT; 196 AA.
AC Q6DUU8;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Vacuolar-type H+-pyrophosphatase (Fragment).
OS Medicago sativa (Alfalfa).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.
OX NCBI_TaxID=3879;

Query Match      59.5%; Score 44; DB 2; Length 181;
Best Local Similarity 66.7%; Pred. No. 19;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DNVSENVGVCVT 13
Db 66 DNVGDNVGDVAG 77

RESULT 8
Q8G446
ID Q8G446 PRELIMINARY; PRT; 464 AA.
AC Q8G446;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=BL1547;
OS Bifidobacterium longum.
OC Bacteria; Actinobacteria; Actinobacteridae; Bifidobacteriales;
OC Bifidobacteriaceae; Bifidobacterium.
OX NCBI_TaxID=216816;

[1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCC 2705;
RX MEDLINE=22294977; PubMed=12381787; DOI=10.1073/pnas.212527599;
RA Schell M.A., Karmirantzou M., Snel B., Vilanova D., Berger B.,
RA Pessi G., Zwaehlen M.-C., Desiere F., Bork P., Delley M.,
RA Pridmore R.D., Arigoni F.;
RT "The genome sequence of Bifidobacterium longum reflects its adaptation
RT to the human gastrointestinal tract.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).
DR EMBL; AE014789; AAN25339.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR006043; Xant/urac/vitC.
DR Pfam; PF00860; Xan_ur_permease; 1.
DR Complete proteome.
KW Complete proteome.
SQ SEQUENCE 464 AA; 48723 MW; CD744DD8CA6AD556 CRC64;

Query Match      59.5%; Score 44; DB 2; Length 464;
Best Local Similarity 38.5%; Pred. No. 51;
Matches 5; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

Qy 2 DNVSENVGVCVT 14
Db 317 DSATSIGAICGT 329

RESULT 9
Q67L99
ID Q67L99 PRELIMINARY; PRT; 659 AA.
AC Q67L99;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Inorganic H+ pyrophosphatase.
GN ORFNames=STH2562;
OS Symbiobacterium thermophilum.
OC Bacteria; Actinobacteria; Symbiobacterium.
OX NCBI_TaxID=2734;
```

```
RP SEQUENCE FROM N.A.
RA Wu M.S., Wang P.Q.;
RC Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL; AY642597; AAT65202.1; -.
DR InterPro; IPR004131; H_PPase.
DR Pfam; PF03030; H_PPase; 1.
DR NON_TER 1
DR NON_TER 196
SQ SEQUENCE 196 AA; 20630 MW; B43885E81B02759E CRC64;

Query Match      59.5%; Score 44; DB 2; Length 196;
Best Local Similarity 66.7%; Pred. No. 21;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DNVSENVGVCVT 13
Db 14 DNVGDNVGDVAG 25

RESULT 8
Q8G446
ID Q8G446 PRELIMINARY; PRT; 464 AA.
AC Q8G446;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=BL1547;
OS Bifidobacterium longum.
OC Bacteria; Actinobacteria; Actinobacteridae; Bifidobacteriales;
OC Bifidobacteriaceae; Bifidobacterium.
OX NCBI_TaxID=216816;

[1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCC 2705;
RX MEDLINE=22294977; PubMed=12381787; DOI=10.1073/pnas.212527599;
RA Schell M.A., Karmirantzou M., Snel B., Vilanova D., Berger B.,
RA Pessi G., Zwaehlen M.-C., Desiere F., Bork P., Delley M.,
RA Pridmore R.D., Arigoni F.;
RT "The genome sequence of Bifidobacterium longum reflects its adaptation
RT to the human gastrointestinal tract.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).
DR EMBL; AE014789; AAN25339.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR006043; Xant/urac/vitC.
DR Pfam; PF00860; Xan_ur_permease; 1.
DR Complete proteome.
KW Complete proteome.
SQ SEQUENCE 464 AA; 48723 MW; CD744DD8CA6AD556 CRC64;

Query Match      59.5%; Score 44; DB 2; Length 464;
Best Local Similarity 38.5%; Pred. No. 51;
Matches 5; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

Qy 2 DNVSENVGVCVT 14
Db 317 DSATSIGAICGT 329

RESULT 9
Q67L99
ID Q67L99 PRELIMINARY; PRT; 659 AA.
AC Q67L99;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Inorganic H+ pyrophosphatase.
GN ORFNames=STH2562;
OS Symbiobacterium thermophilum.
OC Bacteria; Actinobacteria; Symbiobacterium.
OX NCBI_TaxID=2734;
```



```

RN  SEQUENCE FROM N.A.
RC  STRAIN=IAM14863;
RA  Ueda K., Yamashita A., Ishikawa J., Shimada M., Watsuji T.,
RA  Morimura K., Ikeda H., Hattori M., Beppu T.;
RT  "Complete genome sequence of an uncultured bacterium Symbiobacterium
RL  thermophilum.";
RL  Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AP006840; BAD41547.1; -.
DR  InterPro; IPR004131; H_PPase.
DR  Pfam; PF03030; H_PPase; 1.
DR  PIRSF; PIRSF001265; H+-PPase; 1.
DR  TIGRFAMs; TIGR01104; V_PPase; 1.
SQ  SEQUENCE 659 AA; 66602 MW; 67BBIAG2D01BB1A4 CRC64;

Query Match          59.5%; Score 44; DB 2; Length 659;
Best Local Similarity 66.7%; Pred. No. 73;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy  2 DNVSENVGSVCG 13
    |||:|||||
Db  199 DNVGDNVGDVAG 210

RESULT 10
HPPA_FUSNN          STANDARD;          PRT;          671 AA.
AC  Q8RHJ2;
DT  10-OCT-2003 (Rel. 42, Created)
DT  10-OCT-2003 (Rel. 42, Last sequence update)
DT  25-OCT-2004 (Rel. 45, Last annotation update)
DE  Pyrophosphate-energized proton pump (EC 3.6.1.1) (Pyrophosphate-
DE  energized inorganic pyrophosphatase) (H+-PPase) (Membrane-bound
DE  proton-translocating pyrophosphatase).
GN  Name=hppA; OrderedLocusNames=FN2030;
OS  Fusobacterium nucleatum (subsp. nucleatum).
OC  Bacteria; Fusobacteria; Fusobacteriales; Fusobacteriaceae;
OC  Fusobacterium.
OX  NCBI_TaxID=76856;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=ATCC 25586;
RX  MEDLINE=21886394; PubMed=1189109;
RX  DOI=10.1128/JB.184.7.2005-2018.2002;
RA  Kapattal V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,
RA  Bhattacharya A., Bartman A., Gardner W., Grechkin G., Zhu L.,
RA  Vasieva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A.,
RA  Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R.,
RA  Forsteln M., Kyrpides N.C., Overbeek R.;
RT  "Genome sequence and analysis of the oral bacterium Fusobacterium
RT  nucleatum strain ATCC 25586.";
RL  J. Bacteriol. 184:2005-2018 (2002).
CC  -!- FUNCTION: Generates a proton motive force; it probably catalyzes a
CC  fully reversible reaction, thus being able to synthesize
CC  pyrophosphate when the proton motive force is sufficient (By
CC  similarity).
CC  -!- CATALYTIC ACTIVITY: Diphosphate + H(2)O = 2 phosphate.
CC  -!- COFACTOR: Magnesium and potassium (By similarity).
CC  -!- SUBUNIT: Homodimer (Potential).
CC  -!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC  -!- SIMILARITY: Belongs to the H(+)-translocating pyrophosphatase
CC  (TC 3.A.10) family. Subfamily 1.
-----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  HAMAB; MF_01129; -.

```

```

DR  InterPro; IPR004131; H_PPase.
DR  Pfam; PF03030; H_PPase; 1.
DR  PIRSF; PIRSF001265; H+-PPase; 1.
DR  TIGRFAMs; TIGR01104; V_PPase; 1.
KW  Complete proteome; Hydrogen ion transport; Hydrolase; Magnesium;
KW  Potassium; Transmembrane.
FT  TRANSMEM 4 26 Potential.
FT  TRANSMEM 60 94 Potential.
FT  TRANSMEM 126 148 Potential.
FT  TRANSMEM 161 183 Potential.
FT  TRANSMEM 225 247 Potential.
FT  TRANSMEM 254 276 Potential.
FT  TRANSMEM 291 313 Potential.
FT  TRANSMEM 315 337 Potential.
FT  TRANSMEM 361 383 Potential.
FT  TRANSMEM 390 412 Potential.
FT  TRANSMEM 450 472 Potential.
FT  TRANSMEM 493 515 Potential.
FT  TRANSMEM 560 579 Potential.
FT  TRANSMEM 581 603 Potential.
FT  TRANSMEM 646 668 Potential.
FT  SITE 450 450 Determinant of potassium dependence (By
FT  similarity).
SQ  SEQUENCE 671 AA; 68989 MW; B9519DE6D3554ACB CRC64;

Query Match          59.5%; Score 44; DB 1; Length 671;
Best Local Similarity 66.7%; Pred. No. 74;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy  2 DNVSENVGSVCG 13
    |||:|||||
Db  213 DNVGDNVGDVAG 224

RESULT 11
HPPA_CLOTE          STANDARD;          PRT;          673 AA.
AC  Q898Q9;
DT  10-OCT-2003 (Rel. 42, Created)
DT  10-OCT-2003 (Rel. 42, Last sequence update)
DT  25-OCT-2004 (Rel. 45, Last annotation update)
DE  Pyrophosphate-energized proton pump (EC 3.6.1.1) (Pyrophosphate-
DE  energized inorganic pyrophosphatase) (H+-PPase) (Membrane-bound
DE  proton-translocating pyrophosphatase).
GN  Name=hppA; OrderedLocusNames=CTC00383;
OS  Clostridium tetani.
OC  Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC  Clostridium.
OX  NCBI_TaxID=1513;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=Massachusetts / E88;
RX  MEDLINE=22457253; PubMed=12552129; DOI=10.1073/pnas.0335853100;
RA  Brueggemann H., Baeumer S., Fricke W.F., Wierzer A., Liesegang H.,
RA  Decker I., Herzberg C., Martinez-Arias R., Merkl R., Henne A.,
RA  Gottschalk G.;
RT  "The genome sequence of Clostridium tetani, the causative agent of
RT  tetanus disease.";
RL  Proc. Natl. Acad. Sci. U.S.A. 100:1316-1321 (2003).
CC  -!- FUNCTION: Generates a proton motive force; it probably catalyzes a
CC  fully reversible reaction, thus being able to synthesize
CC  pyrophosphate when the proton motive force is sufficient (By
CC  similarity).
CC  -!- CATALYTIC ACTIVITY: Diphosphate + H(2)O = 2 phosphate.
CC  -!- COFACTOR: Magnesium and potassium (By similarity).
CC  -!- SUBUNIT: Homodimer (Potential).
CC  -!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC  -!- SIMILARITY: Belongs to the H(+)-translocating pyrophosphatase
CC  (TC 3.A.10) family. Subfamily 1.
-----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its

```

use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC EMBL; AB015937; AAC035020.1; --
CC HANAP; MF 01129; -- 1.
CC InterPro; IPR004131; H_PPase.
DR Pfam; PF03030; H_PPase; 1.
DR PIRSF; PIRSF001265; H+-PPase; 1.
KW Complete proteome; Hydrogen ion transport; Hydrolase; Magnesium;
KW Potassium; Transmembrane.
FT TRANSMEM 4 26 Potential.
FT TRANSMEM 57 74 Potential.
FT TRANSMEM 78 100 Potential.
FT TRANSMEM 121 143 Potential.
FT TRANSMEM 153 175 Potential.
FT TRANSMEM 245 267 Potential.
FT TRANSMEM 282 304 Potential.
FT TRANSMEM 309 331 Potential.
FT TRANSMEM 360 382 Potential.
FT TRANSMEM 389 411 Potential.
FT TRANSMEM 447 469 Potential.
FT TRANSMEM 482 504 Potential.
FT TRANSMEM 554 573 Potential.
FT TRANSMEM 580 602 Potential.
FT TRANSMEM 650 672 Potential.
FT SITE 449 449 Determinant of potassium dependence (By similarity).
SQ SEQUENCE 673 AA; 69282 MW; E3505682EE10FF56 CRC64;

Query Match 59.5%; Score 44; DB 1; Length 673;
Best Local Similarity 66.7%; Pred. No. 74;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DNVSENVGVCV 13

Db 206 DNVDNVDVAG 217

RESULT 12

Q7P6V4 Q7P6V4 PRELIMINARY; PRT; 673 AA.

AC 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Inorganic pyrophosphatase (EC 3.6.1.1).

GN Name=FN1867;

OS Fusobacterium nucleatum subsp. Vincentii ATCC 49256.

OC Bacteria; Fusobacteria; Fusobacteriales; Fusobacteriaceae;

OX Fusobacterium.

NCBI_TaxID=209882;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 49256;

RA Karpatrial V., Ivanova N., Anderson I., Reznik G., Bhattacharyya A.,

RA Gardner W.L., Mikhailova N., Larsen N., D'Souza M., Walunas T.,

RA Haselkorn R., Overbeek R., Kyrtides N.;

RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.

CC -! CAUTION: The sequence shown here is derived from an

CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is

CC preliminary data.

DR EMBL; AABF0100026; EAA24540.1; --

DR GO; GO:0016020; C-membrane; IEA.

DR GO; GO:0009678; F:hydrogen-translocating pyrophosphatase acti. . .; IEA.

DR GO; GO:0016787; F:hydrolase activity; IEA.

DR GO; GO:0004427; F:inorganic diphosphatase activity; IEA.

DR GO; GO:0015992; P:proton transport; IEA.

DR InterPro; IPR004131; H_PPase.

DR Pfam; PF03030; H_PPase; 1.

DR PIRSF; PIRSF001265; H+-PPase; 1.

DR TIGRFAMs; TIGR01104; V_PPase; 1.

KW Hydrolase.

SQ SEQUENCE 673 AA; 69259 MW; 174E87796E7DE14B CRC64;

Query Match 59.5%; Score 44; DB 2; Length 673;

Best Local Similarity 66.7%; Pred. No. 74;

Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DNVSENVGVCV 13

Db 213 DNVDNVDVAG 224

RESULT 13

Q6MWC1 Q6MWC1 PRELIMINARY; PRT; 688 AA.

AC 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Vacuolar-type H+-pyrophosphatase precursor (EC 3.6.1.1).

GN Name=ppa; OrderedLocustNames=Bd1715;

OS Bdellovibrio bacteriovorus.

OC Bacteria; Proteobacteria; Deltaproteobacteria; Bdellovibrionales;

OC Bdellovibrionaceae; Bdellovibrio.

OX NCBI_TaxID=959;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=HD100 / DSM 50701 / ATCC 15356 / NCIB 9529;

RX PubMed=14752164; DOI=10.1126/science.1093027;

RA Rendulic S., Jagtap P., Rosinus A., Eppinger M., Baar C., Lanz C.,

RA Keller H., Lambert C., Evans K.J., Goesmann A., Meyer F.,

RA Sockett R.E., Schuster S.C.;

RT "A predator unmasked: life cycle of Bdellovibrio bacteriovorus from a

RT genomic perspective."

RL Science 303:689-692(2004).

DR EMBL; BX842650; CAB79584.1; --

DR GO; GO:0016020; C-membrane; IEA.

DR GO; GO:0009678; F:hydrogen-translocating pyrophosphatase acti. . .; IEA.

DR GO; GO:0004427; F:inorganic diphosphatase activity; IEA.

DR GO; GO:0015992; P:proton transport; IEA.

DR InterPro; IPR004131; H_PPase.

DR Pfam; PF03030; H_PPase; 1.

DR TIGRFAMs; TIGR01104; V_PPase; 1.

KW Complete proteome.

FT SIGNAL 1 10 Potential.

SQ SEQUENCE 688 AA; 69153 MW; DB14954596ABB7BC CRC64;

Query Match 59.5%; Score 44; DB 2; Length 688;

Best Local Similarity 66.7%; Pred. No. 76;

Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DNVSENVGVCV 13

Db 212 DNVDNVDVAG 223

RESULT 14

HPA LEPIN

ID _HPA_LEPIN STANDARD; PRT; 704 AA.

AC Q8F641;

DT 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Pyrophosphate-energized proton pump (EC 3.6.1.1) (Pyrophosphate-

DE energized inorganic pyrophosphatase) (H+-PPase) (Membrane-bound

DE proton-translocating pyrophosphatase).

GN Name=hppa; OrderedLocustNames=LAI471;

OS Leptospira interrogans.

OC Bacteria; Spirochaetes; Spirochaetales; Leptospiaceae; Leptospira.

OX NCBI_TaxID=173;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;

RX MEDLINE=22598143; PubMed=12712204; DOI=10.1038/nature01597;
RA Ren S.-X., Fu G., Jiang X.-G., Zeng R., Miao Y.-G., Xu H.,
RA Zhang Y.-X., Xiong H., Lu G., Lu L.-F., Jiang H.-Q., Jia J., Tu Y.-F.,
RA Jiang J.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F.,
RA Zhang Y., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Wang S.-Y., Ma W.,
RA Yao Z.-J., Shen Y., Qiang B.-Q., Xia Q.-C., Guo X.-K., Danchin A.,
RA Saint Girons I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z.,
RA Xu J.-G., Zhao G.-P.;
RT "Unique physiological and pathogenic features of Leptospira
interrogans revealed by whole-genome sequencing.";
RL Nature 422:888-893(2003).
CC -1- FUNCTION: Generates a proton motive force; it probably catalyzes a
CC fully reversible reaction, thus being able to synthesize
CC pyrophosphate when the proton motive force is sufficient (By
CC similarity).
CC
CC -1- CATALYTIC ACTIVITY: Diphosphate + H(2)O = 2 phosphate.
CC -1- COFACTOR: Magnesium and potassium (By similarity).
CC -1- SUBUNIT: Homodimer (Potential).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC -1- SIMILARITY: Belongs to the H(+)-translocating pyrophosphatase
CC (TC 3.A.10) family. Subfamily 1.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC -----
DR EMBL; AB011327; AAM48670.1; -.
DR HAMAP; MF_01129; -; 1.
DR InterPro; IPR004131; H_Ppase.
DR Pfam; PF03030; H_Ppase; 1.
DR PIRSF; PIRSF001265; H+-Ppase; 1.
DR TIGRFAMs; TIGR01104; V_Ppase; 1.
KW Complete proteome; Hydrogen ion transport; Hydrolase; Magnesium;
KW Potassium; Transmembrane.
FT TRANSMEM 4 23 Potential.
FT TRANSMEM 64 81 Potential.
FT TRANSMEM 91 113 Potential.
FT TRANSMEM 143 165 Potential.
FT TRANSMEM 175 197 Potential.
FT TRANSMEM 276 298 Potential.
FT TRANSMEM 308 327 Potential.
FT TRANSMEM 348 370 Potential.
FT TRANSMEM 390 412 Potential.
FT TRANSMEM 419 441 Potential.
FT TRANSMEM 481 503 Potential.
FT TRANSMEM 516 538 Potential.
FT TRANSMEM 586 605 Potential.
FT TRANSMEM 612 634 Potential.
FT TRANSMEM 671 693 Potential.
FT SITE 481 481 Determinant of potassium dependence (By
FT similarity).
SQ SEQUENCE 704 AA; 73105 MW; 9369E135382D96BC CRC64;

Query Match 59.5%; Score 44; DB 1; Length 704;
Best Local Similarity 66.7%; Pred. No. 78;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DNVSNGVSGC 13
Db 232 DNVDNVDVAG 243
|||:|||||
232 DNVDNVDVAG 243

RESULT 15
Q72Q29 PRELIMINARY; PRT; 704 AA.
ID Q72Q29
AC Q72Q29;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE H+-translocating pyrophosphatase.
GN Name:avp; OrderedLocNames=LI02285;
OS Leptospira interrogans (serogroup Icterohaemorrhagiae / serovar
OS Copenhagen).
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
OX NCBI_TaxID=44275;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Floeruz LI-130;
RX PubMed=15028702; DOI=10.1128/JB.186.7.2164-2172.2004;
RA Nascimben A.L.T.O., Ko A.I., Martins E.A.L., Monteiro-Vitorello C.B.,
RA Ho P.L., Haake D.A., Verjovski-Almeida S., Hartsekerl R.A.,
RA Marques M.V., Oliveira M.C., Menck C.F.M., Leite L.C.C., Carrer H.,
RA Coutinho L.R., Degraive W.M., Dellagostin O.A., El-Dorry H.,
RA Ferro E.S., Ferro M.I.T., Furlan L.R., Gamberini M., Gigliotti E.A.,
RA Goes-Neto A., Goldman G.H., Goldman M.H.S., Harakava R.,
RA Jeronimo S.M.B., Junqueira-de-Azevedo J.L.M., Kimura E.T.,
RA Kuranae E.E., Lemos E.G.M., Lemos M.V.F., Marino C.L., Nunes L.R.,
RA de Oliveira R.C., Pereira G.G., Reis M.S., Schriefer A.,
RA Siqueira W.J., Sommer P., Tsai S.M., Simpson A.J.G., Ferro J.A.,
RA Camargo L.E.A., Kitajima J.P., Setubal J.C., Van Sluys M.A.;
RT "Comparative genomics of two Leptospira interrogans serovars reveals
RT novel insights into physiology and pathogenesis.";
RL J. Bacteriol. 186:2164-2172(2004).
DR EMBL; AB017296; AAS70856.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0009678; F:hydrogen-translocating pyrophosphatase acti. .; IEA.
DR GO; GO:0015992; P:proton transport; IEA.
DR InterPro; IPR004131; H_Ppase.
DR Pfam; PF03030; H_Ppase; 1.
DR PIRSF; PIRSF001265; H+-Ppase; 1.
DR TIGRFAMs; TIGR01104; V_Ppase; 1.
SQ SEQUENCE 704 AA; 73105 MW; 9369E135382D96BC CRC64;

Query Match 59.5%; Score 44; DB 2; Length 704;
Best Local Similarity 66.7%; Pred. No. 78;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DNVSNGVSGC 13
Db 232 DNVDNVDVAG 243
|||:|||||
232 DNVDNVDVAG 243

Search completed: February 11, 2005, 03:05:17
Job time : 5.72379 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 11, 2005, 03:18:50 ; Search time 285.586 Seconds
(without alignments)
2375.375 Million cell updates/sec

Title: US-09-736-250-5

Perfect score: 74
Sequence: 1 EDNVSENVGVCVT 14

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO.spool/US09736250/runat_07022005_154924_20406/app.query.fasta_1.718
-DB=GenEmbl -QMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOPEXT=0 -LOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09736250 @CGN 1 1 3890 @runat_07022005_154924_20406 -NCPU=3
-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl:*
1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
4: gb_on:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	74	100.0	136	6 A74835	A74835 Sequence 52
2	74	100.0	136	6 A77814	A77814 Sequence 52
3	74	100.0	288	6 CQ712652	CQ712652 Sequence
4	74	100.0	350	6 CQ675890	CQ675890 Sequence

C	5	74	100.0	444	6	AX397198	Sequence
	6	74	100.0	447	6	AX198885	Sequence
	7	74	100.0	447	6	AX209412	Sequence
C	8	74	100.0	601	11	BV180201	sgml10841
	9	74	100.0	804	6	BD079737	Cancer-as
	10	74	100.0	1131	9	CR541783	Homo sapi
	11	74	100.0	1133	6	AR145734	Sequence
	12	74	100.0	1260	6	AR087353	Sequence
	13	74	100.0	1260	6	CQ812312	Sequence
	14	74	100.0	1260	6	AR281918	Sequence
	15	74	100.0	1260	6	AR380354	Sequence
	16	74	100.0	1260	9	HUMCVI	D50310 Human mRNA
	17	74	100.0	1384	9	AF135162	Homo sapi
	18	74	100.0	1493	6	BD194541	Human nuc
	19	74	100.0	1493	6	AX015395	Sequence
	20	74	100.0	1817	9	BC000420	Homo sapi
	21	74	100.0	1889	9	CQ468129	Sequence
	22	74	100.0	1889	9	BC004975	Homo sapi
	23	74	100.0	2146	6	CQ414223	Sequence
	24	74	100.0	2755	6	CQ414515	Sequence
	25	74	100.0	29867	9	AY207372	Homo sapi
C	26	74	100.0	35191	9	AC111196	Homo sapi
	27	74	100.0	178916	2	AP002874	Homo sapi
C	28	74	100.0	179443	2	AC079051	Homo sapi
	29	70	94.5	308	6	CQ696855	Sequence
	30	69	93.2	304	6	AX914031	Sequence
	31	69	93.2	304	6	BD049564	Sequence
C	32	65	87.8	200850	2	AC101881	Sequence
C	33	65	87.8	202228	2	AC124646	Mus muscu
	34	62	83.8	1535	10	AF005886	Mus muscu
	35	62	83.8	2348	10	BC003290	Mus muscu
	36	62	83.8	11793	10	AF228739S2	Mus muscu
	37	62	83.8	179333	2	AC117658	Mus muscu
	38	62	83.8	193811	10	AC134827	Mus muscu
C	39	62	83.8	241543	2	AC099472	Rattus no
C	40	62	83.8	260517	2	AC111318	Rattus no
	41	62	83.8	270068	2	AC113213	Rattus no
C	42	50	67.6	3039	6	CQ583995	Sequence
C	43	50	67.6	5856	6	CQ583994	Sequence
C	44	50	67.6	15921	3	AF034856	Drosophil
C	45	50	67.6	58569	2	AC015033	Drosophil

ALIGNMENTS

RESULT 1	A74835	A74835	Sequence 521 from Patent WO9401548.	136 bp	DNA	linear	PAT 15-OCT-1999
LOCUS	A74835						
DEFINITION	A74835						
ACCESSION	A74835						
VERSION	A74835.1		GI:6064849				
KEYWORDS							
SOURCE			unidentified				
ORGANISM			unidentified				
			unclassified.				
REFERENCE	1	(bases 1 to 136)					
AUTHORS	Sibson,D.R. and Gross,J.						
TITLE	HUMAN NUCLEIC ACID FRAGMENTS, ISOLATED FROM BRAIN ADRENAL TISSUE,						
	PLACENTA OR BONE MARROW						
JOURNAL	Patent: WO 9401548-A 521 20-JAN-1994;						
	MEDICAL RES COUNCIL (GB); SIBSON DAVID ROSS (GB)						
FEATURES			Location/Qualifiers				
source			1. .136				
			/organism="unidentified"				
			/mol_type="unassigned DNA"				
			/db_xref="taxon:32644"				

ORIGIN							
Alignment Scores:							
Pred. No.:	4.02e-05						136
Score:	74.00						14
Percent Similarity:	100.00%						0
Best Local Similarity:	100.00%						0

Mon Feb 14 12:27:17 2005

```

Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-736-250-5 (1-14) x A74835 (1-136)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 24 GAAGATAATGCTCAGAAATGCGGTCTCTGTGTGGCACT 65

RESULT 2
LOCUS A77814 136 bp DNA linear PAT 19-OCT-1999
DEFINITION Sequence 521 from Patent EP0587279.
ACCESSION A77814
VERSION A77814.1 GI:6089479
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 136)
AUTHORS Sibeon,D.R. and Hadfield,K.M.
TITLE HUMAN NUCLEIC ACID FRAGMENTS ISOLATED FROM BRAIN, ADRENAL TISSUE,
JOURNAL PLACENTA OR BONE MARROW AND THEIR USE
MEDICAL RES COUNCIL (GB)
PATENT: EP 0587279-A 521 16-MAR-1994;
FEATURES
LOCATION/Qualifiers
source 1..136
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
ORIGIN

Alignment Scores:
Pred. No.: 4.02e-05 Length: 136
Score: 74.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-736-250-5 (1-14) x A77814 (1-136)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 24 GAAGATAATGCTCAGAAATGCGGTCTCTGTGTGGCACT 65

RESULT 3
LOCUS CQ712652 288 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 57578 from Patent WO02070737.
ACCESSION CQ712652
VERSION CQ712652.1 GI:42273509
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Liew,C.C., Marshall,W.E. and Zhang,H.
TITLE Compositions and methods relating to osteoarthritis
JOURNAL Patent: WO 02070737-A 57578 12-SEP-2002;
Chondrogene Inc. (CA)
FEATURES
LOCATION/Qualifiers
source 1..288
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.: 8.44e-05 Length: 288
Score: 74.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0

Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-736-250-5 (1-14) x CQ712652 (1-288)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 63 GAAGATAATGCTCAGAAATGCGGTCTCTGTGTGGCACT 104

RESULT 4
LOCUS CQ675890 350 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 20816 from Patent WO02070737.
ACCESSION CQ675890
VERSION CQ675890.1 GI:42180044
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Liew,C.C., Marshall,W.E. and Zhang,H.
TITLE Compositions and methods relating to osteoarthritis
JOURNAL Patent: WO 02070737-A 20816 12-SEP-2002;
Chondrogene Inc. (CA)
FEATURES
LOCATION/Qualifiers
source 1..350
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.: 0.000102 Length: 350
Score: 74.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-736-250-5 (1-14) x CQ675890 (1-350)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 129 GAAGATAATGCTCAGAAATGCGGTCTCTGTGTGGCACT 170

RESULT 5
LOCUS AX397198 444 bp DNA linear PAT 18-MAY-2002
DEFINITION Sequence 1413 from Patent WO0212328.
ACCESSION AX397198
VERSION AX397198.1 GI:21067945
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS King,G.E., Meagher,M.J., Xu,J. and Secrist,H.
TITLE Compositions and methods for the therapy and diagnosis of colon
JOURNAL cancer
PATENT: WO 0212328-A 1413 14-FEB-2002;
CORIXA CORPORATION (US)
FEATURES
LOCATION/Qualifiers
source 1..444
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.: 0.000129 Length: 444
Score: 0.000129 Matches: 144
Percent Similarity: 100.00% Conservative: 0

```

Score: 74.00 Matches: 14
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-09-736-250-5 (1-14) x AX397198 (1-444)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
 |||||
 Db 436 GAAGATAATGCTCAGAAAATGGGTCTCTGTGTGGCACT 395

RESULT 6

AX198885 AX198885 447 bp DNA linear PAT 29-AUG-2001

LOCUS Sequence 1340 from Patent WO015153.

DEFINITION AX198885

ACCESSION AX198885

VERSION AX198885.1 GI:15389211

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 Algate, P.A.

1 Ovarian tumor-associated sequences

TITLE Patent: WO 015153-A 1340 19-JUL-2001;

JOURNAL CORIXA CORPORATION (US)

FEATURES Location/Qualifiers

source
 1..447
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN

Alignment Scores:
 Pred. No.: 0.00013 Length: 447
 Score: 74.00 Matches: 14
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-09-736-250-5 (1-14) x AX198885 (1-447)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
 |||||
 Db 93 GAAGATAATGCTCAGAAAATGGGTCTCTGTGTGGCACT 134

RESULT 7

AX209412 AX209412 447 bp DNA linear PAT 31-AUG-2001

LOCUS Sequence 1252 from Patent WO0157207.

DEFINITION AX209412

ACCESSION AX209412

VERSION AX209412.1 GI:15423835

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 Algate, P.A. and Mannion, J.

1 Compositions and methods for the therapy and diagnosis of ovarian cancer

TITLE Patent: WO 0157207-A 1252 09-AUG-2001;

JOURNAL CORIXA CORPORATION (US)

FEATURES Location/Qualifiers

source
 1..447
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN

Alignment Scores:
 Pred. No.: 0.00013 Length: 447
 Score: 74.00 Matches: 14
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-09-736-250-5 (1-14) x AX209412 (1-447)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
 |||||
 Db 93 GAAGATAATGCTCAGAAAATGGGTCTCTGTGTGGCACT 134

RESULT 8

AX209412 AX209412 601 bp DNA linear STS 10-JUN-2004

LOCUS Sequence 1340 from Patent WO015153.

DEFINITION AX209412

ACCESSION AX209412

VERSION AX209412.1 GI:48017195

KEYWORDS STS

SOURCE Homo sapiens

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 601)

AUTHORS Nelson, R.M., Marnellos, G., Kammerer, S., Hoyal, C.R., Shi, M.M.,

Cantor, C.R. and Braun, A.

Large-Scale Validation of Single Nucleotide Polymorphisms in Gene

Regions

JOURNAL Genome Res. (2004) In press

COMMENT

Contact: Andreas Braun

Pharmaceuticals division

Sequenom, Inc.

3595 John Hopkins Court, San Diego, CA 92121, USA

Tel: 18582029018

Fax: 18582029020

Email: abraum@sequenom.com

Primer A: No primer sequence submitted

Primer B: No primer sequence submitted

STS size: 601.

Location/Qualifiers

1..601

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/clone_lib="Human DNA (Sequenom)"

<1..601

ORIGIN

Alignment Scores:
 Pred. No.: 0.000174 Length: 601
 Score: 74.00 Matches: 14
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 11 Gaps: 0

US-09-736-250-5 (1-14) x BV180201 (1-601)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
 |||||
 Db 327 GAAGATAATGCTCAGAAAATGGGTCTCTGTGTGGCACT 286

RESULT 9

BD079737 BD079737 804 bp DNA linear PAT 27-AUG-2002

LOCUS Cancer-associated nucleic acids and polypeptides.

DEFINITION BD079737

ACCESSION BD079737

VERSION BD079737.1 GI:22625340

KEYWORDS JP 2001516009-A/403.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 804)
 AUTHORS Old, L.J., Scanlan, M.J., Stockert, E., Gure, A., Chen, Y.T., Gout, I.,
 Ogihara, M., Obata, Y., Pfeundschuh, M., Tureci, O. and Sahin, U.
 TITLE Cancer-associated nucleic acids and polypeptides
 JOURNAL Patent: JP 2001516009-A 403 25-SEP-2001;
 LUDWIG INSTITUTE FOR CANCER RESEARCH
 COMMENT OS Homo sapiens (human)
 PN JP 2001516009-A/403
 PD 25-SEP-2001
 PF 15-JUL-1998 JP 2000503425
 PR 17-JUL-1997 US 08/896164, 10-OCT-1997 US 60/061599 PR
 10-OCT-1997 US 60/061765, 10-OCT-1997 US 08/948705 PR
 11-OCT-1997 GB 9721697.2, 22-JUN-1998 US 09/102322 PI LLOYD
 J OLD, MATTHEW J SCANLAN, ELISABETH STOCKERT, ALI GURE, YAO PI
 CHEN,
 PI IVAN GOUT, MICHAEL O'HARE, YUICHI OBATA, MICHAEL PFREUNDSCUH, PI
 OZLEM TURECI,
 PI UGUR SAHIN
 PC GOIN33/574, A61K38/00, A61K39/395, A61K39/395, A61K45/00, A61K48/00, PC
 A61P35/00,
 PC C07K14/82, C07K16/32, C12N15/09//C07K16/46, C12P21/08, A61K37/02,
 PC C12N15/00
 CC Cancer-associated nucleic acids and polypeptides. FH Key
 Location/Qualifiers
 FT source
 1..804
 /organism="Homo sapiens"
 /location/Qualifiers
 FT 1..804
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

FEATURES
 source
 1..804
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

ORIGIN
 Alignment Scores:
 Pred. No.: 0.000232 Length: 804
 Score: 74.00 Matches: 14
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-09-736-250-5 (1-14) x BD079737 (1-804)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
 |||||
 Db 301 GAAGATAATGCTCAGAAATGGTGGTCTGTGTGGCACT 260
 |||||

RESULT 10
 CR541783 1131 bp mRNA linear PRI 29-JUN-2004
 LOCUS Homo sapiens full open reading frame cDNA clone RZPD0834E0730D for
 DEFINITION gene CCNI, cyclin I, complete cds, without stopcodon.
 ACCESSION CR541783
 VERSION CR541783.1 GI:49456522
 KEYWORDS Full ORF shuttle clone, Gateway(TM), complete cds.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1131)
 AUTHORS Halleck, A., Ebert, L., Moundinya, M., Schick, M., Eisenstein, S.,
 Neubert, P., Kstrang, K., Schatten, R., Shen, B., Henze, S., Mar, W.,
 Korn, B., Zuo, D., Hu, Y. and LaBaer, J.
 TITLE Cloning of human full open reading frames in Gateway(TM) system
 entry vector (pDONR201)
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1131)
 AUTHORS Halleck, A., Ebert, L., Moundinya, M., Schick, M., Eisenstein, S.,

TITLE
 JOURNAL

COMMENT
 This clone is available from RZPD;
 Contact RZPD (customer.service@rzpd.de) for further information.
 Clone name at Harvard Institute of Proteomics
 (www.hip.harvard.edu): FLH131015.011
 This CDS clone is part of a collection of human full ORF clones
 jointly established and verified by the Harvard Institute of
 Proteomics (HIP) and RZPD.
 This CDS has been inserted into pDONR201 via a BP Clonase(TM)
 reaction. Additional sequence has been added in front of the start
 codon: att..AAAAA GCA GGC TCC ACC (ATG)
 The last codon is followed by the 3' att site: GACCCAGCTTTT.. att
 The clone is validated by full sequence check.
 Compared to the reference sequence NM_006835 (GI:17738314) we found
 AA exchange(s) at position (first base of changed triplet):
 223(arg->gly) 409(lys->arg)
 Clone distribution: http://www.rzpd.de/products/orfclones/.

FEATURES
 source
 1..1131
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="RZPD0834E0730D"
 /clone_lib="Human Full ORF Clones Gateway(TM) - RZPD"
 /lab_host="DH5Alpha"
 /note="vector: pDONR201, Site_1: attP1; Site_2: attP2"
 1..1131
 /gene="CCNI"
 1..>1131
 /gene="CCNI"
 /codon_start=1
 /protein_id="CAG46582.1"
 /db_xref="GI:49456523"
 /translation="MKPPGPLENQLRSLFLEKAITREAOQMKVNVKMPNSQNSVPSQ
 RDEVIOVLAKLYQNFYLPETALASSLDGFLATVKAHPKYLSCIALSCFPLAAKT
 EDERPVLKVLARDSEFCGSSSEILMERIILDRNWDLTATPLDPLHFAIAVS
 TRQLPLKPLKSPQLAVITKQLHMCACNQLLQFRGMLANVLEKLIPLDW
 LSTIETLLQKQMSQSLIHICRELVAHLSLQSLNSVYVRLPLKHTLVTCDDGV
 FRIHPSPGPFDFSKNSKEPVPGVTAFAFHHPLPAASGCKQTSKTRKVEEMEDDFY
 DGIKRLYNEDNVSENVSGVCGTDLRQEGHASPCPLQPVSM"

ORIGIN
 Alignment Scores:
 Pred. No.: 0.000326 Length: 1131
 Score: 74.00 Matches: 14
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-09-736-250-5 (1-14) x CR541783 (1-1131)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
 |||||
 Db 1027 GAAGATAATGCTCAGAAATGGTGGTCTGTGTGGCACT 1068
 |||||

Neubert, P., Kstrang, K., Schatten, R., Shen, B., Henze, S., Mar, W.,
 Korn, B., Zuo, D., Hu, Y. and LaBaer, J.
 Direct Submission
 Submitted (28-JUN-2004) RZPD Deutsches Ressourcenzentrum fuer
 Genomforschung GmbH, Im Neuenheimer Feld 580, D-69120 Heidelberg,
 Germany
 RZPD; RZPD0834E0730D, ORFNO 3592
 www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=RZPD0834E0730D RZPDLIB;
 Human Full ORF Clones Gateway(TM) - RZPD (kan-resist.) RZPD LIB NO.
 834
 www.rzpd.de/cgi-bin/products/showLib.pl.cgi/response?libNo=834
 www.rzpd.de/products/orfclones/
 Contact: Inge Arlart
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH,
 Heubnerweg 6, D-14059 Berlin, Germany
 Tel: +49 30 32639 100
 Fax: +49 30 32639 111
 www.rzpd.de

This clone is available from RZPD;
 Contact RZPD (customer.service@rzpd.de) for further information.
 Clone name at Harvard Institute of Proteomics
 (www.hip.harvard.edu): FLH131015.011
 This CDS clone is part of a collection of human full ORF clones
 jointly established and verified by the Harvard Institute of
 Proteomics (HIP) and RZPD.
 This CDS has been inserted into pDONR201 via a BP Clonase(TM)
 reaction. Additional sequence has been added in front of the start
 codon: att..AAAAA GCA GGC TCC ACC (ATG)
 The last codon is followed by the 3' att site: GACCCAGCTTTT.. att
 The clone is validated by full sequence check.
 Compared to the reference sequence NM_006835 (GI:17738314) we found
 AA exchange(s) at position (first base of changed triplet):
 223(arg->gly) 409(lys->arg)
 Clone distribution: http://www.rzpd.de/products/orfclones/.

FEATURES
 source

gene
 CDS


```
RESULT 11
ARI45734
LOCUS ARI45734 linear PAT 08-AUG-2001
DEFINITION Sequence 2 from patent US 6218115.
ACCESSION ARI45734
VERSION ARI45734.1 GI:15108923
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1133)
AUTHORS Nakamura,T.
TITLE Human cyclin I and genes encoding same
JOURNAL Patent: US 6218115-A 2 17-APR-2001;
FEATURES
source
1..1133
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Alignment Scores:
Pred. No.: 0.000326 Length: 1133
Score: 74.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB:
US-09-736-250-5 (1-14) x ARI45734 (1-1133)
Qy 1 GluAspAenValSerGluAsnValGlySerValCysGlyThr 14
|||||
Db 1027 GAAGATAATGCTCAGAAATGTGGTTCTGTGTGGCACT 1068
|||||

RESULT 12
AR087353
LOCUS AR087353 linear PAT 07-SEP-2000
DEFINITION Sequence 5 from patent US 5986055.
ACCESSION AR087353
VERSION AR087353.1 GI:10014116
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1260)
AUTHORS Yang,M., Nandabalan,K. and Schultz,V.Peter.
TITLE CDK2 interactions
JOURNAL Patent: US 5986055-A 5 16-NOV-1999;
FEATURES
source
1..1260
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Alignment Scores:
Pred. No.: 0.000362 Length: 1260
Score: 74.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB:
US-09-736-250-5 (1-14) x AR087353 (1-1260)
Qy 1 GluAspAenValSerGluAsnValGlySerValCysGlyThr 14
|||||
Db 1027 GAAGATAATGCTCAGAAATGTGGTTCTGTGTGGCACT 1068
|||||

RESULT 13
CO812312
LOCUS CO812312 linear PAT 24-MAY-2004
DEFINITION Sequence 64 from Patent WO2004038020.
ACCESSION CO812312
VERSION CO812312.1 GI:47601932
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Wittig,R., Poustka,A., Mollenhauer,J. and Schadendorf,D.
TITLE Target genes for the diagnosis and treatment of cancer
JOURNAL Patent: WO 2004038020-A 64 06-MAY-2004;
DEUTSCHES Krebsforschungszentrum Stiftung des oeffentliche n Rechts
(DE)
FEATURES
source
1..1260
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
misc_feature
1..1260
/note="D50310"
ORIGIN
Alignment Scores:
Pred. No.: 0.000362 Length: 1260
Score: 74.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB:
US-09-736-250-5 (1-14) x CO812312 (1-1260)
Qy 1 GluAspAenValSerGluAsnValGlySerValCysGlyThr 14
|||||
Db 1027 GAAGATAATGCTCAGAAATGTGGTTCTGTGTGGCACT 1068
|||||

RESULT 14
AR281918
LOCUS AR281918 linear PAT 10-APR-2003
DEFINITION Sequence 5 from patent US 6521412.
ACCESSION AR281918
VERSION AR281918.1 GI:29717848
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1260)
AUTHORS Yang,M., Nandabalan,K. and Schultz,V.P.
TITLE HsReq*1 and hSReq*2 proteins and use thereof to detect CDK2
JOURNAL Patent: US 6521412-A 5 18-FEB-2003;
FEATURES
source
1..1260
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Alignment Scores:
Pred. No.: 0.000362 Length: 1260
Score: 74.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB:
US-09-736-250-5 (1-14) x AR281918 (1-1260)
Qy 1 GluAspAenValSerGluAsnValGlySerValCysGlyThr 14
|||||
Db 1027 GAAGATAATGCTCAGAAATGTGGTTCTGTGTGGCACT 1068
|||||
```

DEFINITION Sequence 899 from patent US 6607879.
 ACCESSION AR380354
 VERSION AR380354.1 GI:40087988
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 1260)
 AUTHORS Cocks B.G., Stuart S.G. and Seilhamer, J.J.
 TITLE Compositions for the detection of blood cell and immunological
 response gene expression
 JOURNAL Patent: US 6607879-A 899 19-AUG-2003;
 FEATURES
 source
 1..1260
 /organism="unknown"
 /mol_type="genomic DNA"
 ORIGIN
 Alignment Scores:
 Pred. No.: 0.000362 Length: 1260
 Score: 74.00 Matches: 14
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0
 US-09-736-250-5 (1-14) x AR380354 (1-1260)
 QY 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
 DB 1027 GAAGATATATGTCACAGAAATGGGGTTCTGTGTGGCACT 1068

Search completed: February 11, 2005, 05:55:28
 Job time : 288.586 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 11, 2005, 03:18:45 ; Search time 35.2327 Seconds
(without alignments)
2352.255 Million cell updates/sec

Title: US-09-736-250-5

Perfect score: 74

Sequence: 1 EDVSENVGVSGT 14

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US09736250/runat_07022005_154923_20396/app_query.fasta_1.718
-DB=N Geneseq_16Dec04 -QWTF=fastcap -SUFFIX=ring -MINMATCH=0.1 -LOOPGL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=prc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09736250.ecgn_1_1586@runat_07022005_154923_20396 -NCPU=6 -ICPU=3
-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DE TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N Geneseq_16Dec04:
1: Geneseqn1980s:
2: Geneseqn1990s:
3: Geneseqn2000s:
4: Geneseqn2001as:
5: Geneseqn2001bs:
6: Geneseqn2002as:
7: Geneseqn2002bs:
8: Geneseqn2003as:
9: Geneseqn2003bs:
10: Geneseqn2003cs:
11: Geneseqn2003ds:
12: Geneseqn2004as:
13: Geneseqn2004bs:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	74	100.0	136	2	AaQ76921 Human Gen
c 2	74	100.0	351	8	Aad51549 Human BCA
3	74	100.0	389	10	Adk61066 Human c
c 4	74	100.0	444	6	Abk45862 cDNA enco
5	74	100.0	447	4	Aas25071 Human ova

c 6	74	100.0	447	5	Aah83716 Human ova
c 7	74	100.0	597	10	Adk61065 Ovarian c
c 8	74	100.0	804	2	Aax40003 Prostate
9	74	100.0	903	12	Adn01156 Human cel
10	74	100.0	1260	3	Aaz37836 Human cyc
11	74	100.0	1260	6	Abk83672 Human cDN
12	74	100.0	1260	10	Adk61064 Ovarian c
13	74	100.0	1260	11	Adi31573 Human cDN
14	74	100.0	1260	13	Adr25465 Breast ca
15	74	100.0	1328	2	Aat73937 DNA encod
16	74	100.0	1384	8	Acc47339 Human pro
17	74	100.0	1493	2	Aaz41284 Human nor
18	74	100.0	1651	9	Aad57247 Human CGD
19	74	100.0	1889	6	Abi87929 Human ova
20	74	100.0	1890	12	Adp10653 Reference
21	74	100.0	1890	13	Adn38124 Tumour-as
22	74	100.0	2146	5	Adl63082 Human ova
23	74	100.0	2755	5	Adl63374 Human ova
24	69	93.2	304	3	Aac25819 Human sec
25	65	87.8	420	8	Abx44645 Bovine ES
c 26	50	67.6	3039	4	AbL09675
c 27	50	67.6	5856	4	AbL09674
c 28	46	62.2	293	12	AdQ19591
c 29	46	62.2	379	4	Aai89415 Human sof
30	46	62.2	381	4	Aai87049 Human pol
c 31	46	62.2	564	2	Aav49573 Human sco
c 32	46	62.2	601	13	ACN60174 Cotton gy
c 33	46	62.2	798	13	ADR65695
c 34	46	62.2	840	8	ACF64409 Human IP1
c 35	46	62.2	1138	5	ABV22730 Human pro
c 36	46	62.2	1138	5	ABV28557 Human pro
c 37	46	62.2	1175	12	ADL91836
c 38	46	62.2	1186	2	AAV49572 Human sto
c 39	46	62.2	1186	11	ADP65828 Human mRN
c 40	46	62.2	1186	11	ADP65750 Human put
c 41	46	62.2	1187	2	Aax28650 Nucleotid
c 42	46	62.2	1187	3	AAA40570 Human fet
c 43	46	62.2	1206	13	ACN37541 Tumour-as
c 44	46	62.2	1264	4	AAS21244 Human cDN
c 45	46	62.2	1264	8	ACA03603 cDNA enco

ALIGNMENTS

RESULT 1
AAQ76921
ID AAQ76921 standard; DNA; 136 BP.
XX
AC AAQ76921;
XX
DT 25-MAR-2003 (revised)
DT 23-SEP-1994 (first entry)
XX
DE Human genome fragment.
XX
KW Brain; placenta; bone marrow; genetic analysis; gene mapping; detection;
KW homology; human; adrenal tissue; ds.
XX
OS Homo sapiens.
PN WO9401548-A2.
XX
PD 20-JAN-1994.
XX
PF 13-JUL-1993; 93WO-GB001467.
XX
PR 13-JUL-1992; 92GB-00014857.
XX
PA (MEDI-) MEDICAL RES COUNCIL.
XX
PI Sibson DR, Gross J, Hadfield KM, Howells D, Starkey M, Kelly M,
PI Shaw D,
XX

DR WPI; 1994-035056/04.

XX New nucleic acid fragment encoding gene products - can be used for

PT genetic analysis and mapping.

XX Claim 1; Page 272; 616pp; English.

XX Human nucleic acid fragments, isolated from brain adrenal tissue, the

CC placenta or bone marrow comprise any of: (A) a sequence selected from

CC (AAQ76401-Q77613), (B) an allelic variation of a sequence as described in

CC (A), or (C) a sequence complementary to (A) or (B). (Updated on 25-MAR-

XX 2003 to correct FN field.)

XX Sequence 136 BP; 36 A; 28 C; 29 G; 43 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 5.39e-05 Length: 136

Score: 74.00 Matches: 14

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 2 Gaps: 0

US-09-736-250-5 (1-14) x AAQ76921 (1-136)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14

Db 24 GAAGATAATGCTCAGAAATGTCGGTCTCTGTGTGGCACT 65

RESULT 2

AAD51549/c

ID AAD51549 standard; cDNA; 351 BP.

XX AC AAD51549;

DT 16-APR-2003 (first entry)

DE Human BCA7 cDNA.

XX Human; breast cancer-associated gene; BCA-related disorder; lymphoma;

KW infectious disease; eating disorder; cancer; Ewing's tumour; allergy;

KW tumour; polycythaemia vera; forensic biology; gene therapy; leukaemia;

KW bone disease; sarcoma; vaccine; gene; ss.

XX Homo sapiens.

XX Key

FH Location/Qualifiers

FT 1. .351

FT /*tag= a

FT /product= "BCA protein"

FT /transl_except= (pos:22. .24, aa:Xaa)

FT /transl_except= (pos:28. .30, aa:Xaa)

FT /transl_except= (pos:202. .204, aa:Xaa)

FT /transl_except= (pos:313. .315, aa:Xaa)

FT /transl_except= (pos:334. .336, aa:Xaa)

FT /note= "Xaa corresponds to in-frame stop codon; No start

FT and stop codon"

FT /partial

XX WO200287507-A2.

XX 07-NOV-2002.

XX 29-APR-2002; 2002WO-US013584.

XX 27-APR-2001; 2001US-0287170P.

XX (SUNN-) SUNNYBROOK & WOMEN'S COLLEGE HEALTH SCI.

XX Seth A;

XX WPI; 2003-120443/11.

DR P-PSDB; AAE33644.

XX New breast cancer-associated (BCA) genes and polypeptides, useful for

PT preventing, treating, diagnosing or staging breast cancer, or other BCA-

PT related disorders, e.g. prostate cancer, sarcoma, Ewing's tumor, leukemia

XX or lymphomas.

XX Disclosure; Page 188; 195pp; English.

XX The invention relates to human breast cancer-associated (BCA) genes and

CC polypeptides. BCA sequences are useful for preventing or treating breast

CC cancer. Other BCA-related disorders that may be treated include allergy,

CC bone disease, eating disorder, infectious disease, ovarian cancer,

CC prostate cancer, skin cancer or brain cancer, malignant or non-malignant

CC tumours, sarcoma, Ewing's tumour, leukaemia, lymphomas, or polycythaemia

CC vera. BCA sequences are also useful in forensic biology, diagnostic

CC assays, prognostic assays or pharmacogenomics or for monitoring clinical

CC trials. The invention is useful in gene therapy and as vaccines. The

CC present sequence is human BCA cDNA

XX Sequence 351 BP; 98 A; 77 C; 60 G; 116 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0.000163 Length: 351

Score: 74.00 Matches: 14

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 8 Gaps: 0

US-09-736-250-5 (1-14) x AAD51549 (1-351)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14

Db 308 GAAGATAATGCTCAGAAATGTCGGTCTCTGTGTGGCACT 267

RESULT 3

ADK61066

ID ADK61066 standard; DNA; 389 BP.

XX AC ADK61066;

DT 06-MAY-2004 (first entry)

XX Ovarian cancer-related DNA #221 with altered ovarian cancer expression.

XX ds; Gene; ovarian tumor; BRCA-1-like; BRCA-2-like; non-BRCA-like;

KW gene expression; primer; cancer.

XX Homo sapiens.

XX WO2003068054-A2.

XX 21-AUG-2003.

XX 13-FEB-2003; 2003WO-US004688.

XX 13-FEB-2002; 2002US-0357031P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX (SLOK) SLOAN KETTERING INST CANCER RES.

XX Jazaeri AA, Boyd J, Liu ET;

XX WPI; 2003-689589/65.

XX Classifying an ovarian tumor as a BRCA-1-like or BRCA-2-like or non-BRCA-

PT like tumor by determining a pattern of expression in the ovarian tumor of

PT several markers.

XX Disclosure; SEQ ID NO 236; 137pp; English.

XX The invention relates to a method of classifying an ovarian tumor as a

CC BRCA-1-like or BRCA-2-like or non-BRCA-like tumor by: (1) determining a

CC pattern of expression in the ovarian tumor of several markers given in
CC the specification; and (2) comparing a similarity of the pattern of
CC expression of the markers in the ovarian tumor to a pattern of expression
CC of the markers in a comparison tissue of a known BRCA-1-like or BRCA-2-
CC like or non-BRCA-like tumor. The method is useful for classifying an
CC ovarian tumor as a BRCA-1-like or BRCA-2-like or non-BRCA-like tumor.
CC This sequence corresponds to an ovarian cancer -related gene having an
CC altered pattern of expression in ovarian cancer. (Note: The sequence data
CC for this patent did not form part of the printed specification but was
CC obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences).

XX Sequence 389 BP; 97 A; 99 C; 84 G; 100 T; 0 U; 9 Other;

Alignment Scores:
Pred. No.: 0.000184 Length: 389
Score: 74.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-736-250-5 (1-14) x ADK61066 (1-389)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 286 GAAGATAATGCTCAGAAATGCGGTCTGTGTGCGACT 327

RESULT 4
ABK45862/c

ID ABK45862 standard; cDNA; 444 BP.

XX AC ABK45862;
XX
XX
XX 05-JUN-2002 (first entry)
XX cDNA encoding colon tumour protein, SEQ ID No 1413.
XX Human; colon tumour; vaccine; colon cancer; immunogenic; immunotherapy;
XX gene; ss.

XX Homo sapiens.

XX WO200212328-A2.

XX 14-FEB-2002.

XX 31-JUL-2001; 2001WO-US024218.

XX 03-AUG-2000; 2000US-0223283P.

XX 28-MAR-2001; 2001US-0279763P.

XX 29-JUN-2001; 2001US-0302051P.

XX (CORI-) CORIXA CORP.

XX King GE, Meagher MJ, Xu J, Secretist H;

XX WPI; 2002-241739/29.

XX New colon cancer polypeptides and polynucleotides, useful as vaccines,
XX for diagnosing, preventing, and treating colon cancer, and as markers for
XX the progression of cancer.

XX Claim 1; SEQ ID NO 1413; 147pp; English.

XX The invention relates to polynucleotides encoding colon tumour proteins.
XX The polynucleotides and encoded polypeptides are useful in pharmaceutical
XX compositions, such as vaccines, for the diagnosis, prevention, and
XX treatment of colon cancer. Polynucleotide sequences may be used as
XX hybridisation probes or primers, and in the design and preparation of
XX ribozyme molecules for inhibiting expression of tumour polypeptides and
XX proteins in tumour cells. The compositions are useful for stimulating an
XX immune response against cancer, particularly for the immunotherapy of

CC colon cancer, and as markers for the progression of cancer. ABK44450-
CC ABK46237 represent coding sequences of human colon tumour proteins of the
CC invention. Note: With the exception of SEQ ID No 1 and 2, the sequence
CC data for this patent did not form part of the printed specification but
CC was supplied by the European Patent Office

XX Sequence 444 BP; 134 A; 81 C; 74 G; 155 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0.000215 Length: 444
Score: 74.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-736-250-5 (1-14) x ABK45862 (1-444)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 436 GAAGATAATGCTCAGAAATGCGGTCTGTGTGCGACT 395

RESULT 5

AAS25071

ID AAS25071 standard; cDNA; 447 BP.

XX AC AAS25071;

XX 07-NOV-2001 (first entry)

XX Human ovarian PCR-subtracted cDNA library clone #1252.

XX Immunogenic protein; cancer; ovarian tumour; T-cell stimulation; ss;
XX Gene therapy; cytostatic; T-cell expansion; nucleic acid hybridisation;
XX primer; probe.

XX Homo sapiens.

XX WO200157207-A2.

XX 09-AUG-2001.

XX 05-FEB-2001; 2001WO-US003733.

XX 04-FEB-2000; 2000US-0180403P.

XX 28-MAR-2000; 2000US-0192745P.

XX (CORI-) CORIXA CORP.

XX Algate PA, Mannion J;

XX WPI; 2001-488879/53.

XX New polynucleotides encoding ovarian tumor proteins, useful for treating
XX ovarian cancer, and as probes, primers, and markers of cancer
XX progression.

XX Example 1; Page 304; 378pp; English.

XX The invention comprises compositions used for the therapy and diagnosis
XX of ovarian cancer. The compositions comprise one or more ovarian tumour
XX proteins, their associated polynucleotides, or immunogenic portions of
XX the proteins. The ovarian tumour polynucleotides and polypeptides are
XX useful for stimulating and/or expanding T cells specific for a tumour
XX protein. They are also useful for inhibiting the development of cancer in
XX a patient with an ovarian tumour DNA or protein by incubating isolated T-
XX cells allowing them to proliferate, and administering to the patient. The
XX sequences can be used as markers for cancer, for example, to monitor
XX ovarian cancer progression. Probes and primers are useful in nucleic acid
XX hybridisation, in detecting the presence of complementary sequences in a
XX given sample, for preparing mutant species and for preparing other
XX genetic constructions. Sequences AAS23820-AAS25231 and AAS25328-AAS25549
XX represent human ovarian tumour protein cDNA clones

```
XX SQ Sequence 447 BP; 157 A; 79 C; 92 G; 115 T; 0 U; 4 Other;
Alignment Scores:
Pred. No.: 0.000217 Length: 447
Score: 74.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
US-09-736-250-5 (1-14) x AAS25071 (1-447)
Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
|||||
Db 93 GAAGATAATGCTCAGAAAATGGGTCTCTGTGTGGCACT 134
RESULT 6
AAH83716
ID AAH83716 standard; cDNA; 447 BP.
XX
AC AAH83716;
XX
DT 25-SEP-2001 (first entry)
XX
DE Human ovarian tumour associated polynucleotide sequence SEQ ID NO:1340.
XX
KW Human; ovarian tumour; ovarian cancer; diagnosis; gene therapy;
KW immunogenic; vaccine; ss.
XX
OS Homo sapiens.
XX
PN WO200151513-A2.
XX
PD 19-JUL-2001.
XX
PF 16-JAN-2001; 2001WO-US001575.
XX
PR 14-JAN-2000; 2000US-0176722P.
XX
PA (CORI-) CORIXA CORP.
XX
PI Algate PA;
XX
DR WPI; 2001-425866/45.
XX
PT Novel ovarian tumor proteins, and nucleic acids encoding them, used to
XX treat and diagnose cancers, particularly ovarian cancer.
XX Claim 5; Page 308; 338pp; English.
XX
CC AAH82377 to AAH83878 represent human ovarian tumour-associated
CC polynucleotide sequences which encode ovarian tumour proteins. The
CC ovarian tumour protein and polynucleotide sequences have cytostatic
CC activity, and can be used in gene therapy and vaccine production. The
CC ovarian tumour proteins and polynucleotides can be used to inhibit the
CC development of cancer, particularly ovarian cancer. They can also be used
CC to diagnose the onset and progression of cancer
XX
SQ Sequence 447 BP; 157 A; 79 C; 92 G; 115 T; 0 U; 4 Other;
Alignment Scores:
Pred. No.: 0.000217 Length: 447
Score: 74.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0
US-09-736-250-5 (1-14) x AAH83716 (1-447)
Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
|||||
```

```
Db 93 GAAGATAATGCTCAGAAAATGGGTCTCTGTGTGGCACT 134
RESULT 7
ADK61065/c
ID ADK61065 standard; DNA; 597 BP.
XX
AC ADK61065;
XX
DT 06-MAY-2004 (first entry)
XX
DE Ovarian cancer-related DNA #220 with altered ovarian cancer expression.
XX
KW ds; gene; ovarian tumor; BRCA-1-like; BRCA-2-like; non-BRCA-like;
KW gene expression; primer; cancer.
XX
OS Homo sapiens.
XX
PN WO2003068054-A2.
XX
PD 21-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004688.
XX
PR 13-FEB-2002; 2002US-0357031P.
XX
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA (SLOK ) SLOAN KETTERING INST CANCER RES.
XX
PI Jazaeri AA, Boyd J, Liu ET;
XX
DR WPI; 2003-689589/65.
XX
PT Classifying an ovarian tumor as a BRCA-1-like or BRCA-2-like or non-BRCA-
PT like tumor by determining a pattern of expression in the ovarian tumor of
PT several markers.
XX
PS Disclosure; SEQ ID NO 235; 137pp; English.
XX
CC The invention relates to a method of classifying an ovarian tumor as a
CC BRCA-1-like or BRCA-2-like or non-BRCA-like tumor by: (1) determining a
CC pattern of expression in the ovarian tumor of several markers given in
CC the specification; and (2) comparing a similarity of the pattern of
CC expression of the markers in the ovarian tumor to a pattern of expression
CC of the markers in a comparison tissue of a known BRCA-1-like or BRCA-2-
CC like or non-BRCA-like tumor. The method is useful for classifying an
CC ovarian tumor as a BRCA-1-like or BRCA-2-like or non-BRCA-like tumor.
CC This sequence corresponds to an ovarian cancer -related gene having an
CC altered pattern of expression in ovarian cancer. (Note: The sequence data
CC for this patent did not form part of the printed specification but was
CC obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences).
XX
SQ Sequence 597 BP; 152 A; 126 C; 143 G; 171 T; 0 U; 5 Other;
Alignment Scores:
Pred. No.: 0.000304 Length: 597
Score: 74.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0
US-09-736-250-5 (1-14) x ADK61065 (1-597)
Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
|||||
Db 303 GAAGATAATGCTCAGAAAATGGGTCTCTGTGTGGCACT 262
RESULT 8
AAX40003/c
ID AAX40003 standard; DNA; 804 BP.
XX
AC AAX40003;
```

XX	02-JUL-1999	(first entry)	Prostate cancer associated gene.
XX	DE	XX	Cancer associated antigen; diagnosis; research; treatment; human;
XX	DE	XX	breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer;
XX	DE	XX	prostate cancer; ss.
XX	OS	XX	Homo sapiens.
XX	OS	XX	WO9904265-A2.
XX	PN	XX	28-JAN-1999.
XX	PD	XX	15-JUL-1998; 98WO-US014679.
XX	PF	XX	17-JUL-1997; 97US-00896164.
XX	PR	XX	10-OCT-1997; 97US-0061599P.
XX	PR	XX	10-OCT-1997; 97US-0061765P.
XX	PR	XX	10-OCT-1997; 97US-00948705.
XX	PR	XX	11-OCT-1997; 97GB-00021697.
XX	PR	XX	22-JUN-1998; 98US-00102322.
XX	PA	XX	(LUDW-) LUDWIG INST CANCER RES.
XX	PI	XX	Old LJ, Scanlan MJ, Stockert E, Gure A, Chen Y, Gout I;
XX	PI	XX	O'hare M, Obata Y, Pfreundschuh M, Tureci O, Sahin U;
XX	PI	XX	WPI; 1999-1324448/11.
XX	DR	XX	New isolated cancer associated nucleic acids and polypeptides - isolated
XX	PT	XX	using sera from cancer patients, used to develop products for the
XX	PT	XX	diagnosis, monitoring or treatment of cancers.
XX	PS	XX	Claim 67; Page 630; 787pp; English.
XX	PS	XX	The invention relates to a method for diagnosing a disorder characterised
XX	CC	XX	by expression of a human cancer associated antigen precursor coded for by
XX	CC	XX	a nucleic acid molecule (NAM). The method comprises: (a) contacting a
XX	CC	XX	biological sample isolated from a subject with an agent that specifically
XX	CC	XX	binds to the NAM, an expression product or a fragment of an expression
XX	CC	XX	product complexed with an HNA molecule; and (b) determining the
XX	CC	XX	interaction between the agent and the NAM or the expression product as a
XX	CC	XX	determination of the disorder. The products and methods can be used in
XX	CC	XX	the diagnosis, monitoring, research, or treatment of conditions
XX	CC	XX	characterised by the expression of various cancer associated antigens.
XX	CC	XX	The invention provides nucleic acid sequences and encoded polypeptides
XX	CC	XX	which are cancer associated antigen precursors expressed in human breast
XX	CC	XX	cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and
XX	CC	XX	lung cancer
XX	CC	XX	Sequence 804 BP; 208 A; 172 C; 188 G; 222 T; 0 U; 14 Other;
XX	CC	XX	Alignment Scores:
XX	CC	XX	Pred. No.: 0.000431 Length: 804
XX	CC	XX	Score: 74.00 Matches: 14
XX	CC	XX	Percent Similarity: 100.00% Conservative: 0
XX	CC	XX	Best Local Similarity: 100.00% Mismatches: 0
XX	CC	XX	Query Match: 100.00% Indels: 0
XX	CC	XX	DB: 2 Gaps: 0
XX	CC	XX	US-09-736-250-5 (1-14) x AAX40003 (1-804)
XX	CC	XX	QY 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
XX	CC	XX	301 GAAGATTAATGTCTCAGAAATATGGTGTCTGTGTGGCACT 260
XX	CC	XX	Db
XX	CC	XX	RESULT 9
XX	CC	XX	ADN01156
XX	CC	XX	ID ADN01156 standard; DNA; 903 BP.
XX	CC	XX	XX
XX	CC	XX	ADN01156;
XX	CC	XX	AC
XX	01-JUL-2004	(first entry)	Human cell growth, differentiation, and death-associated coding seq #15.
XX	DE	XX	human; cell growth; cell differentiation; cell death; CGDD;
XX	DE	XX	cell proliferative disorder; arteriosclerosis; atherosclerosis; bursitis;
XX	DE	XX	cirrhosis; hepatitis; polycythaemia vera; psoriasis; cancer;
XX	DE	XX	developmental disorder; Cushing's syndrome; hypothyroidism;
XX	DE	XX	neurological disorder; epilepsy; stroke; Alzheimer's disease;
XX	DE	XX	Pick's disease; Huntington's disease; Parkinson's disease;
XX	DE	XX	multiple sclerosis; autoimmune disorder; inflammatory disorder; AIDS;
XX	DE	XX	allergy; anaemia; asthma; contact dermatitis; diabetes mellitus;
XX	DE	XX	reproductive disorder; infertility; endometriosis; uterine fibroid; gene;
XX	DE	XX	ds.
XX	OS	XX	Homo sapiens.
XX	PN	XX	WO2004031364-A2.
XX	PD	XX	15-APR-2004.
XX	XX	XX	03-OCT-2003; 2003WO-US031441.
XX	XX	XX	03-OCT-2002; 2002US-0416205P.
XX	XX	XX	25-OCT-2002; 2002US-0421521P.
XX	XX	XX	21-NOV-2002; 2002US-0428376P.
XX	XX	XX	23-DEC-2002; 2002US-0436258P.
XX	XX	XX	10-JAN-2003; 2003US-0439292P.
XX	XX	XX	13-FEB-2003; 2003US-0447578P.
XX	XX	XX	(INCY-) INCYTE CORP.
XX	PA	XX	(BURR/) BURRILL J D.
XX	PI	XX	Elliott VS, Swarnakar A, Tang YT, Yue H, Lu DAM, Khare R;
XX	PI	XX	Chawla NK, Richardson TW, Marquis JP, Lal PG, Nguyen DB, Lee SY;
XX	PI	XX	Tran UK, Bhatia UG, Lee S, Blake JU, Ho A, Zheng W, Gao J, Tran B;
XX	PI	XX	Yang YG, Gietzen KJ, Hafalia AJA;
XX	XX	XX	WPI: 2004-330172/30.
XX	XX	XX	P-PSDB; ADN01131.
XX	XX	XX	New isolated polypeptides associated with cell growth, differentiation
XX	XX	XX	and death, useful for diagnosing, treating or preventing e.g.
XX	XX	XX	atherosclerosis, psoriasis, cancers, Alzheimer's disease, AIDS, anemia,
XX	XX	XX	diabetes mellitus or infertility.
XX	XX	XX	Claim 5; SEQ ID NO 40; 213pp; English.
XX	XX	XX	The invention comprises the amino acid and coding sequences of human
XX	XX	XX	proteins that are associated with cell growth, differentiation, and death
XX	XX	XX	(CGDD). The DNA and protein sequences of the invention are useful for
XX	XX	XX	diagnosing, treating or preventing disorders associated with aberrant
XX	XX	XX	expression of CGDD, such as: cell proliferative disorders (e.g.
XX	XX		

US-09-736-250-5 (1-14) x ADN01156 (1-303)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
 Db 797 GAAGATAATGCTCAGAAATGTGGTTCTGTGTGGCACT 838

RESULT 10

AAZ37836
 ID AAZ37836 standard; DNA; 1260 BP.

XX AAZ37836;

XX 09-FEB-2000 (first entry)

XX Human cyclin I nucleotide sequence.

XX Cyclin-dependent kinase 2; CDK2; hsReq; hsReq*-1; hsReq*-2; cyclin I;
 KW ERH; cell cycle; proliferation; cancer; hyperproliferative disorder;
 KW atherosclerosis; tumour; ss.

XX Homo sapiens.

XX Key Location/Qualifiers
 FH 1. .1134
 FT CDS /*tag= a
 FT /product= "Cyclin_I"

XX WO925829-A2.

XX 27-MAY-1999.

XX 12-NOV-1998; 98WO-US024095.

XX 13-NOV-1997; 97US-00969106.

XX (CURA-) CURAGEN CORP.

XX Yang M, Nandabalan K, Schulz VP;

XX WPI; 2000-061923/05.

XX P-PSDB; AAY52185.

XX New complexes of the cyclin-dependent kinase 2 protein with its
 PT interacting proteins, used to treat, e.g. atherosclerosis.

XX Example; Fig 2; 90pp; English.

XX This sequence is the human Cyclin I nucleotide sequence. Cyclin I is
 CC expressed at almost constant levels throughout the cell cycle, and is
 CC implicated in controlling cell cycle progression and transcriptional
 CC control. Cyclins form complexes with cyclin-dependent kinases. CDK2,
 CC cyclin-dependent kinase 2, is used in the invention which relates to
 CC complexes of the CDK2 protein with other proteins, selected from cyclin
 CC I, ERH, hsReq, hsReq*-1 and hsReq*-2 (AAY52185-Y52188). CDK2 is expressed
 CC late in G1 or early in S phase of the cell cycle, and is pivotal for G1/S
 CC transition. Compositions containing a CDK2 complex, or its derivatives
 CC the complex, and nucleotide sequences encoding CDK2 or its derivatives
 CC can be used therapeutically. The complexes and their nucleotide sequences
 CC can be used to treat diseases or disorders associated with increased or
 CC decreased levels of the complex. Screening the complex, or a derivative
 CC or a modulator of the complex for neoplastic activity by measuring the
 CC survival or proliferation of cells from a malignant cell line when in
 CC contact with the complex can be used to indicate if the the complex has
 CC anti-neoplastic activity. Screening for molecules that modulate the
 CC formation of the complexes can be used for treating or preventing
 CC atherosclerosis or atherosclerosis-associated disease by contacting cells
 CC or using a test animal, in which tumour growth or regression is measured
 CC to test whether anti-neoplastic activity is displayed. Diseases which can
 CC be treated or prevented by molecule/s which modulate the function of the
 CC complex include cancer, hyperproliferative disorders and atherosclerosis

XX Sequence 1260 BP; 352 A; 283 C; 274 G; 351 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0.000729 Length: 1260
 Score: 74.00 Matches: 14
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 3 Gaps: 0

US-09-736-250-5 (1-14) x AAZ37836 (1-1260)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
 Db 1027 GAAGATAATGCTCAGAAATGTGGTTCTGTGTGGCACT 1068

RESULT 11

ABK83672

ID ABK83672 standard; cDNA; 1260 BP.

XX AC ABK83672;

XX 14-AUG-2002 (first entry)

XX Human cDNA differentially expressed in granulocytic cells #243.

XX Human; ss; granulocytic cell; DNA chip; bacterial infection;
 KW viral infection; parasitic infection; protozoal infection;
 KW fungal infection; sterile inflammatory disease; psoriasis;
 KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
 KW cardiac reperfusion injury; renal reperfusion injury; AIDS;
 KW adult respiratory distress syndrome; inflammatory bowel disease;
 KW Crohn's disease; ulcerative colitis; periodontal disease;
 KW granulocyte activation; chronic inflammation; allergy.

XX Homo sapiens.

XX WO200228999-A2.

XX 11-APR-2002.

XX 03-OCT-2001; 2001WO-US030821.

XX 03-OCT-2000; 2000US-0237189P.

XX (GENE-) GENE LOGIC INC.

XX Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;

XX WPI; 2002-435328/46.

XX Detecting granulocyte activation by detecting differential expression of
 CC genes associated with granulocyte activation, which serves as diagnostic
 CC markers that is useful for monitoring disease states and drug toxicity.

XX Claim 1; SEQ ID NO 243; 114pp; English.

XX The invention relates to detecting (M1) granulocyte (GC) activation
 CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by
 CC DNA chip analysis as given in the specification, and comparing the
 CC expression level to an expression level in an unactivated GC, where
 CC differential expression of Gs is indicative of GCA. Also included are
 CC modulating (M2) GA by contacting GC with an agent that alters the
 CC expression of at least one gene in Gs; (2) screening (M3) for an agent
 CC capable of modulating GCA or an inflammation (especially chronic) in a
 CC tissue, an allergic response in a subject, exposure of a subject to a
 CC pathogen or sterile inflammatory disease using the gene expression
 CC profile; (3) detecting (M4) an inflammation (especially chronic) in a
 CC tissue, an allergic response in a subject, exposure of a subject to a
 CC pathogen or sterile inflammatory disease, by detecting the level of
 CC expression in a sample of the tissue of gene(s) from Gs, where the level
 CC of expression of the gene is indicative of inflammation; (4) treating
 CC (M5) an inflammation (especially chronic) or in a tissue, an allergic
 CC response in a subject, exposure of a subject to a pathogen or sterile

CC inflammatory disease, by contacting a tissue having inflammation with an
CC agent that modulates the expression of gene(s) from Gs in the tissue. M1
CC is useful for detecting GCA; M2 is useful for modulating GA; M3 is useful
CC for screening an agent capable of modulating GCA preferably in an
CC inflammation in a tissue; M4 is useful for detecting an inflammation
CC (especially chronic) in a tissue, an allergic response in a subject,
CC exposure of a subject to a pathogen or sterile inflammatory disease (e.g.
CC psoriasis, rheumatoid arthritis, glomerulonephritis, asthma, thrombosis,
CC cardiac reperfusion injury, renal reperfusion injury, ARDS, adult
CC respiratory distress syndrome, inflammatory bowel disease, Crohn's
CC disease, ulcerative colitis, periodontal disease; also bacterial
CC infection, viral infection, parasitic infection, protozoal infection,
CC fungal infection and M5 is useful for treating one of the above
CC conditions. The present sequence represents a gene differentially
CC expressed in granulocytes. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1260 BP; 352 A; 283 C; 274 G; 351 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0.000729 Length: 1260
Score: 74.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-736-250-5 (1-14) x ABK83672 (1-1260)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 1027 GAAGATAATGCTCAGAAATGTGGGTCTGTGTGGCACT 1068

RESULT 12

ADK61064

ID ADK61064 standard; DNA; 1260 BP.

XX AC ADK61064;

XX DT 06-MAY-2004 (first entry)

XX DE Ovarian cancer-related DNA #219 with altered ovarian cancer expression.

XX KW ds; gene; ovarian tumor; BRCA-1-like; BRCA-2-like; non-BRCA-like;

XX KW gene expression; primer; cancer.

XX XX Homo sapiens.

XX OS WO2003068054-A2.

XX PN 21-AUG-2003.

XX PD 13-FEB-2003; 2003WO-US004688.

XX PF (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PA (SLOK) SLOAN KETTERING INST CANCER RES.

XX PI Jazaeri AA, Boyd J, Liu ET;

XX XX WPI; 2003-689589/65.

XX DR Classifying an ovarian tumor as a BRCA-1-like or BRCA-2-like or non-BRCA-
PT like tumor by determining a pattern of expression in the ovarian tumor of
PT several markers.

XX PS Disclosure; SEQ ID NO 234; 137pp; English.

XX CC The invention relates to a method of classifying an ovarian tumor as a
CC BRCA-1-like or BRCA-2-like or non-BRCA-like tumor by: (1) determining a

CC pattern of expression in the ovarian tumor of several markers given in
CC the specification; and (2) comparing a similarity of the pattern of
CC expression of the markers in the ovarian tumor to a pattern of expression
CC of the markers in a comparison tissue of a known BRCA-1-like or BRCA-2-
CC like or non-BRCA-like tumor. The method is useful for classifying an
CC ovarian tumor as a BRCA-1-like or BRCA-2-like or non-BRCA-like tumor.
CC This sequence corresponds to an ovarian cancer -related gene having an
CC altered pattern of expression in ovarian cancer. (Note: The sequence data
CC for this patent did not form part of the printed specification but was
CC obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences).

SQ Sequence 1260 BP; 352 A; 283 C; 274 G; 351 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0.000729 Length: 1260
Score: 74.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-736-250-5 (1-14) x ADK61064 (1-1260)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 1027 GAAGATAATGCTCAGAAATGTGGGTCTGTGTGGCACT 1068

RESULT 13

AD131573

ID AD131573 standard; cDNA; 1260 BP.

XX AC AD131573;

XX DT 17-JUN-2004 (first entry)

XX DE Human cDNA #899.

XX KW Human; gene; ss; immunological response; immunopathological condition;
KW Crohn's disease; asthma; ulcerative colitis; hyperosinophilia;
KW irritable bowel syndrome; osteoarthritis; rheumatoid arthritis;
KW acute monocytic leukaemia; antiinflammatory; antiasthmatic; antiulcer;
KW osteopathic; antiarthritic; antirheumatic; cytostatic.

XX OS Homo sapiens.

XX XX US6607879-B1.

XX PN 19-AUG-2003.

XX XX 09-FEB-1998; 98US-00023655.

XX XX 09-FEB-1998; 98US-00023655.

XX XX (INCY-) INCYTE CORP.

XX XX Cocks BG, Stuart SG, Seilhamer JJ;

XX XX WPI; 2003-895307/82.

XX XX A composition comprising a plurality of cDNAs, useful for detecting
PT altered expression of genes in an immunological response or for
PT diagnosing and treating an immunopathology, e.g. Crohn's disease, asthma
PT or osteoarthritis.

XX PS Claim 1; SEQ ID NO 899; 50pp; English.

XX CC The invention relates to a composition comprising a plurality of cDNAs
CC for detecting the altered expression of genes in an immunological
CC response. The invention also relates to a method of diagnosing or
CC monitoring the treatment of an immunopathological condition in a sample,
CC comprising obtaining nucleic acids from a sample, contacting the nucleic
CC acids of the sample with an array comprising the plurality of cDNAs under

CC conditions to form one or more hybridisation complexes, detecting the
CC hybridisation complexes and comparing the levels of the detected
CC hybridisation complexes with the level of hybridisation complexes
CC detected in a non-diseased sample, where an altered level of the detected
CC hybridisation complexes correlates with the presence of an
CC immunopathological condition. Also disclosed are an expression profile
CC comprising a microarray and a plurality of detectable probes. The cDNAs
CC method for identifying a plurality of polynucleotide probes. The cDNAs
CC are useful as hybridisable array elements in a microarray for monitoring
CC the expression of target polynucleotides. The microarray can be used in
CC the diagnosis of an immunopathology, such as Crohn's disease, asthma,
CC ulcerative colitis, hyperesinophilia, irritable bowel syndrome,
CC osteoarthritis, rheumatoid arthritis or acute monocytic leukaemia, and in
CC identifying agents for the treatment of the diseases. The microarray may
CC also be used in drug discovery and development, toxicological and
CC carcinogenicity studies, forensic or pharmacogenomics. The composition
CC may also be used in purification of a subpopulation of mRNAs, cDNAs or
CC genomic fragments. This sequence represents a human cDNA of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification but was obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html.

XX SQ Sequence 1260 BP; 352 A; 283 C; 274 G; 351 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0.000729 Length: 1260
Score: 74.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 11 Gaps: 0

US-09-736-250-5 (1-14) x ADI31573 (1-1260)

Qy 1 GluAspAnValSerGluAsnValGlySerValCysGlyThr 14
Db 1027 GAAGATAATGCTCAGAAATGTGGTTCTGTGTGGCACT 1068

RESULT 14
ID ADR25465
ID ADR25465 standard; DNA; 1260 BP.
XX AC ADR25465;
XX DT 21-OCT-2004 (first entry)
XX DE Breast cancer prognosis marker #1326.
XX KW ds; breast cancer; prognosis; gene expression; diagnosis.
XX OS Homo sapiens.
XX PN WO2004065545-A2.
XX PD 05-AUG-2004.
XX PF 15-JAN-2004; 2004WO-US001100.
XX PR 15-JAN-2003; 2003US-00342887.
XX (ROSE-) ROSETTA INPHARMATICS LLC.
XX (NECA-) NETHERLANDS CANCER INST.

XX Van't Veer LJ, He Y;

XX WPI; 2004-593473/57.

XX Classifying a breast cancer patient according to prognosis comprises
XX determining the similarity between the level of expression of each of
XX five genes in a cell sample taken from patient, to control levels.

XX Disclosure; SEQ ID NO 1326; 226pp; English.

CC The invention relates to a method of classifying a breast cancer patient
CC according to prognosis by determining the similarity between the level of
CC expression of each of five genes for which markers are listed in the
CC specification, in a cell sample taken from the breast cancer patient, to
CC control levels of expression for each respective five genes to obtain a
CC patient similarity value. The methods are useful for classifying a breast
CC cancer patient according to prognosis. Kits and computer program products
CC are useful for data analysis using the diagnostic, prognostic and
CC statistical methods of the invention. This sequence corresponds to a
CC marker used in the method of the invention.

XX SQ Sequence 1260 BP; 352 A; 283 C; 274 G; 351 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0.000729 Length: 1260
Score: 74.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-09-736-250-5 (1-14) x ADR25465 (1-1260)

Qy 1 GluAspAnValSerGluAsnValGlySerValCysGlyThr 14
Db 1027 GAAGATAATGCTCAGAAATGTGGTTCTGTGTGGCACT 1068

RESULT 15
ID AAT73937
ID AAT73937 standard; DNA; 1328 BP.
XX AC AAT73937;

XX DT 02-DEC-1997 (first entry)

XX DE DNA encoding human cyclin I.

XX KW human; cyclin I; antisense; probe; neurone; cancer; antibody; ds.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
XX CDS 69..1202
XX FT /*tag= a

XX PN WO9712973-A1.

XX PD 10-APR-1997.

XX PF 07-OCT-1996; 96WO-JP002905.

XX PR 05-OCT-1995; 95JP-00284663.

XX (SUME) SUMITOMO ELECTRIC IND CO.

XX Nakamura T;

XX WPI; 1997-226217/20.

XX P-PSDB; AAW21965.

XX Human cyclin I protein and related (anti:sense) DNA - used for neuron
XX labelling method and cancer cell detection.

XX Example 1; Fig 1; 45pp; Japanese.

XX This sequence encodes human cyclin I. Antisense polynucleotides are
XX useful for as probes and can be labelled and used for detection of
XX neurones by hybridisation with mRNA for cyclin I (contained in these
XX cells). The gene can be used for detection of cancer cells by detecting
XX the expression of the cyclin I gene in these cells. Also antibodies
XX specific for the fragments of the protein (especially AAW21966) can be
XX used for detection

```

XX
SQ Sequence 1328 BP; 376 A; 292 C; 302 G; 358 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:      0.000775      Length:      1328
Score:          74.00         Matches:     14
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00%  Mismatches:  0
Query Match:      100.00%      Indels:     0
DB:               2           Gaps:       0

US-09-736-250-5 (1-14) x AAT73937 (1-1328)

Qy      1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db      1095 GAAGATAATGTCACAAAAATGTTGGGTTCTGTGTGGCACT 1136

Search completed: February 11, 2005, 03:41:49
Job time : 39.2327 secs

```

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 11, 2005, 03:24:00 ; Search time 11.2072 Seconds
(without alignments)
2044.039 Million cell updates/sec

Title: US-09-736-250-5

Perfect score: 74

Sequence: 1 EDVSENVGVCGT 14

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US09736250/runat 07022005 154924 20422/app query.fasta_1.718
-DB=Issued Patents NA -QWMT=fastap -SUFFIX=rni -MINWATCH=0.1 -LOPFCI=0
-LOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09736250 @CGN 1 1 93 @runat 07022005 154924 20422 -NCPU=6 -ICPU=3
-NO_MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents NA:
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:
5: /cgn2_6/ptodata/1/ina/PTCUS_COMB.seq:
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	74	100.0	1133	3	US-09-054-492B-2
2	74	100.0	1260	2	Sequence 2, Appli
3	74	100.0	1260	4	Sequence 5, Appli
4	74	100.0	1260	4	Sequence 338-125-5
5	69	93.2	304	4	US-09-023-655-899
6	44	59.5	2080	4	Sequence 899, App
7	44	59.5	5299	4	Sequence 28894, A
8	44	59.5	53165	4	Sequence 7092, Ap
9	43	58.1	601	4	US-09-513-999C-29894
10	43	58.1	601	4	Sequence 7092, Ap
11	43	58.1	601	4	US-09-214-808-1
12	43	58.1	601	4	Sequence 1, Appli
					Sequence 29572, A
					Sequence 124453, A
					Sequence 164761, A
					Sequence 164762, A

c 13	58.1	601	4	US-09-949-016-164763	Sequence 164763, A
14	58.1	2614	4	US-09-999-699A-3	Sequence 3, Appli
15	58.1	113042	4	US-09-949-016-12343	Sequence 12343, A
16	58.1	113042	4	US-09-949-016-15246	Sequence 15246, A
17	58.1	1136917	4	US-09-949-016-16369	Sequence 16369, A
18	56.8	601	4	US-09-949-016-187338	Sequence 187338, A
19	56.8	601	4	US-09-949-016-187339	Sequence 187339, A
20	56.8	601	4	US-09-949-016-187340	Sequence 187340, A
21	56.8	78269	4	US-09-949-016-17099	Sequence 17099, A
22	56.8	78269	4	US-09-949-016-12497	Sequence 12497, A
23	56.8	392000	4	US-10-027-983-11	Sequence 11, Appl
24	55.4	601	4	US-09-949-016-68033	Sequence 68033, A
25	55.4	601	4	US-09-949-016-147945	Sequence 147945, A
26	55.4	601	4	US-09-949-016-196181	Sequence 196181, A
27	55.4	942	4	US-09-543-681A-1078	Sequence 1078, Ap
28	55.4	1128	4	US-09-270-767-14909	Sequence 14909, A
29	55.4	1938	4	US-09-270-767-12995	Sequence 12995, A
30	55.4	2061	1	US-08-472-028A-7	Sequence 7, Appli
31	55.4	2061	2	US-08-808-931-7	Sequence 7, Appli
32	55.4	2061	3	US-08-808-323-7	Sequence 7, Appli
33	55.4	2061	3	US-09-050-603A-7	Sequence 7, Appli
34	55.4	2061	3	US-09-102-420B-7	Sequence 7, Appli
35	55.4	2061	3	US-09-071-296-7	Sequence 7, Appli
36	55.4	2061	3	US-09-196-268-7	Sequence 7, Appli
37	55.4	2061	3	US-09-015-683-7	Sequence 7, Appli
38	55.4	2061	3	US-09-191-998-7	Sequence 7, Appli
39	55.4	2061	3	US-09-497-698-7	Sequence 7, Appli
40	55.4	2061	4	US-09-730-525-7	Sequence 7, Appli
41	55.4	2276	3	US-08-946-026-11	Sequence 11, Appl
42	55.4	2983	3	US-09-058-489-86	Sequence 86, Appl
43	55.4	4134	3	US-09-162-021B-1	Sequence 1, Appli
44	55.4	4134	3	US-09-687-477-17	Sequence 17, Appl
45	55.4	4134	4	US-09-687-476-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1

US-09-054-492B-2
; Sequence 2, Application US/09054492B
; Patent No. 6218115
; GENERAL INFORMATION:
; APPLICANT: TAKESHI NAKAMURA
; TITLE OF INVENTION: HUMAN CYCLIN I AND GENES ENCODING SAME
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY, MADISON & SUTRO
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/054,492B
; FILING DATE: APRIL 3, 1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: PAUL E. WHITE, JR.
; REGISTRATION NUMBER: 32,011
; REFERENCE/DOCKET NUMBER: 7898/252159
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; TELEX: 6714627CUSH
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1133
; TYPE: nucleic acid

```

; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-054-492B-2
Alignment Scores:
Pred. No.: 2.83e-05 Length: 1133
Score: 74.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-09-736-250-5 (1-14) x US-09-054-492B-2 (1-1133)
Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 1027 GAAGATAATGCTCAGAAATGTGGTTCTGTGTGGCACT 1068

RESULT 2
US-08-969-106-5
; Sequence 5, Application US/08969106
; Patent No. 5986055
; GENERAL INFORMATION:
; APPLICANT: Yang, M.
; APPLICANT: Nandabalan, K.
; APPLICANT: Schulz, V.
; TITLE OF INVENTION: CDK2 INTERACTIONS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/969,106
; FILING DATE: 13-NOV-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/969,106
; FILING DATE: 13-NOV-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7934-057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1260 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1..1131
; OTHER INFORMATION:
US-09-736-250-5
Alignment Scores:
Pred. No.: 3.24e-05 Length: 1260
Score: 74.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-08-969-106-5
Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 1027 GAAGATAATGCTCAGAAATGTGGTTCTGTGTGGCACT 1068

RESULT 3
US-09-338-125-5
; Sequence 5, Application US/09338125
; Patent No. 6521412
; GENERAL INFORMATION:
; APPLICANT: Yang, M.
; APPLICANT: Nandabalan, K.
; APPLICANT: Schulz, V.
; TITLE OF INVENTION: CDK2 INTERACTIONS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/338,125
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/969,106
; FILING DATE: 13-NOV-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7934-057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1260 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1..1131
; OTHER INFORMATION:
US-09-338-125-5
Alignment Scores:
Pred. No.: 3.24e-05 Length: 1260
Score: 74.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-736-250-5 (1-14) x US-09-338-125-5 (1-1260)
Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 1027 GAAGATAATGCTCAGAAATGTGGTTCTGTGTGGCACT 1068

RESULT 4
US-09-023-655-899
```

Sequence 899, Application US/09023655
Patent No. 6607879
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023.655
FILING DATE: HERewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 899:
SEQUENCE CHARACTERISTICS:
LENGTH: 1260 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: g1183161
US-09-023-655-899

Alignment Scores:
Pred. No.: 3.24e-05 Length: 1260
Score: 74.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-736-250-5 (1-14) x US-09-023-655-899 (1-1260)

Qy 1 GluAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 1027 GAAGATATGCTCAGAAATGCGGTCTGTGTGGCACT 1068

RESULT 5
US-09-513-999C-29894
Sequence 29894, Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513.999C

CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 29894
LENGTH: 304
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 230
OTHER INFORMATION: m-a or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: 231
OTHER INFORMATION: n-a, g, c or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: 268
OTHER INFORMATION: w-a or t
US-09-513-999C-29894

Alignment Scores:
Pred. No.: 5.23e-05 Length: 304
Score: 69.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 93.24% Indels: 0
DB: 4 Gaps: 0

US-09-736-250-5 (1-14) x US-09-513-999C-29894 (1-304)

Qy 2 AspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 2 GATAATGCTCAGAAATGCGGTCTGTGTGGCACT 40

RESULT 6
US-09-902-540-7092
Sequence 7092, Application US/09902540
Patent No. 6833447
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 7092
LENGTH: 2080
TYPE: DNA
ORGANISM: Myxococcus xanthus
US-09-902-540-7092

Alignment Scores:
Pred. No.: 65.2 Length: 2080
Score: 44.00 Matches: 8
Percent Similarity: 75.00% Conservative: 1
Best Local Similarity: 66.67% Mismatches: 3
Query Match: 59.46% Indels: 0
DB: 4 Gaps: 0

US-09-736-250-5 (1-14) x US-09-902-540-7092 (1-2080)

Qy 2 AspAsnValSerGluAsnValGlySerValCysGly 13
Db 649 GACAACGTGGCGACAAACGTGGGTGACGTGCCGCG 684

US-09-736-250-5 (1-14) x US-09-949-016-124453 (1-601)
Qy 1 GluAspAsnValSerGluAsnValGlySerValCys 12
Db 325 GAAGATTCAATGAATGAACGTAAGTAGTTGTGC 360

RESULT 11

US-09-949-016-164761/c
; Sequence 164761, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 164761

; LENGTH: 601

; TYPE: DNA

; ORGANISM: Human

US-09-949-016-164761

Alignment Scores:

Pred. No.: 20.9 Length: 601
Score: 43.00 Matches: 7
Percent Similarity: 83.33% Conservative: 3
Best Local Similarity: 58.33% Mismatches: 2
Query Match: 58.11% Indels: 0
DB: 4 Gaps: 0

US-09-736-250-5 (1-14) x US-09-949-016-164761 (1-601)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCys 12
Db 437 CAGAGCAACTGCAGCCAGAAATCTGGGTCAGTATGC 402

RESULT 12

US-09-949-016-164762/c

; Sequence 164762, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 164762

; LENGTH: 601

; TYPE: DNA

; ORGANISM: Human

US-09-949-016-164762

Alignment Scores:

Pred. No.: 20.9 Length: 601

Score: 43.00 Matches: 7
Percent Similarity: 83.33% Conservative: 3
Best Local Similarity: 58.33% Mismatches: 2
Query Match: 58.11% Indels: 0
DB: 4 Gaps: 0

US-09-736-250-5 (1-14) x US-09-949-016-164762 (1-601)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCys 12

Db 96 CAGAGCAACTGCAGCCAGAAATCTGGGTCAGTATGC 61

RESULT 13

US-09-949-016-164763/c

; Sequence 164763, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 164763

; LENGTH: 601

; TYPE: DNA

; ORGANISM: Human

US-09-949-016-164763

Alignment Scores:

Pred. No.: 20.9 Length: 601
Score: 43.00 Matches: 7
Percent Similarity: 83.33% Conservative: 3
Best Local Similarity: 58.33% Mismatches: 2
Query Match: 58.11% Indels: 0
DB: 4 Gaps: 0

US-09-736-250-5 (1-14) x US-09-949-016-164763 (1-601)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCys 12

Db 84 CAGAGCAACTGCAGCCAGAAATCTGGGTCAGTATGC 49

RESULT 14

US-09-999-699A-3

; Sequence 3, Application US/09999699A

; Patent No. 6794139

; GENERAL INFORMATION:

; APPLICANT: SCHIEMANN, Sabine

; APPLICANT: WEIDLE, Ulrich

; TITLE OF INVENTION: BREAST CARCINOMA-ASSOCIATED GENE

; FILE REFERENCE: 20221US1

; CURRENT APPLICATION NUMBER: US/09/999,699A

; CURRENT FILING DATE: 2001-10-24

; PRIOR APPLICATION NUMBER: PCT/EP97/04785

; PRIOR FILING DATE: 1997-09-02

; PRIOR APPLICATION NUMBER: EP 96114098.5

; PRIOR FILING DATE: 1996-09-03

; PRIOR APPLICATION NUMBER: US 09/254,129

; PRIOR FILING DATE: 2002-05-12

; NUMBER OF SEQ ID NOS: 10

; SEQ ID NO 3

; LENGTH: 2614

; TYPE: DNA

; ORGANISM: Murinae gen. sp.

FEATURE:
; NAME/KEY: CDS
; LOCATION: (90)..(569)
US-09-999-699A-3

Alignment Scores:
Pred. No.: 139 Length: 2614
Score: 43.00 Matches: 9
Percent Similarity: 52.17% Conservative: 3
Best Local Similarity: 39.13% Mismatches: 1
Query Match: 58.11% Indels: 10
DB: 4 Gaps: 1

US-09-736-250-5 (1-14) x US-09-999-699A-3 (1-2614)

Qy 1 GluAepAenValSerGluAenValGlySer----- 10
Db 1377 GATGATATGCTCACAAACATAGGGTCAAAGCATATGCCACCGAGTGCTATAGTAA 1436
Qy 11 ValCysGly 13
Db 1437 GTTTGTGG 1445

RESULT 15

US-09-949-016-12343
; Sequence 12343, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12343
; LENGTH: 113042
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12343

Alignment Scores:
Pred. No.: 1.79e+04 Length: 113042
Score: 43.00 Matches: 7
Percent Similarity: 91.67% Conservative: 4
Best Local Similarity: 58.33% Mismatches: 1
Query Match: 58.11% Indels: 0
DB: 4 Gaps: 0

US-09-736-250-5 (1-14) x US-09-949-016-12343 (1-113042)

Qy 1 GluAepAenValSerGluAenValGlySerValCys 12
Db 101983 GAAGATTCATGAATGAACGTAAGTAGTTGTGC 102018

Search completed: February 11, 2005, 07:42:13
Job time : 41.2072 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model
Run on: February 11, 2005, 05:55:30 ; Search time 59.9028 Seconds
(without alignments)
1379.008 Million cell updates/sec

Title: US-09-736-250-5
Perfect score: 74
Sequence: 1 BDVSENVGVSGT 14

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5378673 seqs, 2950229984 residues

Total number of hits satisfying chosen parameters: 10757346

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
-O=/cgn2_1/USPTO_spool/US09736250/runat_07022005_154926_20490/app_query.fasta_1.718
-DB=Published Applications NA -OFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPEXT=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09736250 @CGN 1 1 582 @runat_07022005_154926_20490
-NCPU=6 -ICPU=3 -NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:
18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:
19: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:
20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:
21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:
22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	74	100.0	288	17	US-10-242-535A-57578
2	74	100.0	288	17	US-10-085-783A-57578
3	74	100.0	350	17	US-10-242-535A-20816
4	74	100.0	350	17	US-10-085-783A-20816
c 5	74	100.0	444	9	US-09-920-300A-1413
c 6	74	100.0	444	13	US-10-033-528-1413
c 7	74	100.0	444	16	US-10-099-926-1413
8	74	100.0	447	9	US-09-777-564-1252
9	74	100.0	447	14	US-10-015-219-1252
10	74	100.0	1134	12	US-09-736-250-2
11	74	100.0	1260	17	US-10-172-118-1326
12	74	100.0	1260	17	US-10-342-887-1326
13	74	100.0	1260	17	US-10-641-643-899
14	74	100.0	1889	9	US-09-867-701-10907
15	74	100.0	2145	10	US-09-814-353-21294
16	74	100.0	2755	10	US-09-814-353-21586
17	70	94.6	308	17	US-10-242-535A-41781
18	70	94.6	308	17	US-10-085-783A-41781
19	65	87.8	420	9	US-09-960-352-9810
20	49	66.2	200	17	US-10-242-535A-5568
21	49	66.2	200	17	US-10-085-783A-5568
c 22	46	62.2	293	18	US-10-723-860-2410
c 23	46	62.2	401	17	US-10-242-535A-3486
c 24	46	62.2	401	17	US-10-085-783A-3486
c 25	46	62.2	474	17	US-10-242-535A-57273
c 26	46	62.2	474	17	US-10-085-783A-57273
c 27	46	62.2	564	10	US-09-284-320-37
c 28	46	62.2	601	18	US-10-021-323-14955
c 29	46	62.2	798	18	US-10-767-795-6476
c 30	46	62.2	1110	18	US-10-842-740-40
c 31	46	62.2	1138	18	US-10-357-930-22723
c 32	46	62.2	1138	18	US-10-357-930-28570
c 33	46	62.2	1186	10	US-09-284-320-62
c 34	46	62.2	1264	14	US-10-028-072-1
c 35	46	62.2	1264	14	US-10-140-808-1
c 36	46	62.2	1264	14	US-10-121-049-1
c 37	46	62.2	1264	14	US-10-123-904-1
c 38	46	62.2	1264	14	US-10-140-470-1
c 39	46	62.2	1264	14	US-10-175-746-1
c 40	46	62.2	1264	14	US-10-176-918-1
c 41	46	62.2	1264	14	US-10-137-865-1
c 42	46	62.2	1264	14	US-10-140-474-1
c 43	46	62.2	1264	14	US-10-142-431-1
c 44	46	62.2	1264	14	US-10-143-114-1
c 45	46	62.2	1264	14	US-10-143-114-1

ALIGNMENTS

RESULT 1
US-10-242-535A-57578
; Sequence 57578, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242.535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994

; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57578
; LENGTH: 288
; TYPE: DNA
; ORGANISM: Human
US-10-242-535A-57578

Alignment Scores:
Pred. No.: 4.01e-05 Length: 288
Score: 74.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-09-736-250-5 (1-14) x US-10-242-535A-57578 (1-288)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 63 GAAGATAATGCTCAGAAATGTGGTTCTGTGTGGCACT 104

RESULT 2

US-10-085-783A-57578
; Sequence 57578, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57578
; LENGTH: 288
; TYPE: DNA
; ORGANISM: Human
US-10-085-783A-57578

Alignment Scores:
Pred. No.: 4.01e-05 Length: 288
Score: 74.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-09-736-250-5 (1-14) x US-10-085-783A-57578 (1-288)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 63 GAAGATAATGCTCAGAAATGTGGTTCTGTGTGGCACT 104

RESULT 3

US-10-242-535A-20816
; Sequence 20816, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28

; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20816
; LENGTH: 350
; TYPE: DNA
; ORGANISM: Human
US-10-242-535A-20816

Alignment Scores:
Pred. No.: 5.03e-05 Length: 350
Score: 74.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-09-736-250-5 (1-14) x US-10-242-535A-20816 (1-350)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 129 GAAGATAATGCTCAGAAATGTGGTTCTGTGTGGCACT 170

RESULT 4

US-10-085-783A-20816
; Sequence 20816, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20816
; LENGTH: 350
; TYPE: DNA
; ORGANISM: Human
US-10-085-783A-20816

Alignment Scores:
Pred. No.: 5.03e-05 Length: 350
Score: 74.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-09-736-250-5 (1-14) x US-10-085-783A-20816 (1-350)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 129 GAAGATAATGCTCAGAAATGTGGTTCTGTGTGGCACT 170

RESULT 5

US-09-920-300A-1413/c
; Sequence 1413, Application US/09920300A
; Patent No. US20020136728A1
; GENERAL INFORMATION:
; APPLICANT: King, Gordon E.

```

; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; APPLICANT: Jjang, Yugu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.547C2
; CURRENT APPLICATION NUMBER: US/10/099,926
; CURRENT FILING DATE: 2002-03-17
; NUMBER OF SEQ ID NOS: 1982
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1413
; LENGTH: 444
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-099-926-1413

Alignment Scores:
Pred. No.: 6.63e-05 Length: 444
Score: 74.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 16 Gaps: 0

US-09-736-250-5 (1-14) x US-10-099-926-1413 (1-444)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
|||||
Db 436 GAAGATAATGCTCTCAGAAATGTGGTTCTGTGTGGCACT 395
|||||

RESULT 8
US-09-777-564-1252
; Sequence 1252, Application US/09777564
; Patent No. US20020022591A1
; GENERAL INFORMATION:
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.493
; CURRENT APPLICATION NUMBER: US/09/777,564
; CURRENT FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 1730
; SOFTWARE: FastSeq for Window Version 4.0
; SEQ ID NO 1252
; LENGTH: 447
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(447)
; OTHER INFORMATION: n = A,T,C or G
US-09-777-564-1252

Alignment Scores:
Pred. No.: 6.69e-05 Length: 447
Score: 74.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-736-250-5 (1-14) x US-09-777-564-1252 (1-447)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
|||||
Db 93 GAAGATAATGCTCTCAGAAATGTGGTTCTGTGTGGCACT 134
|||||

RESULT 9
US-10-015-219-1252
; Sequence 1252, Application US/10015219
; Publication No. US20030008299A1
; GENERAL INFORMATION:

```

APPLICANT: Algate, Paul A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.493C1
CURRENT APPLICATION NUMBER: US/10/015,219
CURRENT FILING DATE: 2002-03-02
NUMBER OF SEQ ID NOS: 1739
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1252
LENGTH: 447
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: 424, 428, 437, 440
OTHER INFORMATION: n = A,T,C or G
US-10-015-219-1252

Alignment Scores:
Pred. No.: 6.69e-05 Length: 447
Score: 74.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-09-736-250-5 (1-14) x US-10-015-219-1252 (1-447)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 93 GAAGATAATGCTCAGAAATGCGGTCTCTGTGTGGCACT 134

RESULT 10

US-09-736-250-2
Sequence 2, Application US/09736250
Publication No. US20050014139A1
GENERAL INFORMATION:
APPLICANT: SUMITOMO ELECTRIC INDUSTRIES, LTD.
TITLE OF INVENTION: NAKAMURA, Takeshi
FILE REFERENCE: 050212-0278
CURRENT APPLICATION NUMBER: US/09/736,250
CURRENT FILING DATE: 2006-12-15
PRIOR APPLICATION NUMBER: 09/054,492
PRIOR FILING DATE: 1998-04-03
PRIOR APPLICATION NUMBER: PCT/JF96/02905
PRIOR FILING DATE: 1996-10-07
PRIOR APPLICATION NUMBER: 284663/1995
PRIOR FILING DATE: 1995-10-05
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.3
SEQ ID NO 2
LENGTH: 1134
TYPE: DNA
ORGANISM: Homo sapiens
US-09-736-250-2

Alignment Scores:
Pred. No.: 0.000197 Length: 1134
Score: 74.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-09-736-250-5 (1-14) x US-09-736-250-2 (1-1134)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 1027 GAAGATAATGCTCAGAAATGCGGTCTCTGTGTGGCACT 1068

RESULT 11

US-10-172-118-1326

Sequence 1326, Application US/10172118
Publication No. US20030224374A1
GENERAL INFORMATION:
APPLICANT: Dai, Hongyue
APPLICANT: He, Yudong
APPLICANT: Linsley, Peter
APPLICANT: Mao, Mao
APPLICANT: Roberts, Chris
APPLICANT: Van 't Veer, Laura
APPLICANT: Van de Vijver, Marc
APPLICANT: Bernards, Rene
TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
FILE REFERENCE: 9301-175-999
CURRENT APPLICATION NUMBER: US/10/172,118
CURRENT FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: 60/380,770
PRIOR FILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 2699
SEQ ID NO 1326
LENGTH: 1260
TYPE: DNA
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: NM_006835
DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-1326

Alignment Scores:
Pred. No.: 0.000223 Length: 1260
Score: 74.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-09-736-250-5 (1-14) x US-10-172-118-1326 (1-1260)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 1027 GAAGATAATGCTCAGAAATGCGGTCTCTGTGTGGCACT 1068

RESULT 12

US-10-342-887-1326
Sequence 1326, Application US/10342887
Publication No. US20040058340A1
GENERAL INFORMATION:
APPLICANT: Dai, Hongyue
APPLICANT: He, Yudong
APPLICANT: Linsley, Peter S.
APPLICANT: Mao, Mao
APPLICANT: Roberts, Christopher J.
APPLICANT: Van 't Veer, Laura Johanna
APPLICANT: Van de Vijver, Marc J.
APPLICANT: Bernards, Rene
TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
FILE REFERENCE: 9301-188-999
CURRENT APPLICATION NUMBER: US/10/342,887
CURRENT FILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: 60/298,918
PRIOR FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: 60/380,710
PRIOR FILING DATE: 2002-05-14
PRIOR APPLICATION NUMBER: 10/172,118
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 2699
SEQ ID NO 1326
LENGTH: 1260
TYPE: DNA
ORGANISM: Homo sapiens
US-10-342-887-1326

Alignment Scores:
Pred. No.: 0.000223 Length: 1260

Score: 74.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-09-736-250-5 (1-14) x US-10-342-887-1326 (1-1260)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
|||||
Db 1027 GAAGATAATGCTCAGAAATGTGGTCTCTGTGTGGCACT 1068
|||||

RESULT 13
US-10-641-643-899
; Sequence 899, Application US/10641643
; Publication No. US20040077003A1
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; Susan G. Stuart
; Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
; GENE EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/641,643
; FILING DATE: 14-Aug-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 899:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1260 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g1183161
; SEQUENCE DESCRIPTION: SEQ ID NO: 899 :
US-10-641-643-899

Alignment Scores:
Pred. No.: 0.000223 Length: 1260
Score: 74.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-09-736-250-5 (1-14) x US-10-641-643-899 (1-1260)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
|||||

Db 1027 GAAGATAATGCTCAGAAATGTGGTCTCTGTGTGGCACT 1068
|||||

RESULT 14
US-09-867-701-10907
; Sequence 10907, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10907
; LENGTH: 1889
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-867-701-10907

Alignment Scores:
Pred. No.: 0.000356 Length: 1889
Score: 74.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-736-250-5 (1-14) x US-09-867-701-10907 (1-1889)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
|||||
Db 1570 GAAGATAATGCTCAGAAATGTGGTCTCTGTGTGGCACT 1611
|||||

RESULT 15
US-09-814-353-21294
; Sequence 21294, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21294
; LENGTH: 2146
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-814-353-21294

Alignment Scores:
Pred. No.: 0.000413 Length: 2146

Score: 74.00 Matches: 14

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 10 Gaps: 0

US-09-736-250-5 (1-14) x US-09-814-353-21294 (1-2146)

QY 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14

Db 1213 GAAGATATATGCTCAGAAATGTGGGTTCTGTGTGGCACT 1254

Search completed: February 11, 2005, 10:20:38

Job time : 61.9028 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 11, 2005, 03:23:50 ; Search time 218.235 Seconds
(without alignments)
2441.859 Million cell updates/sec

Title: US-09-736-250-5

Perfect score: 74

Sequence: 1 EDNVSENVGVCVT 14

Scoring table:

	BLOSUM62	Xgapop 10.0	Xgapext 0.5
Ygapop 10.0			0.5
Ygapop 6.0			7.0
Delop 6.0			7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2 1/USPTO/spool/US09736250/runat_07022005 154924 20414/app query.fasta_1.718
-DB-EST_QFMT-fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09736250 -CGN 1 1 4385 @runat_07022005 154924 20414 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*

1:	gb_est1.*
2:	gb_est2.*
3:	gb_hcc.*
4:	gb_est3.*
5:	gb_est4.*
6:	gb_est5.*
7:	gb_est6.*
8:	gb_gsl1.*
9:	gb_gsl2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	74	100.0	136	7	Z20123
2	74	100.0	139	1	AA678060
3	74	100.0	139	1	AA094874
4	74	100.0	197	1	AA659220
5	74	100.0	234	1	AA058781
6	74	100.0	246	4	BG180306
7	74	100.0	251	5	BQ327548
8	74	100.0	251	5	BQ327560
9	74	100.0	265	7	R85184

C 10	74	100.0	269	1	AA680208
C 11	74	100.0	275	1	AA011113
C 12	74	100.0	278	1	AA778982
C 13	74	100.0	296	7	F32546
C 14	74	100.0	302	4	BI493342
C 15	74	100.0	302	7	N84129
C 16	74	100.0	321	7	R87368
C 17	74	100.0	323	2	BE245492
C 18	74	100.0	325	1	AI383113
C 19	74	100.0	328	2	BE675114
C 20	74	100.0	331	2	BF109323
C 21	74	100.0	340	2	AW993907
C 22	74	100.0	340	4	BI491010
C 23	74	100.0	340	7	R83731
C 24	74	100.0	341	1	AA055821
C 25	74	100.0	341	5	AW019986
C 26	74	100.0	341	5	BM894061
C 27	74	100.0	343	2	BF901867
C 28	74	100.0	344	1	AI735109
C 29	74	100.0	346	7	H80782
C 30	74	100.0	347	1	AA248313
C 31	74	100.0	347	6	CB135564
C 32	74	100.0	348	1	AA018692
C 33	74	100.0	348	4	BG943235
C 34	74	100.0	348	5	BM894332
C 35	74	100.0	349	1	AI857246
C 36	74	100.0	350	1	AA730298
C 37	74	100.0	350	7	R88164
C 38	74	100.0	351	2	AW225340
C 39	74	100.0	352	2	BE539946
C 40	74	100.0	352	7	H38301
C 41	74	100.0	353	1	AA558174
C 42	74	100.0	357	7	H84151
C 43	74	100.0	357	7	N45919
C 44	74	100.0	358	2	AW408405
C 45	74	100.0	358	6	CD678566

ALIGNMENTS

RESULT 1

LOCUS	Z20123	136 bp	mrna	linear	EST 07-FEB-1995
DEFINITION	HSAAABALIE P, Human foetal Brain Whole tissue Homo sapiens CDNA,				
ACCESSION	Z20123				
VERSION	Z20123.1	GI:26868			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	1 (bases 1 to 136)				
TITLE	MRC Human Genome Mapping Project Resource Centre.				
JOURNAL	The UK-HGMP CDNA program				
COMMENT	Unpublished (1993) Contact: MRC Human Genome Mapping Project Resource Centre Clinical Research Centre Watford Road, Harrow, Middlesex HA1 3UJ, U.K. Email: biolhelp@hgm.mrc.ac.uk single read.				
FEATURES	Location/Qualifiers				
source	1..136				
	/organism="Homo sapiens"				
	/mol_type="mrna"				
	/db_xref="taxon:9606"				
	/clone_lib="P, Human foetal Brain Whole tissue"				
	/notes="vector: Bluescript; clone_library=P, Human foetal Brain Whole tissue; cloning vector is Bluescript."				

ORIGIN

Alignment Scores: 0.000573 Length: 136
Pred. No.: 136

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 197)
 NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaps-remail.nih.gov
 Tissue Procurement: W. Douglas Figg, Ph.D., Paul H. Duray, M.D.,
 Rodrigo F. Chuacui, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: David B. Krizman, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone Distribution: NCI-CCAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
 Insert Length: 288 Std Error: 0.00
 Seq primer: -40m13 fwd. ET from Amersham
 High quality sequence stop: 161.
 Location/Qualifiers
 FEATURES
 source
 1..197
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clones="IMAGE:1205972"
 /sex="male"
 /tissue_type="metastatic prostate bone lesion"
 /lab_host="DH10B"
 /clone_lib="NCI-CCAP Pr12"
 /notes="vector: pAMP10; mRNA made from metastatic prostate
 lesion of the bone, cDNA made by oligo-dT priming.
 Non-directionally cloned. Size-selected on agarose gel,
 average insert size 600 bp. Library made by D. Krizman,
 NIH."
 ORIGIN
 Alignment Scores: Length: 197
 Pred. No.: 0.00087 Matches: 14
 Score: 74.00
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 1 Gaps: 0
 US-09-736-250-5 (1-14) x AA659220 (1-197)
 Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
 Db 93 GAAGATAATGCTCAGAAATGTGGTCTCTGTGTGGCACT 134
 RESULT 5
 AA058781/c
 LOCUS
 DEFINITION
 zf58f03.r1 Soares retina N2b4HR Homo sapiens cDNA clone
 IMAGE:381149 5' similar to TR:G1183162 G1183162 CYCLIN I. 1, mRNA
 sequence.
 ACCESSION
 AA058781
 AA058781.1 GI:1551591
 VERSION
 EST.
 KEYWORDS
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 234)
 Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
 Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W.,
 Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N.,
 Mardis, E., Moore, B., Morris, M., Parsons, J., Pange, C., Rifkin, L.,
 Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J.,
 Travaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
 and Marra, M.
 Generation and analysis of 280,000 human expressed sequence tags

JOURNAL
 MEDLINE
 PUBMED
 COMMENT
 Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Possible reversed clone: similarity on wrong strand
 Insert Length: 1691 Std Error: 0.00
 Seq primer: -28M13 rev2 from Amersham
 High quality sequence stop: 191.
 Location/Qualifiers
 FEATURES
 source
 1..234
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="GDB:1289406"
 /db_xref="taxon:9606"
 /clone="IMAGE:381149"
 /sex="male"
 /tissue_type="retina"
 /dev_stage="55 year old"
 /lab_host="DH10B (ampicillin resistant)"
 /clone_lib="Soares retina N2b4HR"
 /notes="Organ: eye; Vector: pT7T3D (Pharmacia) with a
 modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
 strand cDNA was primed with a Not I - oligo(dT) primer [5'
 TGTACCAATCTGAAGTGGAGCGCGCCCTTTTCTTTTCTTTT 3'],
 double-stranded cDNA was size selected, ligated to Eco RI
 adapters (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of a modified pT7T3 vector
 (Pharmacia). The retinas were obtained from a 55 year old
 Caucasian and total cellular poly(A)+ RNA was extracted 6
 hrs after their removal. The retina RNA was kindly
 provided by Roderick R. McInnes M.D. Ph.D. from the
 University of Toronto. Library constructed by Bento
 Soares and M.Fatima Bonaldo."
 ORIGIN
 Alignment Scores: Length: 234
 Pred. No.: 0.00106 Matches: 14
 Score: 74.00
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 1 Gaps: 0
 US-09-736-250-5 (1-14) x AA058781 (1-234)
 Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
 Db 189 GAAGATAATGCTCAGAAATGTGGTCTCTGTGTGGCACT 148
 RESULT 6
 BG180306
 LOCUS
 DEFINITION
 602331150f1 NIH_MGC_91 Homo sapiens cDNA clone IMAGE:4432452 5',
 mRNA sequence.
 ACCESSION
 BG180306
 BG180306.1 GI:12687009
 VERSION
 EST.
 KEYWORDS
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 246)
 NIH-MGC <http://mgs.nci.nih.gov/>.
 AUTHORS
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 COMMENT
 Contact: Robert Strausberg, Ph.D.

Email: cgapbs@mail.nih.gov
 Tissue Procurement: DCTD/DRP
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 cDNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LAM10189 row: c column: 13
 High quality sequence stop: 243.
 Location/Qualifiers
 1. 246
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4432452"
 /tissue_type="adenocarcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_91"
 /note="Organ: prostate; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.4 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."

FEATURES

source

ORIGIN

Alignment Scores:
 Pred. No.: 0.00112 Length: 246
 Score: 74.00 Matches: 14
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 4 Gaps: 0

US-09-736-250-5 (1-14) x BG180306 (1-246)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
 |||||
 Db 44 GAAGATAATGCTCAGAAATGGGTTCTGTGTGGCACT 85

RESULT 7

BQ327548

LOCUS CM0-RT0017-211100-702-e07 RT0017 Homo sapiens linear EST 17-MAY-2002

DEFINITION

BQ327548

ACCESSION

VERSION

BQ327548.1 GI:20944770

EST.

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

REFERENCE

AUTHORS

1 (bases 1 to 251)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,

Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,

Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,

Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,

O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and

Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20202663

PUBLISHED

10737800

COMMENT

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(<http://www.ludwig.org.br/scripts/gethtml2.pl?t1=CM0&t2=CM0-RT0017-211100-702-e07&t3=2000-11-21&t4=1>)
 Seq primer: puc 18 forward
 High quality sequence start: 7
 High quality sequence stop: 25.
 Location/Qualifiers
 1. 251
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="RT0017"
 /note="Organ: kidney tumor; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

FEATURES

source

ORIGIN

Alignment Scores:
 Pred. No.: 0.00114 Length: 251
 Score: 74.00 Matches: 14
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 5 Gaps: 0

US-09-736-250-5 (1-14) x BQ327548 (1-251)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
 |||||
 Db 163 GAAGATAATGCTCAGAAATGGGTTCTGTGTGGCACT 204

RESULT 8

BQ327560

LOCUS

CM0-RT0017-221100-705-e07 RT0017 Homo sapiens linear EST 17-MAY-2002

DEFINITION

BQ327560

ACCESSION

VERSION

BQ327560.1 GI:20944806

EST.

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

REFERENCE

AUTHORS

1 (bases 1 to 251)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,

Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,

Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,

Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,

O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and

Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20202663

PUBLISHED

10737800

COMMENT

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(<http://www.ludwig.org.br/scripts/gethtml2.pl?t1=CM0&t2=CM0-RT0017-211100-705-e07&t3=2000-11-22&t4=1>)

Seq primer: puc 18 forward

High quality sequence start: 7

High quality sequence stop: 25.

FEATURES
source

Location/Qualifiers
1..251
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="RT0017"
/note="Organ: kidney_tumor; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN

Alignment Scores:
Pred. No.: 0.00114 Length: 251
Score: 74.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0

US-09-736-250-5 (1-14) x BQ327560 (1-251)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
|||||
Db 163 GAAGATAATGCTCAGAAATGCGTCTCTGTGTGGCACT 204
|||||

RESULT 9
R85184/c

LOCUS R85184 265 bp mRNA linear EST 14-AUG-1995
DEFINITION yo43f02.x1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone
IMAGE:180699 5', mRNA sequence.

ACCESSION R85184
VERSION R85184.1 GI:943590

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 265)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.

TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilton RK

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

Insert Size: 1058

High quality sequence stops: 220

Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 1058 Std Error: 0.00

Seq primer: M13RP1

High quality sequence stop: 220.

FEATURES
source

Location/Qualifiers
1..265
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3827349"
/db_xref="taxon:9606"
/clone="IMAGE:180699"
/sex="Male"
/dev_stage="55-year old"

/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares adult brain N2b4HB55Y"

/note="Organ: brain; Vector: pT73D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5',
TGTTACCAATCTGAAGTGGAGCGCGCGCTTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 53. Library constructed by Bento
Soares and M. Fatima Bonaldo. The adult brain RNA was
provided by Dr. Donald H. Gilden. Tissue was acquired
17-18 hours after death which occurred in consequence of a
ruptured aortic aneurysm. RNA was prepared from a pool of
tissues representing the following areas of the brain:
frontal, parietal, temporal and occipital cortex from the
left and right hemispheres, subcortical white matter,
basal ganglia, thalamus, cerebellum, midbrain, pons and
medulla."

ORIGIN

Alignment Scores:
Pred. No.: 0.00121 Length: 265
Score: 74.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0

US-09-736-250-5 (1-14) x R85184 (1-265)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
|||||
Db 234 GAAGATAATGCTCAGAAATGCGTCTCTGTGTGGCACT 193
|||||

RESULT 10

AA680208/c

LOCUS

DEFINITION

ac82d11.s1 Stratagene lung (#937210) Homo sapiens cDNA clone

IMAGE:869109 3' similar to TR:G1183162 G1183162 CYCLIN I. ; mRNA

sequence.

ACCESSION AA680208

VERSION AA680208.1 GI:2656176

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 269)

Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,

Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M.,

Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F.,

Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.

WashU-NCI human EST Project

Unpublished (1997)

TITLE

JOURNAL

COMMENT

Contact: Wilton RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Possible reversed clone: similarity on wrong strand

Seq primer: -40ml3 fwd. ET from Amersham

High quality sequence stop: 215.

Location/Qualifiers

1..269

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:869109"

```

/sex="male"
/dev_stage="72 years"
/lab_host="SOLR cells (kanamycin resistant)"
/clone_lib="Stratagene lung (#937210)"
/notes="Organ: lung; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo dt. normal lung. Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCAGCAG 3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'"

ORIGIN
Alignment Scores:
Pred. No.: 0.00123 Length: 269
Score: 74.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-09-736-250-5 (1-14) x AA680208 (1-269)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 116 GAAGATAATGCTCAGAAATGCGGTCTCTGTGTGGCACT 75

RESULT 11
LOCUS AA011113 275 bp mRNA linear EST 29-JUL-1996
DEFINITION ze34d03.r1 Soares retina N2b4HR Homo sapiens cDNA clone
IMAGE:360869 5', mRNA sequence.
ACCESSION AA011113.1 GI:1472160
VERSION AA011113.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 275)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Ellisson,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Travaskis,E., Waterston,R., Williamson,A., Woldmann,P. and
Wilson,R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: mob.REG+ET
High quality sequence stop: 165.
Location/Qualifiers
1..275
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1277414"
/db_xref="taxon:9606"
/clone="IMAGE:360869"
/sex="male"
/tissue_type="retina"
/dev_stage="55 year old"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares retina N2b4HR"
/notes="Organ: eye; Vector: pT73D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dt) primer (5'
TGTTACCATCTGAGTGGAGCGCGCGCTTTTTTTTTTTT 3'),
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into

```

```

the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). The retinas were obtained from a 55 year old
Caucasian and total cellular poly(A)+ RNA was extracted 6
hrs after their removal. The retina RNA was kindly
provided by Roderick R. McInnes M.D. Ph.D. from the
University of Toronto. Library constructed by Bento
Soares and M.Fatima Bonaldo. "

ORIGIN
Alignment Scores:
Pred. No.: 0.00127 Length: 275
Score: 74.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-09-736-250-5 (1-14) x AA011113 (1-275)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 234 GAAGATAATGCTCAGAAATGCGGTCTCTGTGTGGCACT 193

RESULT 12
LOCUS AA778982/c
DEFINITION AA778982 278 bp mRNA linear EST 05-FEB-1998
IMAGE:858661 3', similar to TR:Q14094 Q14094 CYCLIN I.1, mRNA
sequence.
ACCESSION AA778982.1 GI:2838313
VERSION AA778982.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 278)
AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-NCI human EST Project
Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 177.
Location/Qualifiers
1..278
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:858661"
/dev_stage="hnt neurons"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="Stratagene hnt neuron (#937233)"
/notes="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; Cloned unidirectionally. Primer: Oligo dt.
Differentiated, post mitotic hnt neurons. Average insert
size: 1.5 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5'
GAATTCGGCAGCAG 3' -3' adaptor sequence: 5'
CTCGAGTTTTTTTTTTTTTTT 3'"

ORIGIN
Alignment Scores:
Pred. No.: 0.00128 Length: 278

```

Score: 74.00 Matches: 14
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 1 Gaps: 0

US-09-736-250-5 (1-14) x AA778982 (1-278)

Qy 1 GluApAenValSerGluAenValGlySerValCysGlyThr 14
 |||||
 Db 188 GAAGATAATGCTCAGAAATGTGGTCTGTGTGGCACT 147

RESULT 13

F32546 HSPD25369 HM3 Homo sapiens cDNA clone s3000040A06, mRNA sequence.
 DEFINITION
 F32546
 VERSION F32546.1 GI:4818172
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 296)

AUTHORS Lanfranchi, G., Muraro, T., Caldara, F., Pacchioni, B., Pallavicini, A.,
 Pandolfo, D., Toppo, S., Trevisan, S., Scarso, S. and Valle, G.

TITLE Identification of 4370 expressed sequence tags from a
 3'-end-specific cDNA library of human skeletal muscle by DNA
 sequencing and filter hybridization

JOURNAL Genome Res. 6 (1), 35-42 (1996)
 MEDLINE 96276048
 PUBMED 8681137

COMMENT Contact: Valle G.
 CRIBI Biotechnology Centre
 University of Padua
 Via Trieste 75, 35121 Padua, Italy

ABI Chromatograms and other information are available on WWW at
 http://grup.bio.unipd.it.
 Location/Qualifiers
 1..296

FEATURES
 source
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="s3000040A06"
 /sex="female"
 /tissue_type="pectoral muscle (after mastectomy)"
 /clone_lib="HM3"
 /note="Vector: pcDNAII (Invitrogen); Site 1: BstXI;
 Site 2: NotI; The library was constructed by G.
 Lanfranchi. This library is not subtracted nor normalized.
 The first strand cDNA was primed with a biotinylated
 oligo-dT-NotI primer
 (5'-biotin-AACCGCTCGAGCGCGCTTTTCTTTTCTTTT-3'). The
 ds cDNA was sonicated and size-selected in the range
 350-550 bp. The 3' specific fragments were selected by
 streptavidin coated magnetic beads, ligated to
 non-palindromic BstXI adapters, NotI digested and
 directionally cloned into BstXI-NotI cut pcDNAII vector."

ORIGIN
 Alignment Scores:
 Pred. No.: 0.00137 Length: 296
 Score: 74.00 Matches: 14
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 7 Gaps: 0

US-09-736-250-5 (1-14) x F32546 (1-296)

Qy 1 GluApAenValSerGluAenValGlySerValCysGlyThr 14
 |||||
 Db 82 GAAGATAATGCTCAGAAATGTGGTCTGTGTGGCACT 123

RESULT 14

BI493342/c
 LOCUS
 DEFINITION

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

REFERENCE
 AUTHORS
 TITLE

JOURNAL
 MEDLINE
 PUBMED

COMMENT

CONTACT: Morton, C. C.
 Departments of Pathology and Obstetrics, Gynecology and
 Reproductive Biology
 Brigham and Women's Hospital
 75 Francis Street, Harvard Medical School, Boston, MA 02115, USA
 Tel: 617 732 7980
 Fax: 617 738 6996
 Email: cmorton@rics.bwh.harvard.edu
 DNA sequencing and analyses were performed by National Institutes
 of Health Intramural Sequencing Center (NISC; see
 http://www.nisc.nih.gov).

This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Plate: LIAM6328 row: B column: 12
 Seq primer: T7 primer.

FEATURES
 source
 Location/Qualifiers
 1..302

FEATURES
 source
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2540459"
 /tissue_type="cochlea"
 /dev_stage="16-22 week fetus"
 /lab_host="SOLR cells (kanamycin resistant)"
 /clone_lib="Morton Fetal Cochlea"
 /note="Organ: ear; Vector: pBluescript SK-; Site 1: EcoRI;
 Site 2: XhoI; Reference: Genomics 23, 42-50 (1994) Cloned
 unidirectionally. Primer: Oligo dt. Fetal cochlea, normal.
 37% of inserts <0.5 kb, 56% 0.5-1.0 kb, 7% >1 kb. Uni-ZAP
 XR Vector. Library constructed by N. Robertson, C. Morton.
 -5' adaptor sequence: 5' GAATTGGCAGCG 3' -3' adaptor
 sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'

ORIGIN
 Alignment Scores:
 Pred. No.: 0.00141 Length: 302
 Score: 74.00 Matches: 14
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 4 Gaps: 0

US-09-736-250-5 (1-14) x BI493342 (1-302)

Qy 1 GluApAenValSerGluAenValGlySerValCysGlyThr 14
 |||||
 Db 259 GAAGATAATGCTCAGAAATGTGGTCTGTGTGGCACT 218

RESULT 15
 LOCUS
 DEFINITION

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

REFERENCE
 AUTHORS
 TITLE

JOURNAL
 MEDLINE
 PUBMED

COMMENT

CONTACT: Morton, C. C.
 Departments of Pathology and Obstetrics, Gynecology and
 Reproductive Biology
 Brigham and Women's Hospital
 75 Francis Street, Harvard Medical School, Boston, MA 02115, USA
 Tel: 617 732 7980
 Fax: 617 738 6996
 Email: cmorton@rics.bwh.harvard.edu
 DNA sequencing and analyses were performed by National Institutes
 of Health Intramural Sequencing Center (NISC; see
 http://www.nisc.nih.gov).

This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Plate: LIAM6328 row: B column: 12
 Seq primer: T7 primer.

FEATURES
 source
 Location/Qualifiers
 1..302

FEATURES
 source
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2540459"
 /tissue_type="cochlea"
 /dev_stage="16-22 week fetus"
 /lab_host="SOLR cells (kanamycin resistant)"
 /clone_lib="Morton Fetal Cochlea"
 /note="Organ: ear; Vector: pBluescript SK-; Site 1: EcoRI;
 Site 2: XhoI; Reference: Genomics 23, 42-50 (1994) Cloned
 unidirectionally. Primer: Oligo dt. Fetal cochlea, normal.
 37% of inserts <0.5 kb, 56% 0.5-1.0 kb, 7% >1 kb. Uni-ZAP
 XR Vector. Library constructed by N. Robertson, C. Morton.
 -5' adaptor sequence: 5' GAATTGGCAGCG 3' -3' adaptor
 sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'

ORIGIN
 Alignment Scores:
 Pred. No.: 0.00141 Length: 302
 Score: 74.00 Matches: 14
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 4 Gaps: 0

US-09-736-250-5 (1-14) x BI493342 (1-302)

Qy 1 GluApAenValSerGluAenValGlySerValCysGlyThr 14
 |||||
 Db 259 GAAGATAATGCTCAGAAATGTGGTCTGTGTGGCACT 218

RESULT 15
 LOCUS
 DEFINITION

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

REFERENCE
 AUTHORS
 TITLE

JOURNAL
 MEDLINE
 PUBMED

COMMENT

CONTACT: Morton, C. C.
 Departments of Pathology and Obstetrics, Gynecology and
 Reproductive Biology
 Brigham and Women's Hospital
 75 Francis Street, Harvard Medical School, Boston, MA 02115, USA
 Tel: 617 732 7980
 Fax: 617 738 6996
 Email: cmorton@rics.bwh.harvard.edu
 DNA sequencing and analyses were performed by National Institutes
 of Health Intramural Sequencing Center (NISC; see
 http://www.nisc.nih.gov).

This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Plate: LIAM6328 row: B column: 12
 Seq primer: T7 primer.

FEATURES
 source
 Location/Qualifiers
 1..302

FEATURES
 source
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2540459"
 /tissue_type="cochlea"
 /dev_stage="16-22 week fetus"
 /lab_host="SOLR cells (kanamycin resistant)"
 /clone_lib="Morton Fetal Cochlea"
 /note="Organ: ear; Vector: pBluescript SK-; Site 1: EcoRI;
 Site 2: XhoI; Reference: Genomics 23, 42-50 (1994) Cloned
 unidirectionally. Primer: Oligo dt. Fetal cochlea, normal.
 37% of inserts <0.5 kb, 56% 0.5-1.0 kb, 7% >1 kb. Uni-ZAP
 XR Vector. Library constructed by N. Robertson, C. Morton.
 -5' adaptor sequence: 5' GAATTGGCAGCG 3' -3' adaptor
 sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'

ORIGIN
 Alignment Scores:
 Pred. No.: 0.00141 Length: 302
 Score: 74.00 Matches: 14
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 4 Gaps: 0

US-09-736-250-5 (1-14) x BI493342 (1-302)

Qy 1 GluApAenValSerGluAenValGlySerValCysGlyThr 14
 |||||
 Db 259 GAAGATAATGCTCAGAAATGTGGTCTGTGTGGCACT 218

RESULT 15
 LOCUS
 DEFINITION

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

REFERENCE
 AUTHORS
 TITLE

JOURNAL
 MEDLINE
 PUBMED

COMMENT

CONTACT: Morton, C. C.
 Departments of Pathology and Obstetrics, Gynecology and
 Reproductive Biology
 Brigham and Women's Hospital
 75 Francis Street, Harvard Medical School, Boston, MA 02115, USA
 Tel: 617 732 7980
 Fax: 617 738 6996
 Email: cmorton@rics.bwh.harvard.edu
 DNA sequencing and analyses were performed by National Institutes
 of Health Intramural Sequencing Center (NISC; see
 http://www.nisc.nih.gov).

This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Plate: LIAM6328 row: B column: 12
 Seq primer: T7 primer.

FEATURES
 source
 Location/Qualifiers
 1..302

FEATURES
 source
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2540459"
 /tissue_type="cochlea"
 /dev_stage="16-22 week fetus"
 /lab_host="SOLR cells (kanamycin resistant)"
 /clone_lib="Morton Fetal Cochlea"
 /note="Organ: ear; Vector: pBluescript SK-; Site 1: EcoRI;
 Site 2: XhoI; Reference: Genomics 23, 42-50 (1994) Cloned
 unidirectionally. Primer: Oligo dt. Fetal cochlea, normal.
 37% of inserts <0.5 kb, 56% 0.5-1.0 kb, 7% >1 kb. Uni-ZAP
 XR Vector. Library constructed by N. Robertson, C. Morton.
 -5' adaptor sequence: 5' GAATTGGCAGCG 3' -3' adaptor
 sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'

ORIGIN
 Alignment Scores:
 Pred. No.: 0.00141 Length: 302
 Score: 74.00 Matches: 14
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 4 Gaps: 0

US-09-736-250-5 (1-14) x BI493342 (1-302)

Qy 1 GluApAenValSerGluAenValGlySerValCysGlyThr 14
 |||||
 Db 259 GAAGATAATGCTCAGAAATGTGGTCTGTGTGGCACT 218

RESULT 15
 LOCUS
 DEFINITION

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

REFERENCE
 AUTHORS
 TITLE

JOURNAL
 MEDLINE
 PUBMED

COMMENT

CONTACT: Morton, C. C.
 Departments of Pathology and Obstetrics, Gynecology and
 Reproductive Biology
 Brigham and Women's Hospital
 75 Francis Street, Harvard Medical School, Boston, MA 02115, USA
 Tel: 617 732 7980
 Fax: 617 738 6996
 Email: cmorton@rics.bwh.harvard.edu
 DNA sequencing and analyses were performed by National Institutes
 of Health Intramural Sequencing Center (NISC; see
 http://www.nisc.nih.gov).

This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Plate: LIAM6328 row: B column: 12
 Seq primer: T7 primer.

FEATURES
 source
 Location/Qualifiers
 1..302

FEATURES
 source
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2540459"
 /tissue_type="cochlea"
 /dev_stage="16-22 week fetus"
 /lab_host="SOLR cells (kanamycin resistant)"
 /clone_lib="Morton Fetal Cochlea"
 /note="Organ: ear; Vector: pBluescript SK-; Site 1: EcoRI;
 Site 2: XhoI; Reference: Genomics 23, 42-50 (1994) Cloned
 unidirectionally. Primer: Oligo dt. Fetal cochlea, normal.
 37% of inserts <0.5 kb, 56% 0.5-1.0 kb, 7% >1 kb. Uni-ZAP
 XR Vector. Library constructed by N. Robertson, C. Morton.
 -5' adaptor sequence: 5' GAATTGGCAGCG 3' -3' adaptor
 sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'

ORIGIN
 Alignment Scores:
 Pred. No.: 0.00141 Length: 302
 Score: 74.00 Matches: 14
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 4 Gaps: 0

US-09-736-250-5 (1-14) x BI493342 (1-302)

Qy 1 GluApAenValSerGluAenValGlySerValCysGlyThr 14
 |||||
 Db 259 GAAGATAATGCTCAGAAATGTGGTCTGTGTGGCACT 218

RESULT 15
 LOCUS
 DEFINITION

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

REFERENCE
 AUTHORS
 TITLE

JOURNAL
 MEDLINE
 PUBMED

COMMENT

CONTACT: Morton, C. C.
 Departments of Pathology and Obstetrics, Gynecology and
 Reproductive Biology
 Brigham and Women's Hospital
 75 Francis Street, Harvard Medical School, Boston, MA 02115, USA
 Tel: 617 732 7980
 Fax: 617 738 6996
 Email: cmorton@rics.bwh.harvard.edu
 DNA sequencing and analyses were performed by National Institutes
 of Health Intramural Sequencing Center (NISC; see
 http://www.nisc.nih.gov).

This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Plate: LIAM6328 row: B column: 12
 Seq primer: T7 primer.

FEATURES
 source
 Location/Qualifiers
 1..302

FEATURES
 source
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2540459"
 /tissue_type="cochlea"
 /dev_stage="16-22 week fetus"
 /lab_host="SOLR cells (kanamycin resistant)"
 /clone_lib="Morton Fetal Cochlea"
 /note="Organ: ear; Vector: pBluescript SK-; Site 1: EcoRI;
 Site 2: XhoI; Reference: Genomics 23, 42-50 (1994) Cloned
 unidirectionally. Primer: Oligo dt. Fetal cochlea, normal.
 37% of inserts <0.5 kb, 56% 0.5-1.0 kb, 7% >1 kb. Uni-ZAP
 XR Vector. Library constructed by N. Robertson, C. Morton.
 -5' adaptor sequence: 5' GAATTGGCAGCG 3' -3' adaptor
 sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'

ORIGIN
 Alignment Scores:
 Pred. No.: 0.00141 Length: 302
 Score: 74.00 Matches: 14
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 4 Gaps: 0

US-09-736-250-5 (1-14) x BI493342 (1-302)

Qy 1 GluApAenValSerGluAenValGlySerValCysGlyThr 14
 |||||
 Db 259 GAAGATAATGCTCAGAAATGTGGTCTGTGTGGCACT 218

RESULT 15
 LOCUS
 DEFINITION

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

REFERENCE
 AUTHORS
 TITLE

JOURNAL
 MEDLINE
 PUBMED

COMMENT

CONTACT: Morton, C. C.
 Departments of Pathology and Obstetrics, Gynecology and
 Reproductive Biology
 Brigham and Women's Hospital
 75 Francis Street, Harvard Medical School, Boston, MA 02115, USA
 Tel: 617 732 7980
 Fax: 617 738 6996
 Email: cmorton@rics.bwh.harvard.edu
 DNA sequencing and analyses were performed by National Institutes
 of Health Intramural Sequencing Center (NISC; see
 http://www.nisc.nih.gov).

This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Plate: LIAM6328 row: B column: 12
 Seq primer: T7 primer.

FEATURES
 source
 Location/Qualifiers
 1..302

FEATURES
 source
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2540459"
 /tissue_type="cochlea"
 /dev_stage="16-22 week fetus"
 /lab_host="SOLR cells (kanamycin resistant)"
 /clone_lib="Morton Fetal Cochlea"
 /note="Organ: ear; Vector: pBluescript SK-; Site 1: EcoRI;
 Site 2: XhoI; Reference: Genomics 23, 42-50 (1994) Cloned
 unidirectionally. Primer: Oligo dt. Fetal cochlea, normal.
 37% of inserts <0.5 kb, 56% 0.5-1.0 kb, 7% >1 kb. Uni-ZAP
 XR Vector. Library constructed by N. Robertson, C. Morton.
 -5' adaptor sequence: 5' GAATTGGCAGCG 3' -3' adaptor
 sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'

ORIGIN
 Alignment Scores:
 Pred. No.: 0.00141 Length: 302
 Score: 74.00 Matches: 14
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 4 Gaps: 0

US-09-736-250-5 (1-14) x BI493342 (1-302)

Qy 1 GluApAenValSerGluAenValGlySerValCysGlyThr 14
 |||||
 Db 259 GAAGATAATGCTCAGAAATGTGGTCTGTGTGGCACT 218

RESULT 15
 LOCUS
 DEFINITION

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

REFERENCE
 AUTHORS
 TITLE

JOURNAL
 MEDLINE
 PUBMED

COMMENT

CONTACT: Morton, C. C.
 Departments of Pathology and Obstetrics, Gynecology and
 Reproductive Biology
 Brigham and Women's Hospital
 75 Francis Street, Harvard Medical School, Boston, MA 02115, USA
 Tel: 617 732 7980
 Fax: 617 738 6996
 Email: cmorton@rics.bwh.harvard.edu
 DNA sequencing and analyses were performed by National Institutes
 of Health Intramural Sequencing Center (NISC; see
 http://www.nisc.nih.gov).

This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Plate: LIAM6328 row: B column: 12
 Seq primer: T7 primer.

FEATURES
 source
 Location/Qualifiers
 1..302

FEATURES
 source
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2540459"
 /tissue_type="cochlea"
 /dev_stage="16-22 week fetus"
 /lab_host="SOLR cells (kanamycin resistant)"
 /clone_lib="Morton Fetal Cochlea"
 /note="Organ: ear; Vector: pBluescript SK-; Site 1: EcoRI;
 Site 2: XhoI; Reference: Genomics 23, 42-50 (1994) Cloned
 unidirectionally. Primer: Oligo dt. Fetal cochlea, normal.
 37% of inserts <0.5 kb, 56% 0.5-1.0 kb, 7% >1 kb. Uni-ZAP
 XR Vector. Library constructed by N. Robertson, C. Morton.
 -5' adaptor sequence: 5' GAATTGGCAGCG 3' -3' adaptor
 sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'

ORIGIN
 Alignment Scores:
 Pred. No.: 0.00141 Length: 302
 Score: 74.00 Matches: 14
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 4 Gaps: 0

US-09-736-250-5 (1-14) x BI493342 (1-302)

Qy 1 GluApAenValSerGluAenValGlySerValCysGlyThr 14
 |||||
 Db 259 GAAGATAATGCTCAGAAATGTGGTCTGTGTGGCACT 218

RESULT

clone KK6088 5' similar to EST (VP97B03.S1), mRNA sequence.
 N84129
 VERSION N84129.1 GI:1259754
 EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 302)
 AUTHORS Liew, C.C.
 TITLE cDNAs from fetal heart (1996)
 JOURNAL Unpublished (1996)
 COMMENT Contact: Liew CC
 Brigham and Women's Hospital
 Harvard Medical School
 75 Francis St. Boston, MA 02115, USA
 Tel: 6177328915
 Fax: 6179750995
 Email: cliew@rics.bwh.harvard.edu
 Seq primer: GAAATTAACCTCACTAAAGG.

FEATURES
 source
 1..302
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="KK6088"
 /lab_host="E. coli XL1-Blue"
 /clone_lib="Human fetal heart, Lambda ZAP Express"
 /note="Vector: Lambda ZAP Express; Site 1: EcoRI; Site 2:
 XhoI; mRNA was purified from human fetal hearts (8-10
 weeks). cDNA was synthesized using a XhoI-Oligo dt
 adaptor-primer. EcoRI adaptors were ligated, followed by
 digestion with XhoI, for directional cloning into
 predigested lambda ZAP Express."

ORIGIN

Alignment Scores:
 Pred. No.: 0.00141 Length: 302
 Score: 74.00 Matches: 14
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 7 Gaps: 0
 US-09-736-250-5 (1-14) x N84129 (1-302)
 Oy 1 GluAspAsnValSerGluAsnValClySerValCysGlyThr 14
 Db 50 GAGGATAATGTCAGAAAATGGGGTCTGTGTGGCACT 91

Search completed: February 11, 2005, 07:36:35
 Job time : 225.235 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 11, 2005, 03:05:54 ; Search time 3.93862 Seconds
(without alignments)
1374.757 Million cell updates/sec

Title: US-09-736-250-5

Perfect score: 14

Sequence: 1 EDNVSENVGVCVT 14

Scoring table:
OLIGO
Gap 60.0 , Gapext 60.0

Searched: 2105692 seqs, 386760381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : A Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14	100.0	14	2	AAW21966 Human cyc
2	14	100.0	300	8	ADN01131 Human cel
3	14	100.0	334	7	AAE37938 Human CGD
4	14	100.0	377	2	AAW21965 Human cyc
5	14	100.0	377	3	AAW52185 Human cyc
6	14	100.0	377	6	ABR39934 Human pro
7	14	100.0	377	8	ADP12615 Protein e
8	14	100.0	377	8	ABM80569 Tumour-as
9	7	50.0	446	5	ABP35708 Fungal ZB
10	7	50.0	446	8	ADJ93495 RDS2. 5/2
11	7	50.0	556	4	ABB69870 Human chr
12	7	50.0	1068	6	ABP78187 N. gonorr
13	7	50.0	1190	8	ADS29513 Bacterial
14	6	42.9	13	2	AAW74214 Internal
15	6	42.9	63	4	ABG23791 Novel hum
16	6	42.9	63	4	AAW29530 Human chr
17	6	42.9	81	5	ABP42754 Human Cr2
18	6	42.9	118	5	ABB49682 Listeria
19	6	42.9	169	8	ADS28328 Bacterial
20	6	42.9	194	4	ABB65029 Drosophil
21	6	42.9	219	6	ADA54813 Human pro
22	6	42.9	224	5	ABU05664 M. tuberc
23	6	42.9	231	8	ADN23823 Bacterial
24	6	42.9	233	5	ABB49740 Listeria
25	6	42.9	233	6	ABU32874 Protein e

26	6	42.9	248	3	AAW10786 Arabidops
27	6	42.9	249	3	AAW47125 Arabidops
28	6	42.9	260	3	AAW47124 Arabidops
29	6	42.9	260	3	AAW10785 Arabidops
30	6	42.9	278	6	AAO16277 Human CD2
31	6	42.9	282	2	AAW74217 Bryodin-2
32	6	42.9	310	3	AAW53037 Human sec
33	6	42.9	330	8	ADO41954 Human CD5
34	6	42.9	334	8	ADO41950 Human CR2
35	6	42.9	381	5	ABB49806 Listeria
36	6	42.9	381	6	ABU32409 Protein e
37	6	42.9	383	7	ADM25476 Hyperther
38	6	42.9	419	4	AAW75602 Human sec
39	6	42.9	419	4	AAW75601 Gene 45 h
40	6	42.9	456	4	ABG21589 Novel hum
41	6	42.9	495	8	ADO41948 Human CR2
42	6	42.9	510	8	ADO41963 Human CR2
43	6	42.9	518	8	ADO41952 Human DAF
44	6	42.9	603	6	ABU20315 Protein e
45	6	42.9	634	6	ABU20978 Protein e
46	6	42.9	709	8	ADI40865 Human kin
47	6	42.9	721	8	ADI40866 Human kin
48	6	42.9	732	4	AAW67574 Amino aci
49	6	42.9	733	7	ABM85399 Human pro
50	6	42.9	745	6	ABR41368 Human DIT
51	6	42.9	785	8	ADN72669 Thale cre
52	6	42.9	794	5	ABBS7307 Mouse isc
53	6	42.9	794	7	ADD48931 Rat Prote
54	6	42.9	794	7	ADD47982 Rat Prote
55	6	42.9	794	7	ADD47984 Human pro
56	6	42.9	794	7	ADD48933 Human pro
57	6	42.9	794	8	ADQ39213 Human myo
58	6	42.9	819	4	ABG13725 Novel hum
59	6	42.9	875	6	ABU24883 Protein e
60	6	42.9	884	6	ABU25371 Protein e
61	6	42.9	890	6	ABU25357 Protein e
62	6	42.9	892	8	ADO62059 Transcrip
63	6	42.9	1033	7	ADD67538 Human Lyl
64	6	42.9	1033	8	ADI05797 Human com
65	6	42.9	1033	8	ADO41968 Human com
66	6	42.9	1033	8	ADO41971 Human com
67	6	42.9	1033	8	ADP56042 Human PRO
68	6	42.9	1048	4	ABBS9245 Drosophil
69	6	42.9	1066	4	AAW67418 Amino aci
70	6	42.9	1066	6	ABG72693 Fruit fly
71	6	42.9	1066	7	ADG98862 Fruit fly
72	6	42.9	1084	8	ADM90837 Human pha
73	6	42.9	1087	2	AAW11139 B lymphoc
74	6	42.9	1367	4	ABG25023 Novel hum
75	6	42.9	1415	7	ABO77692 Pseudomon
76	6	42.9	2520	8	ADN11586 Human CD9
77	6	42.9	2565	8	ADN11585 Human CD9
78	6	42.9	3029	8	ADP25433 Plasmodi
79	6	42.9	4183	7	ABM85419 Human pro
80	6	42.9	4419	8	ADN11590 Human CD9
81	6	42.9	4419	8	ADN11588 Human CD9
82	6	42.9	4464	8	ADN11587 Human CD9
83	6	42.9	4464	8	ADN11589 Human CD9
84	6	42.9	4529	5	AAU81016 Mouse alp
85	6	42.9	4544	2	AAW47861 Alpha 2-M
86	6	42.9	4544	2	AAW60517 Human alp
87	6	42.9	4544	4	AAW79091 Human pro
88	6	42.9	4544	5	AAU81019 Human alp
89	6	42.9	4544	6	ABP56839 Human LRP
90	6	42.9	4544	6	ABU89744 Protein d
91	6	42.9	4544	7	ADN14025 Human src
92	6	42.9	4544	8	ADI27167 Human LRP
93	6	42.9	4544	8	ADL15636 Human lip
94	6	42.9	4544	8	ADN11584 Human CD9
95	6	42.9	4545	5	AAU74797 Mouse alp
96	6	42.9	4545	8	ADI27166 Mouse LRP
97	6	42.9	4545	8	ADI27170 Mouse LRP
98	6	42.9	4545	8	ADT49882 Murine LR

99	6	42.9	4563	4	ABBI1353	Abbi1353 Human LDL	172	5	35.7	68	5	ABR04908	Abb04908 LRPB huma
100	6	42.9	4599	6	ABP56837	Abp56837 Human LRP	173	5	35.7	68	5	ABG44988	Abg44988 Human pep
101	6	42.9	4599	8	ADI27168	Adi27168 Mouse LRP	174	5	35.7	70	7	ADC94966	Adc94966 E. faeciu
102	6	42.9	4599	8	ADI27169	Adi27169 Mouse LRP	175	5	35.7	70	7	ADC94965	Adc94965 E. faeciu
103	6	42.9	4636	4	AAE11937	AAe11937 Human CG1	176	5	35.7	77	3	AAE11937	AAe11937 Human CG1
104	6	42.9	4636	8	AAE10474	AAe10474 Human the	177	5	35.7	77	3	AAE10474	AAe10474 Human the
105	5	35.7	9	4	AAE10474	AAe10474 Human the	178	5	35.7	77	3	AAE10474	AAe10474 Human the
106	5	35.7	9	7	AAE10474	AAe10474 Human the	179	5	35.7	77	3	AAE10474	AAe10474 Human the
107	5	35.7	9	7	AAE10474	AAe10474 Human the	180	5	35.7	78	4	AAE10474	AAe10474 Human the
108	5	35.7	9	7	AAE10474	AAe10474 Human the	181	5	35.7	78	4	AAE10474	AAe10474 Human the
109	5	35.7	9	7	AAE10474	AAe10474 Human the	182	5	35.7	78	4	AAE10474	AAe10474 Human the
110	5	35.7	9	7	AAE10474	AAe10474 Human the	183	5	35.7	79	6	AAE10474	AAe10474 Human the
111	5	35.7	9	7	AAE10474	AAe10474 Human the	184	5	35.7	81	4	AAE10474	AAe10474 Human the
112	5	35.7	9	7	AAE10474	AAe10474 Human the	185	5	35.7	81	4	AAE10474	AAe10474 Human the
113	5	35.7	9	7	AAE10474	AAe10474 Human the	186	5	35.7	81	4	AAE10474	AAe10474 Human the
114	5	35.7	9	7	AAE10474	AAe10474 Human the	187	5	35.7	81	4	AAE10474	AAe10474 Human the
115	5	35.7	11	6	ABO10711	ABO10711 Murine J4	188	5	35.7	81	4	ABO10711	ABO10711 Murine J4
116	5	35.7	11	6	ABR44655	ABr44655 Murine J4	189	5	35.7	81	4	ABR44655	ABr44655 Murine J4
117	5	35.7	11	8	ADQ09783	ADq09783 Mouse com	190	5	35.7	83	2	ADQ09783	ADq09783 Mouse com
118	5	35.7	12	8	ADP21839	ADp21839 Branched	191	5	35.7	83	2	ADP21839	ADp21839 Branched
119	5	35.7	15	7	ADK82700	ADk82700 Beta-amy1	192	5	35.7	83	2	ADK82700	ADk82700 Beta-amy1
120	5	35.7	15	7	ADM64487	ADM64487 human zin	193	5	35.7	83	2	ADM64487	ADM64487 human zin
121	5	35.7	16	7	ADM52322	ADM52322 Human LY1	194	5	35.7	83	2	ADM52322	ADM52322 Human LY1
122	5	35.7	28	5	ABA47915	ABa47915 EETI-2 va	195	5	35.7	83	2	ABA47915	ABa47915 EETI-2 va
123	5	35.7	30	7	ADM35227	ADM35227 Human LY1	196	5	35.7	83	2	ADM35227	ADM35227 Human LY1
124	5	35.7	30	7	ADM35226	ADM35226 Human LY1	197	5	35.7	83	2	ADM35226	ADM35226 Human LY1
125	5	35.7	35	2	RAY05330	RAY05330 Inflamat	198	5	35.7	83	2	RAY05330	RAY05330 Inflamat
126	5	35.7	37	4	AM88488	AM88488 Human imm	199	5	35.7	83	2	AM88488	AM88488 Human imm
127	5	35.7	37	6	ABP80484	ABp80484 N. gonorr	200	5	35.7	83	2	ABP80484	ABp80484 N. gonorr
128	5	35.7	37	6	ABP77386	ABp77386 N. gonorr	201	5	35.7	83	2	ABP77386	ABp77386 N. gonorr
129	5	35.7	39	2	AAW03644	AAw03644 Rat FC5R	202	5	35.7	83	2	AAW03644	AAw03644 Rat FC5R
130	5	35.7	39	6	ABP77797	ABp77797 N. gonorr	203	5	35.7	83	2	ABP77797	ABp77797 N. gonorr
131	5	35.7	42	6	ABP97890	ABp97890 Amino aci	204	5	35.7	83	2	ABP97890	ABp97890 Amino aci
132	5	35.7	44	7	ADC24831	ADc24831 Human bre	205	5	35.7	83	2	ADC24831	ADc24831 Human bre
133	5	35.7	46	8	ADM63393	ADM63393 Tobamovir	206	5	35.7	83	2	ADM63393	ADM63393 Tobamovir
134	5	35.7	47	4	AAE18291	AAE18291 Peptide #	207	5	35.7	83	2	AAE18291	AAE18291 Peptide #
135	5	35.7	47	4	ABE37326	ABe37326 Peptide #	208	5	35.7	83	2	ABE37326	ABe37326 Peptide #
136	5	35.7	47	4	AAE37079	AAe37079 Peptide #	209	5	35.7	83	2	AAE37079	AAe37079 Peptide #
137	5	35.7	47	4	ABE37079	ABe37079 Peptide #	210	5	35.7	83	2	ABE37079	ABe37079 Peptide #
138	5	35.7	47	4	ABE37079	ABe37079 Peptide #	211	5	35.7	83	2	ABE37079	ABe37079 Peptide #
139	5	35.7	47	4	ABE37079	ABe37079 Peptide #	212	5	35.7	83	2	ABE37079	ABe37079 Peptide #
140	5	35.7	47	4	ABE37079	ABe37079 Peptide #	213	5	35.7	83	2	ABE37079	ABe37079 Peptide #
141	5	35.7	47	4	ABE37079	ABe37079 Peptide #	214	5	35.7	83	2	ABE37079	ABe37079 Peptide #
142	5	35.7	47	4	ABE37079	ABe37079 Peptide #	215	5	35.7	83	2	ABE37079	ABe37079 Peptide #
143	5	35.7	51	4	AAU43192	AAu43192 Propionib	216	5	35.7	83	2	AAU43192	AAu43192 Propionib
144	5	35.7	51	4	AAU43192	AAu43192 Propionib	217	5	35.7	83	2	AAU43192	AAu43192 Propionib
145	5	35.7	53	4	ABE15233	ABe15233 Human ner	218	5	35.7	83	2	ABE15233	ABe15233 Human ner
146	5	35.7	56	4	AAW92619	AAw92619 Human dig	219	5	35.7	83	2	AAW92619	AAw92619 Human dig
147	5	35.7	56	4	AAU22613	AAu22613 Novel hum	220	5	35.7	83	2	AAU22613	AAu22613 Novel hum
148	5	35.7	56	7	ADN63392	ADn63392 Tobamovir	221	5	35.7	83	2	ADN63392	ADn63392 Tobamovir
149	5	35.7	56	8	ADN63392	ADn63392 Tobamovir	222	5	35.7	83	2	ADN63392	ADn63392 Tobamovir
150	5	35.7	60	4	AAE69147	AAe69147 M. catarr	223	5	35.7	83	2	AAE69147	AAe69147 M. catarr
151	5	35.7	61	3	AAE55738	AAe55738 Arabidops	224	5	35.7	83	2	AAE55738	AAe55738 Arabidops
152	5	35.7	61	8	ADL05381	ADl05381 M. catarr	225	5	35.7	83	2	ADL05381	ADl05381 M. catarr
153	5	35.7	62	2	AAU11422	AAu11422 Human 5'	226	5	35.7	83	2	AAU11422	AAu11422 Human 5'
154	5	35.7	62	2	AAU11422	AAu11422 Human 5'	227	5	35.7	83	2	AAU11422	AAu11422 Human 5'
155	5	35.7	65	4	ABE40009	ABe40009 Peptide #	228	5	35.7	83	2	ABE40009	ABe40009 Peptide #
156	5	35.7	65	4	ABE40009	ABe40009 Peptide #	229	5	35.7	83	2	ABE40009	ABe40009 Peptide #
157	5	35.7	65	4	ABE40009	ABe40009 Peptide #	230	5	35.7	83	2	ABE40009	ABe40009 Peptide #
158	5	35.7	65	4	ABE40009	ABe40009 Peptide #	231	5	35.7	83	2	ABE40009	ABe40009 Peptide #
159	5	35.7	65	4	ABE40009	ABe40009 Peptide #	232	5	35.7	83	2	ABE40009	ABe40009 Peptide #
160	5	35.7	65	4	ABE40009	ABe40009 Peptide #	233	5	35.7	83	2	ABE40009	ABe40009 Peptide #
161	5	35.7	65	4	ABE40009	ABe40009 Peptide #	234	5	35.7	83	2	ABE40009	ABe40009 Peptide #
162	5	35.7	65	4	ABE40009	ABe40009 Peptide #	235	5	35.7	83	2	ABE40009	ABe40009 Peptide #
163	5	35.7	65	4	ABE40009	ABe40009 Peptide #	236	5	35.7	83	2	ABE40009	ABe40009 Peptide #
164	5	35.7	65	4	ABE40009	ABe40009 Peptide #	237	5	35.7	83	2	ABE40009	ABe40009 Peptide #
165	5	35.7	65	4	ABE40009	ABe40009 Peptide #	238	5	35.7	83	2	ABE40009	ABe40009 Peptide #
166	5	35.7	65	4	ABE40009	ABe40009 Peptide #	239	5	35.7	83	2	ABE40009	ABe40009 Peptide #
167	5	35.7	65	4	ABE40009	ABe40009 Peptide #	240	5	35.7	83	2	ABE40009	ABe40009 Peptide #
168	5	35.7	65	4	ABE40009	ABe40009 Peptide #	241	5	35.7	83	2	ABE40009	ABe40009 Peptide #
169	5	35.7	65	4	ABE40009	ABe40009 Peptide #	242	5	35.7	83	2	ABE40009	ABe40009 Peptide #
170	5	35.7	65	4	ABE40009	ABe40009 Peptide #	243	5	35.7	83	2	ABE40009	ABe40009 Peptide #
171	5	35.7	65	4	ABE40009	ABe40009 Peptide #	244	5	35.7	83	2	ABE40009	ABe40009 Peptide #

245 ABR44621 Murine J4 107 6 ABR44621 5 35.7 107 6 ABR44621 5 35.7 107 6 ABR44621 Murine J4 318
246 ABR44679 Murine J4 107 6 ABR44679 5 35.7 107 6 ABR44679 Murine J4 319
247 ABR44681 Murine J4 107 6 ABR44681 5 35.7 107 6 ABR44681 Murine J4 320
248 ABR44671 Murine J4 107 6 ABR44671 5 35.7 107 6 ABR44671 Murine J4 321
249 ABR44671 Murine J4 107 6 ABR44671 5 35.7 107 6 ABR44671 Murine J4 322
250 ABR44671 Murine J4 107 6 ABR44671 5 35.7 107 6 ABR44671 Murine J4 323
251 ABR44671 Murine J4 107 6 ABR44671 5 35.7 107 6 ABR44671 Murine J4 324
252 ABR44671 Murine J4 107 6 ABR44671 5 35.7 107 6 ABR44671 Murine J4 325
253 ABR44671 Murine J4 107 6 ABR44671 5 35.7 107 6 ABR44671 Murine J4 326
254 ABR44671 Murine J4 107 6 ABR44671 5 35.7 107 6 ABR44671 Murine J4 327
255 ABR44671 Murine J4 107 6 ABR44671 5 35.7 107 6 ABR44671 Murine J4 328
256 ABR44671 Murine J4 107 6 ABR44671 5 35.7 107 6 ABR44671 Murine J4 329
257 ABR44671 Murine J4 107 6 ABR44671 5 35.7 107 6 ABR44671 Murine J4 330
258 ABR44671 Murine J4 107 6 ABR44671 5 35.7 107 6 ABR44671 Murine J4 331
259 ABR44671 Murine J4 107 6 ABR44671 5 35.7 107 6 ABR44671 Murine J4 332
260 ABR44671 Murine J4 107 6 ABR44671 5 35.7 107 6 ABR44671 Murine J4 333
261 ABR44671 Murine J4 107 6 ABR44671 5 35.7 107 6 ABR44671 Murine J4 334
262 ABR44671 Murine J4 107 6 ABR44671 5 35.7 107 6 ABR44671 Murine J4 335
263 ABR44671 Murine J4 107 6 ABR44671 5 35.7 107 6 ABR44671 Murine J4 336
264 ABR44671 Murine J4 107 6 ABR44671 5 35.7 107 6 ABR44671 Murine J4 337
265 ABR44671 Murine J4 107 6 ABR44671 5 35.7 107 6 ABR44671 Murine J4 338
266 ABR44671 Murine J4 107 6 ABR44671 5 35.7 107 6 ABR44671 Murine J4 339
267 ABR44671 Murine J4 107 6 ABR44671 5 35.7 107 6 ABR44671 Murine J4 340
268 ABR44671 Murine J4 107 6 ABR44671 5 35.7 107 6 ABR44671 Murine J4 341
269 ABR44671 Murine J4 107 6 ABR44671 5 35.7 107 6 ABR44671 Murine J4 342
270 ABR44671 Murine J4 107 6 ABR44671 5 35.7 107 6 ABR44671 Murine J4 343
271 ABR44671 Murine J4 107 6 ABR44671 5 35.7 107 6 ABR44671 Murine J4 344
272 ABR44671 Murine J4 107 6 ABR44671 5 35.7 107 6 ABR44671 Murine J4 345
273 ABR44671 Murine J4 107 6 ABR44671 5 35.7 107 6 ABR44671 Murine J4 346
274 ABR44671 Murine J4 107 6 ABR44671 5 35.7 107 6 ABR44671 Murine J4 347
275 ABR44671 Murine J4 107 6 ABR44671 5 35.7 107 6 ABR44671 Murine J4 348
276 ABR44671 Murine J4 107 6 ABR44671 5 35.7 107 6 ABR44671 Murine J4 349
277 ABR44671 Murine J4 107 6 ABR44671 5 35.7 107 6 ABR44671 Murine J4 350
278 ABR44671 Murine J4 107 6 ABR44671 5 35.7 107 6 ABR44671 Murine J4 351
279 ABR44671 Murine J4 107 6 ABR44671 5 35.7 107 6 ABR44671 Murine J4 352
280 ABR44671 Murine J4 107 6 ABR44671 5 35.7 107 6 ABR44671 Murine J4 353
281 ABR44671 Murine J4 107 6 ABR44671 5 35.7 107 6 ABR44671 Murine J4 354
282 ABR44671 Murine J4 107 6 ABR44671 5 35.7 107 6 ABR44671 Murine J4 355
283 ABR44671 Murine J4 107 6 ABR44671 5 35.7 107 6 ABR44671 Murine J4 356
284 ABR44671 Murine J4 107 6 ABR44671 5 35.7 107 6 ABR44671 Murine J4 357
285 ABR44671 Murine J4 107 6 ABR44671 5 35.7 107 6 ABR44671 Murine J4 358
286 ABR44671 Murine J4 107 6 ABR44671 5 35.7 107 6 ABR44671 Murine J4 359
287 ABR44671 Murine J4 107 6 ABR44671 5 35.7 107 6 ABR44671 Murine J4 360
288 ABR44671 Murine J4 107 6 ABR44671 5 35.7 107 6 ABR44671 Murine J4 361
289 ABR44671 Murine J4 107 6 ABR44671 5 35.7 107 6 ABR44671 Murine J4 362
290 ABR44671 Murine J4 107 6 ABR44671 5 35.7 107 6 ABR44671 Murine J4 363
291 ABR44671 Murine J4 107 6 ABR44671 5 35.7 107 6 ABR44671 Murine J4 364
292 ABR44671 Murine J4 107 6 ABR44671 5 35.7 107 6 ABR44671 Murine J4 365
293 ABR44671 Murine J4 107 6 ABR44671 5 35.7 107 6 ABR44671 Murine J4 366
294 ABR44671 Murine J4 107 6 ABR44671 5 35.7 107 6 ABR44671 Murine J4 367
295 ABR44671 Murine J4 107 6 ABR44671 5 35.7 107 6 ABR44671 Murine J4 368
296 ABR44671 Murine J4 107 6 ABR44671 5 35.7 107 6 ABR44671 Murine J4 369
297 ABR44671 Murine J4 107 6 ABR44671 5 35.7 107 6 ABR44671 Murine J4 370
298 ABR44671 Murine J4 107 6 ABR44671 5 35.7 107 6 ABR44671 Murine J4 371
299 ABR44671 Murine J4 107 6 ABR44671 5 35.7 107 6 ABR44671 Murine J4 372
300 ABR44671 Murine J4 107 6 ABR44671 5 35.7 107 6 ABR44671 Murine J4 373
301 ABR44671 Murine J4 107 6 ABR44671 5 35.7 107 6 ABR44671 Murine J4 374
302 ABR44671 Murine J4 107 6 ABR44671 5 35.7 107 6 ABR44671 Murine J4 375
303 ABR44671 Murine J4 107 6 ABR44671 5 35.7 107 6 ABR44671 Murine J4 376
304 ABR44671 Murine J4 107 6 ABR44671 5 35.7 107 6 ABR44671 Murine J4 377
305 ABR44671 Murine J4 107 6 ABR44671 5 35.7 107 6 ABR44671 Murine J4 378
306 ABR44671 Murine J4 107 6 ABR44671 5 35.7 107 6 ABR44671 Murine J4 379
307 ABR44671 Murine J4 107 6 ABR44671 5 35.7 107 6 ABR44671 Murine J4 380
308 ABR44671 Murine J4 107 6 ABR44671 5 35.7 107 6 ABR44671 Murine J4 381
309 ABR44671 Murine J4 107 6 ABR44671 5 35.7 107 6 ABR44671 Murine J4 382
310 ABR44671 Murine J4 107 6 ABR44671 5 35.7 107 6 ABR44671 Murine J4 383
311 ABR44671 Murine J4 107 6 ABR44671 5 35.7 107 6 ABR44671 Murine J4 384
312 ABR44671 Murine J4 107 6 ABR44671 5 35.7 107 6 ABR44671 Murine J4 385
313 ABR44671 Murine J4 107 6 ABR44671 5 35.7 107 6 ABR44671 Murine J4 386
314 ABR44671 Murine J4 107 6 ABR44671 5 35.7 107 6 ABR44671 Murine J4 387
315 ABR44671 Murine J4 107 6 ABR44671 5 35.7 107 6 ABR44671 Murine J4 388
316 ABR44671 Murine J4 107 6 ABR44671 5 35.7 107 6 ABR44671 Murine J4 389
317 ABR44671 Murine J4 107 6 ABR44671 5 35.7 107 6 ABR44671 Murine J4 390

ADN73803 Thale cre 145 8 ADN73803 35.7 145 8 ADN73803 Thale cre
ABG23799 Novel hum 146 5 ABG23799 35.7 146 5 ABG23799 Novel hum
AGR41557 Human CD- 147 4 AGR41557 35.7 147 4 AGR41557 Human CD-
ABG12343 Novel hum 147 4 ABG12343 35.7 147 4 ABG12343 Novel hum
ABG23801 Novel hum 147 4 ABG23801 35.7 147 4 ABG23801 Novel hum
ABU10250 Mammalian 147 6 ABU10250 35.7 147 6 ABU10250 Mammalian
ADE80904 Mammalian 147 6 ADE80904 35.7 147 6 ADE80904 Mammalian
ABM73894 DNA clone 147 7 ABM73894 35.7 147 7 ABM73894 DNA clone
AGS00176 Human sec 148 3 AGS00176 35.7 148 3 AGS00176 Human sec
ABG23800 Novel hum 148 3 ABG23800 35.7 148 3 ABG23800 Novel hum
AGS56381 Arabidops 151 3 AGS56381 35.7 151 3 AGS56381 Arabidops
AGS60992 Arabidops 151 3 AGS60992 35.7 151 3 AGS60992 Arabidops
AGS37153 Arabidops 151 3 AGS37153 35.7 151 3 AGS37153 Arabidops
AGS93315 Human pro 151 4 AGS93315 35.7 151 4 AGS93315 Human pro
AGS38476 Arabidops 154 3 AGS38476 35.7 154 3 AGS38476 Arabidops
ABD49339 Listeria 154 5 ABD49339 35.7 154 5 ABD49339 Listeria
ABG58936 Breast an 156 3 ABG58936 35.7 156 3 ABG58936 Breast an
AGS60991 Arabidops 156 3 AGS60991 35.7 156 3 AGS60991 Arabidops
AGS56380 Arabidops 156 3 AGS56380 35.7 156 3 AGS56380 Arabidops
AGS08644 Arabidops 159 3 AGS08644 35.7 159 3 AGS08644 Arabidops
AGS29977 Arabidops 160 3 AGS29977 35.7 160 3 AGS29977 Arabidops
AGS65870 Novel hum 160 8 AGS65870 35.7 160 8 AGS65870 Novel hum
ADN22897 Bacterial 161 6 ADN22897 35.7 161 6 ADN22897 Bacterial
ADP77628 N. gonorr 161 6 ADP77628 35.7 161 6 ADP77628 N. gonorr
AAR25124 Hepatitis 162 2 AAR25124 35.7 162 2 AAR25124 Hepatitis
AAW56730 Novel dis 163 2 AAW56730 35.7 163 2 AAW56730 Novel dis
AAB64463 Human sec 163 2 AAB64463 35.7 163 2 AAB64463 Human sec
AAB19038 Amino aci 163 3 AAB19038 35.7 163 3 AAB19038 Amino aci
AAB19037 Amino aci 163 3 AAB19037 35.7 163 3 AAB19037 Amino aci
AAY93601 Protein e 163 3 AAY93601 35.7 163 3 AAY93601 Protein e
ADC38660 Human sec 163 7 ADC38660 35.7 163 7 ADC38660 Human sec
ADI63102 Human apo 163 7 ADI63102 35.7 163 7 ADI63102 Human apo
ADN95501 Human BEC 163 7 ADN95501 35.7 163 7 ADN95501 Human BEC
ADN55179 Protein # 163 8 ADN55179 35.7 163 8 ADN55179 Protein #
ADQ20841 Human sof 166 6 ADQ20841 35.7 166 6 ADQ20841 Human sof
ADP23602 PRO polyp 166 8 ADP23602 35.7 166 8 ADP23602 PRO polyp
ADP5642 Human pro 166 8 ADP5642 35.7 166 8 ADP5642 Human pro
AGS38475 Arabidops 166 3 AGS38475 35.7 166 3 AGS38475 Arabidops
AAU16609 Human nov 166 4 AAU16609 35.7 166 4 AAU16609 Human nov
AAU10452 Immunolog 166 6 AAU10452 35.7 166 6 AAU10452 Immunolog
ABU5678 Human nov 166 6 ABU5678 35.7 166 6 ABU5678 Human nov
ADG80906 Mammalian 166 8 ADG80906 35.7 166 8 ADG80906 Mammalian
AGS20163 Arabidops 168 3 AGS20163 35.7 168 3 AGS20163 Arabidops
AAU45536 Propionib 168 4 AAU45536 35.7 168 4 AAU45536 Propionib
ADM42055 Propionib 168 6 ADM42055 35.7 168 6 ADM42055 Propionib
ABG23793 Novel hum 170 4 ABG23793 35.7 170 4 ABG23793 Novel hum
AGS60990 Arabidops 171 3 AGS60990 35.7 171 3 AGS60990 Arabidops
AGS56379 Arabidops 171 3 AGS56379 35.7 171 3 AGS56379 Arabidops
AAU53524 Propionib 172 4 AAU53524 35.7 172 4 AAU53524 Propionib
ADM50043 Propionib 172 6 ADM50043 35.7 172 6 ADM50043 Propionib
AAM25771 Human pro 173 4 AAM25771 35.7 173 4 AAM25771 Human pro
AGS90845 C. glutam 174 7 AGS90845 35.7 174 7 AGS90845 C. glutam
ADD13208 C. glutam 174 7 ADD13208 35.7 174 7 ADD13208 C. glutam
AGS59801 Arabidops 175 3 AGS59801 35.7 175 3 AGS59801 Arabidops
AGS58326 Arabidops 175 3 AGS58326 35.7 175 3 AGS58326 Arabidops
AGS20162 Arabidops 180 3 AGS20162 35.7 180 3 AGS20162 Arabidops
ADF06164 Bacterial 185 7 ADF06164 35.7 185 7 ADF06164 Bacterial
AAW81026 PAS domai 186 2 AAW81026 35.7 186 2 AAW81026 PAS domai
ADA89678 Staphyloc 188 6 ADA89678 35.7 188 6 ADA89678 Staphyloc
ADA89666 Staphyloc 188 6 ADA89666 35.7 188 6 ADA89666 Staphyloc
AGS59800 Arabidops 190 3 AGS59800 35.7 190 3 AGS59800 Arabidops
ADO58830 Human gen 190 8 ADO58830 35.7 190 8 ADO58830 Human gen
ADM03992 Human pro 191 7 ADM03992 35.7 191 7 ADM03992 Human pro
AAR33985 HCT33 E1 193 2 AAR33985 35.7 193 2 AAR33985 HCT33 E1
ADB11810 Alloiooc 193 6 ADB11810 35.7 193 6 ADB11810 Alloiooc
ADC00075 Enterohae 194 7 ADC00075 35.7 194 7 ADC00075 Enterohae
AOL16405 Human nuc 196 6 AOL16405 35.7 196 6 AOL16405 Human nuc
ABG23794 Novel hum 199 4 ABG23794 35.7 199 4 ABG23794 Novel hum
ADB11808 Alloiooc 203 6 ADB11808 35.7 203 6 ADB11808 Alloiooc
ABB04904 Meg human 204 5 ABB04904 35.7 204 5 ABB04904 Meg human
ABG25323 Novel hum 205 4 ABG25323 35.7 205 4 ABG25323 Novel hum
ABP39921 Staphyloc 205 5 ABP39921 35.7 205 5 ABP39921 Staphyloc
ADE06997 Staphyloc 205 8 ADE06997 35.7 205 8 ADE06997 Staphyloc

391	5	35.7	206	6	ADB11806	Adb11806 Alloiococ	464	258	2	AAW10154	Aaw10154 Callose
392	5	35.7	207	2	AAR97213	Aar97213 Human cal	465	258	6	ABR52901	AbR52901 Protein s
393	5	35.7	207	2	AAW26770	Aaw26770 Calcium s	466	258	7	ADK62442	AdK62442 Disease t
394	5	35.7	212	6	ADA34545	Ada34545 Acinetoba	466	258	8	ADN62547	Adn62547 A. thalia
395	5	35.7	213	2	AAAY42374	Aay42374 Amino aci	468	258	8	ADN43930	Adn43930 Bacterial
396	5	35.7	214	8	ADL22485	Adl22485 Human tau	469	260	2	AAM52944	Aam52944 Agkistrod
397	5	35.7	214	8	ADL22485	Adl22485 Human tau	470	260	8	ADL65425	Adl65425 DNA gyras
398	5	35.7	216	2	AAAY73908	Aay73908 Human pro	471	261	7	ADM34373	Adm34373 Human LV1
399	5	35.7	216	3	AAAB24648	Aab24648 Plant SDF	472	261	7	ADM35281	Adm35281 Human LV1
400	5	35.7	216	3	AAAB25090	Aab25090 Plant SDF	472	261	8	ADR96378	Adr96378 Novel S.
401	5	35.7	217	8	ADN21492	Adn21492 Bacterial	473	262	3	ABR52901	AbR52901 Protein s
402	5	35.7	218	5	ABB09590	Abb09590 Deinagkis	474	262	3	ABR52901	AbR52901 Protein s
403	5	35.7	219	2	AAAY34450	Aay34450 Porphyrom	475	262	3	ABR52901	AbR52901 Protein s
404	5	35.7	221	4	ABG30016	Abg30016 Novel hum	476	262	6	AAE38420	Aae38420 Arabidops
405	5	35.7	223	4	ABR65564	AbR65564 Drosophil	477	262	6	ADK62442	AdK62442 Disease t
406	5	35.7	224	7	ADM25534	Adm25534 Hyperther	478	266	3	AAE38420	Aae38420 Arabidops
407	5	35.7	225	2	AAAR09846	Aar09846 Hybrid co	479	266	3	ADK62442	AdK62442 Disease t
408	5	35.7	225	7	ADH10110	Adh10110 Human IL-	480	266	3	ABG30016	Abg30016 Novel hum
409	5	35.7	225	7	ADG48164	Adg48164 Human IL-	481	266	3	ABG30016	Abg30016 Novel hum
410	5	35.7	226	4	AAU60973	Aau60973 Propionib	482	266	4	ABG12593	Abg12593 Novel hum
411	5	35.7	226	6	ABM57492	Abm57492 Propionib	483	266	8	ADN63337	Adn63337 Tobamovir
412	5	35.7	226	6	ABM57492	Abm57492 Propionib	484	266	8	ADN63337	Adn63337 Tobamovir
413	5	35.7	227	3	AAAG37427	Aag37427 Arabidops	485	269	3	AAAG37427	Aag37427 Arabidops
414	5	35.7	227	6	ABP78057	Abp78057 N. gonorr	486	271	3	AAAG37427	Aag37427 Arabidops
415	5	35.7	227	6	ABB48998	Abb48998 Listeria	487	271	3	AAAG37427	Aag37427 Arabidops
416	5	35.7	228	5	ABR08510	AbR08510 A recombi	488	271	7	ABO68546	AbO68546 Pseudomon
417	5	35.7	230	3	AAAB08511	Aab08511 A. contor	489	272	7	ADM35274	Adm35274 Human LV1
418	5	35.7	231	2	AAW76538	Aaw76538 A. contor	491	272	7	AAV11104	Aay11104 H. pylori
419	5	35.7	231	2	AAW76538	Aaw76538 A. contor	492	275	2	AAV11104	Aay11104 H. pylori
420	5	35.7	231	4	AAAM52946	Aam52946 Batroxobi	493	276	3	AAAG50848	Aag50848 Arabidops
421	5	35.7	233	4	AAAG79000	Aag79000 Mamushi f	494	276	8	ADS22549	AdS22549 Bacterial
422	5	35.7	233	4	ADM19989	Adm19989 Protein e	495	278	2	AAV11105	Aay11105 H. pylori
423	5	35.7	234	2	AAAR20554	Aar20554 Fibrinoge	496	278	3	AAAG37980	Aag37980 Arabidops
424	5	35.7	234	6	ABR09589	AbR09589 Deinagkis	497	278	3	AAAG37980	Aag37980 Arabidops
425	5	35.7	234	6	ABU02455	Abu02455 S. pneumo	498	278	7	ADK97046	AdK97046 E. faeciu
426	5	35.7	234	6	ABU46243	Abu46243 Protein e	499	280	4	ABR59077	AbR59077 Drosophil
427	5	35.7	235	3	AAAR20555	Aar20555 Fibrinoge	500	280	6	ABU70931	Abu70931 Human adi
428	5	35.7	235	3	AAAG43026	Aag43026 Arabidops	501	280	6	AAW93214	Aaw93214 A. Gelati
429	5	35.7	235	8	ADS27596	AdS27596 Bacterial	502	282	2	AAW93214	Aaw93214 A. Gelati
430	5	35.7	235	8	ADS30303	AdS30303 Bacterial	503	282	8	ADP08244	AdP08244 Neisseria
431	5	35.7	236	2	AAAR20556	Aar20556 Fibrinoge	504	282	8	AAW98446	Aaw98446 H. pylori
432	5	35.7	236	2	AAAM52945	Aam52945 Flabobobi	505	282	8	AAW98446	Aaw98446 H. pylori
433	5	35.7	238	2	AAAY34327	Aay34327 Porphyrom	506	282	8	AAW98446	Aaw98446 H. pylori
434	5	35.7	238	2	AAAG12185	Aag12185 Arabidops	507	282	8	AAW98446	Aaw98446 H. pylori
435	5	35.7	239	5	ABG93879	Abg93879 Rice form	508	282	8	AAW98446	Aaw98446 H. pylori
436	5	35.7	239	7	ADK66715	AdK66715 Rice form	509	282	8	AAW98446	Aaw98446 H. pylori
437	5	35.7	242	5	ABP28763	Abp28763 Streptoco	510	289	7	ADF07713	AdF07713 Bacterial
438	5	35.7	242	8	ADN25724	Adn25724 Bacterial	511	289	7	ADF07713	AdF07713 Bacterial
439	5	35.7	244	8	ADL91043	Adl91043 Rat manno	512	290	8	ADS42038	AdS42038 Bacterial
440	5	35.7	246	5	ABP51447	Abp51447 Human MDD	513	291	8	ADS42038	AdS42038 Bacterial
441	5	35.7	246	6	ABU49450	Abu49450 Protein e	514	292	5	ABR91255	AbR91255 Herbicida
442	5	35.7	249	5	AAU80221	Aau80221 B. cereus	515	292	5	ABR91255	AbR91255 Herbicida
443	5	35.7	249	5	AAU97277	Aau97277 Bacillus	516	296	4	ABR91255	AbR91255 Herbicida
444	5	35.7	249	5	AAU97279	Aau97279 Bacillus	517	297	5	ABR91255	AbR91255 Herbicida
445	5	35.7	250	8	AAOI4629	Aaoi4629 Pig scave	518	297	5	ABR91255	AbR91255 Herbicida
446	5	35.7	250	8	ADS24547	AdS24547 Bacterial	519	307	7	ADM26232	Adm26232 Hyperther
447	5	35.7	252	2	AAW15773	Aaw15773 Protein c	520	309	4	ABR91255	AbR91255 Herbicida
448	5	35.7	252	7	ADG87416	Adg87416 Meloidogy	521	311	8	ADM48298	Adm48298 Polypepti
449	5	35.7	252	8	ADM27941	Adm27941 Bacterial	522	312	5	ABR91255	AbR91255 Herbicida
450	5	35.7	254	3	AAAG32812	Aag32812 Arabidops	523	312	6	AAO29575	Aao29575 Human wou
451	5	35.7	254	8	ADO67052	AdO67052 Novel hum	524	312	8	ADH74487	Adh74487 Human end
452	5	35.7	254	8	ADS26684	AdS26684 Bacterial	525	312	8	ADH74487	Adh74487 Human end
453	5	35.7	255	1	AAAP81333	Aap81333 Batroxobi	526	313	6	ABP81489	AbP81489 Streptoco
454	5	35.7	255	2	AAAR05436	Aar05436 Batroxobi	527	313	6	ABP81489	AbP81489 Streptoco
455	5	35.7	255	2	AAAY17869	Aay17869 Araraca b	528	314	3	AAAB01831	Aab01831 Haemophil
456	5	35.7	255	7	ADM34374	Adm34374 Human LV1	529	314	3	AAAB01831	Aab01831 Haemophil
457	5	35.7	255	7	ADM34374	Adm34374 Human LV1	530	315	8	ADR95071	Adr95071 Novel S.
458	5	35.7	255	8	ADF89716	AdF89716 Human can	531	316	8	ADJ19957	AdJ19957 Human sof
459	5	35.7	256	8	ADN633275	Adn633275 Tobamovir	532	317	3	AAAG32611	Aag32611 Arabidops
460	5	35.7	256	8	ADN63338	Adn63338 Tobamovir	533	319	2	AAAG32611	Aag32611 Arabidops
461	5	35.7	256	8	ADN63278	Adn63278 Tobamovir	534	319	4	ABG12844	AbG12844 Novel hum
462	5	35.7	257	8	ADK26317	AdK26317 Bacterial	535	319	8	ADJ19957	AdJ19957 Human sof
463	5	35.7	257	8	ADS25217	AdS25217 Bacterial	536	319	8	ADO15738	AdO15738 African c

537	5	35.7	320	3	AAy84613	Amino aci	610	5	35.7	367	3	AAg06096	Arabidops
538	5	35.7	320	3	AABo1829	Haemophil	611	5	35.7	367	3	AAg49374	Arabidops
539	5	35.7	320	3	ADm35267	Human LY1	612	5	35.7	367	6	AAU35480	Protein e
540	5	35.7	320	8	ABm83639	Human dia	613	5	35.7	367	3	AAg35275	Human LY1
541	5	35.7	320	8	ABm83639	Immune Re	614	5	35.7	370	3	AAg49396	Arabidops
542	5	35.7	323	7	ADd24330	Mouse PST	615	5	35.7	371	5	ABp73608	Candida a
543	5	35.7	323	7	ABW02023	Murine mu	616	5	35.7	371	8	ADG27332	Candida a
544	5	35.7	323	7	ABW02020	Murine mu	617	5	35.7	371	8	ADN21175	Bacterial
545	5	35.7	323	8	ADJ48543	Oil-absoc	618	5	35.7	374	4	AAb42328	Human ORF
546	5	35.7	324	3	AAg39403	Arabidops	619	5	35.7	374	4	ABG00048	Novel hum
547	5	35.7	325	8	ADs25592	Bacterial	620	5	35.7	375	7	ADm26000	Hyperther
548	5	35.7	325	8	ADs26043	Bacterial	621	5	35.7	376	7	ABO80426	Pseudomon
549	5	35.7	328	4	AAb63244	Human bre	622	5	35.7	376	7	ABO71181	Pseudomon
550	5	35.7	328	4	ABG13237	Novel hum	623	5	35.7	377	2	AAW98246	H. pylori
551	5	35.7	328	4	ABG13476	Novel hum	624	5	35.7	377	3	AAy75615	Neisseria
552	5	35.7	329	3	AAg49375	Arabidops	625	5	35.7	379	5	ABU50882	Helicobac
553	5	35.7	329	3	AAg06097	Arabidops	626	5	35.7	379	7	ADD30156	Plant yie
554	5	35.7	331	6	ABr58009	Mouse GI	627	5	35.7	379	7	ADe31537	Plant yie
555	5	35.7	331	8	ADN20053	Bacterial	628	5	35.7	379	8	ADi41953	Plant tra
556	5	35.7	332	3	AAg49397	Arabidops	629	5	35.7	381	5	AAU98989	Oestrogen
557	5	35.7	332	8	ADs29795	Bacterial	630	5	35.7	381	8	ADK16395	Nanoarcha
558	5	35.7	334	5	ABU51084	Helicobac	631	5	35.7	382	4	AAE08001	Rat neuro
559	5	35.7	335	6	ABU16367	Protein e	632	5	35.7	382	6	ABU45726	Protein e
560	5	35.7	336	2	AAW77400	Absidia b	633	5	35.7	384	4	AAg70863	C albican
561	5	35.7	337	2	AAW26688	Absidia b	634	5	35.7	385	8	ADs27721	Bacterial
562	5	35.7	337	4	AAU34121	Staphyloc	635	5	35.7	386	8	ADs24119	Bacterial
563	5	35.7	337	4	AAU37283	Staphyloc	636	5	35.7	389	5	ABU51383	Helicobac
564	5	35.7	337	6	AAU36946	Staphyloc	637	5	35.7	389	5	AAU75907	Human epi
565	5	35.7	337	6	ABU42965	Protein e	638	5	35.7	391	6	ADa55534	Human pro
566	5	35.7	337	6	ABU43809	Protein e	639	5	35.7	391	8	ADs44135	Bacterial
567	5	35.7	337	6	ABU16072	Protein e	640	5	35.7	392	6	ABU45725	Protein e
568	5	35.7	337	6	ABM72240	Staphyloc	641	5	35.7	395	2	AAW34308	Mouse neu
569	5	35.7	339	3	AAg41814	Arabidops	642	5	35.7	395	2	AAW23347	Novel mur
570	5	35.7	340	7	ADf05682	Bacterial	643	5	35.7	395	3	AAy77536	Murine ne
571	5	35.7	340	8	ADi67230	Lactobaci	644	5	35.7	395	3	AAy53254	Mouse neu
572	5	35.7	341	8	ADf89714	Human can	645	5	35.7	395	4	AAy69176	Murine ne
573	5	35.7	343	6	ABU33511	Protein e	646	5	35.7	395	6	ADa47992	Rice prot
574	5	35.7	345	4	ABE67087	Drosophil	647	5	35.7	395	8	ADH10676	Murine fr
575	5	35.7	347	6	ABP78216	N. gonorr	648	5	35.7	395	8	ADJ76268	Marker ge
576	5	35.7	349	4	AAAB79726	Corynebac	649	5	35.7	395	8	ADP98875	C. albica
577	5	35.7	349	4	AAU71897	C. glutam	650	5	35.7	396	8	ADr01259	Farnesyl
578	5	35.7	349	4	AAg90683	C. glutam	651	5	35.7	397	2	AAy28292	Amino aci
579	5	35.7	350	5	ABE84724	DNA polym	652	5	35.7	398	2	AAy29822	Arabidops
580	5	35.7	350	5	ABE84804	Aquifex a	653	5	35.7	400	3	AAy81929	Human EST
581	5	35.7	350	5	ABE84812	DNA polym	654	5	35.7	400	8	ADN46344	Thermococ
582	5	35.7	350	8	ADJ67894	A. aeolic	655	5	35.7	404	7	ADK68537	Mycoplasma
583	5	35.7	350	8	ADJ68106	A. aeolic	656	5	35.7	404	7	ADK68536	Mycoplasma
584	5	35.7	350	8	ADK01184	DNA polym	657	5	35.7	406	3	AAg37979	Arabidops
585	5	35.7	350	8	ADJ79403	A. aeolic	658	5	35.7	407	3	ABs20939	Drosophil
586	5	35.7	350	8	ADJ84843	A. aeolic	659	5	35.7	407	7	ADD15320	Fruitfly
587	5	35.7	350	8	ADm77631	DNA polym	660	5	35.7	408	2	AAW71465	Glycosylt
588	5	35.7	350	8	ADm66298	A. aeolic	661	5	35.7	411	5	ABp7549	A. Orient
589	5	35.7	350	8	ADm04351	A. aeolic	662	5	35.7	411	5	ABp7295	Novel hum
590	5	35.7	350	8	ADP82428	Aquifex a	663	5	35.7	413	6	AAW46822	Amino aci
591	5	35.7	351	3	AAg39402	Arabidops	664	5	35.7	413	6	ADa32940	Acinetoba
592	5	35.7	352	8	ADs41644	Bacterial	665	5	35.7	413	7	ADm35265	Human LY1
593	5	35.7	353	5	ABP40666	Staphyloc	666	5	35.7	415	2	AAW71595	Murine ty
594	5	35.7	353	8	ADs07922	Staphyloc	667	5	35.7	415	3	AAb53180	Macaca mu
595	5	35.7	354	6	ADa34348	Acinetoba	668	5	35.7	415	3	AAy81928	Murine PS
596	5	35.7	355	3	ADs32610	Arabidops	669	5	35.7	415	3	ABm08486	A murine
597	5	35.7	355	8	ABO58499	Human gen	670	5	35.7	415	7	ADm35266	Human LY1
598	5	35.7	356	5	ABU51625	Helicobac	671	5	35.7	416	2	AAy28291	Amino aci
599	5	35.7	358	5	ABG77256	Selected	672	5	35.7	416	3	AAy68782	Amino aci
600	5	35.7	358	5	ABj11127	Yeast sel	673	5	35.7	416	4	ABG28750	Novel hum
601	5	35.7	359	2	AAr88871	Sardinian	674	5	35.7	416	6	ABM67905	Photorhab
602	5	35.7	359	2	AAr88870	Sardinian	675	5	35.7	416	7	ADD24329	Human CD2
603	5	35.7	359	2	AAr88872	Sardinian	676	5	35.7	416	7	ADD24348	Human CD2
604	5	35.7	359	2	AAy05667	Maize cin	677	5	35.7	416	7	ADD24350	Human CD2
605	5	35.7	360	7	ADc61397	Nicotiana	678	5	35.7	416	7	ABW02019	Human CD2
606	5	35.7	361	8	ADp29940	Human sec	679	5	35.7	416	7	ABW02022	Human CD2
607	5	35.7	362	5	ABO5006	Mouse ser	680	5	35.7	416	8	ADL22901	Human MP2
608	5	35.7	365	7	ADm35272	Human LY1	681	5	35.7	416	8	ADs29579	Bacterial
609	5	35.7	366	7	ABM74139	DNA clone	682	5	35.7	419	4	ABs58148	Drosophil

683	5	35.7	419	5	AAU99075	Aau99075 Human Pro	756	5	35.7	473	8	ADQ65367	Adq65367 Novel hum
684	5	35.7	420	5	ABU51367	Abu51367 Helicobac	757	5	35.7	473	8	ABM83797	Abm83797 Human dia
685	5	35.7	420	5	ABB48624	Abb48624 Listeria	758	5	35.7	473	8	ADN21319	Adn21319 Bacterial
686	5	35.7	422	5	ABU51614	Abu51614 Helicobac	759	5	35.7	474	3	AAU56509	Aay56509 Human Jur
687	5	35.7	423	3	AAU37978	Aag37978 Arabidops	760	5	35.7	475	6	ABU43179	Abu43179 Protein e
688	5	35.7	424	2	AAW23818	Aaw23818 Arabidops	761	5	35.7	478	3	AAU44073	Aag44073 Arabidops
689	5	35.7	424	2	AAW45512	Aaw45512 LEAFY gen	762	5	35.7	478	3	AAU47163	Aag47163 Arabidops
690	5	35.7	424	2	AAW43332	Aaw43332 Arabidops	763	5	35.7	479	4	ABBS1020	Abb53020 Escherich
691	5	35.7	424	2	AAW39138	Aaw39138 Arabidops	764	5	35.7	479	7	ADU7046	Adf07046 Bacterial
692	5	35.7	424	3	AAU67557	Aay67557 A. thalia	765	5	35.7	479	8	ADN24682	Adn24682 Bacterial
693	5	35.7	424	3	AAU19248	Abi19248 Amino aci	766	5	35.7	481	4	ABM62987	Abm62987 Drosophil
694	5	35.7	424	3	AAU78886	Aay78886 A. thalia	767	5	35.7	481	8	ABM83796	Abm83796 Human dia
695	5	35.7	424	6	ABR42687	Abd42687 Arabidops	768	5	35.7	482	6	ABU31996	Abu31996 Protein e
696	5	35.7	424	7	ADU56541	Adf56541 Thale cre	769	5	35.7	483	6	ADU44061	Adu44061 Bacterial
697	5	35.7	424	8	ADG47860	Adg47860 Arabidops	770	5	35.7	485	6	ABU37935	Abu37935 Protein e
698	5	35.7	426	8	ADU61643	Adu61643 Transcrip	771	5	35.7	485	6	ABU37322	Abu37322 Protein e
699	5	35.7	426	8	ADU42621	Adu42621 Bacterial	772	5	35.7	488	5	ABP39401	Abp39401 Staphyloc
700	5	35.7	428	2	AAU05332	Aay05332 Inflammat	773	5	35.7	488	8	ADU4592	Adu4592 Staphyloc
701	5	35.7	428	6	ABP71709	Abp71709 M161 anti	774	5	35.7	489	7	ADU74316	Adf74316 Human FCR
702	5	35.7	428	7	ADK68538	Adk68538 Mycoplasma	775	5	35.7	490	2	AAU05375	Aay05375 Human HCM
703	5	35.7	428	7	ADK68531	Adk68531 Mycoplasma	776	5	35.7	490	7	ADU76387	Adf76387 Novel hum
704	5	35.7	429	2	AAU22727	Aaw22727 Membrane	777	5	35.7	490	8	ADU75340	Adj75340 Marker ge
705	5	35.7	430	4	ABM60505	Abm60505 Drosophil	778	5	35.7	490	8	ADL61272	Adl61272 Human int
706	5	35.7	432	3	AAU48078	Aag48078 Arabidops	779	5	35.7	490	8	ADN06003	Adn06003 Antipsoi
707	5	35.7	432	8	ADK60819	Adk60819 Lycopersi	780	5	35.7	490	8	ADO24395	Ado24395 Human PRO
708	5	35.7	432	8	ABM83798	Abm83798 Human dia	781	5	35.7	490	8	ADQ19383	Adq19383 Human sof
709	5	35.7	433	3	AAU41651	Aag41651 Arabidops	782	5	35.7	490	8	ADL14255	Adl14255 Human NF-
710	5	35.7	433	3	AAU43025	Aag43025 Arabidops	783	5	35.7	491	4	AAU33137	Aau33137 Novel hum
711	5	35.7	433	5	ABM92056	Abm92056 Herbicida	784	5	35.7	493	7	ABG75409	Abg75409 Xenopus B
712	5	35.7	433	6	ABR52885	Abd52885 Protein s	785	5	35.7	494	3	AAU44072	Aag44072 Arabidops
713	5	35.7	433	7	ADU79808	Adu79808 Mouse put	786	5	35.7	494	8	ADQ19013	Ado19013 Amino aci
714	5	35.7	433	7	ADK62398	Adk62398 Disease t	787	5	35.7	495	3	AAU94280	Aay94280 Corri hist
715	5	35.7	435	3	AAU29821	Aag29821 Arabidops	788	5	35.7	497	2	AAU74187	Aay74187 Human pro
716	5	35.7	436	2	AAU04391	Aay04391 Human ori	789	5	35.7	500	6	ABP78407	Abp78407 N. gonorr
717	5	35.7	436	8	ABM80350	Abm80350 Tumour-as	790	5	35.7	502	8	ADS42440	Ads42440 Bacterial
718	5	35.7	437	5	ABM97913	Abm97913 Human sec	791	5	35.7	503	6	AAO23320	Aao23320 Rhesus mo
719	5	35.7	437	8	ADN24334	Adn24334 Bacterial	792	5	35.7	503	6	AAO23312	Aao23312 Cynomolg
720	5	35.7	438	8	ADN01257	Adn01257 Farnesyl	793	5	35.7	503	6	ABU28414	Abu28414 Protein e
721	5	35.7	442	8	ADN04828	Adn04828 Antipsoi	794	5	35.7	504	3	ABU18228	Abu18228 Plasmodiu
722	5	35.7	442	8	ABM81629	Abm81629 Tumour-as	795	5	35.7	505	3	AAU17004	Aag17004 Arabidops
723	5	35.7	444	4	AAU40722	Aau40722 Human pol	796	5	35.7	505	6	AAO23316	Aao23316 Rhesus mo
724	5	35.7	445	6	ABU23382	Abu23382 Protein e	797	5	35.7	506	4	ABM64792	Abm64792 Drosophil
725	5	35.7	446	8	ADN73299	Adn73299 Thale cre	798	5	35.7	506	7	ADU75344	Adu75344 Putative
726	5	35.7	447	3	AAU74915	Aay74915 Neisseria	799	5	35.7	506	8	ADM74217	Adm74217 Human NOV
727	5	35.7	447	3	AAU41813	Aag41813 Arabidops	800	5	35.7	506	8	ADM74215	Adm74215 Human NOV
728	5	35.7	447	4	ABM61990	Abm61990 Drosophil	801	5	35.7	506	8	ADR14579	Adr14579 Human NF-
729	5	35.7	447	7	ADM64482	Adm64482 human zin	802	5	35.7	506	8	ADS24106	Ads24106 Bacterial
730	5	35.7	448	8	ADS23705	Ads23705 Bacterial	803	5	35.7	507	4	AAU96433	Aau96433 Putative
731	5	35.7	451	3	AAU74916	Aay74916 Neisseria	804	5	35.7	508	4	AAU82317	Aau82317 Human imm
732	5	35.7	451	3	AAU74914	Aay74914 Neisseria	805	5	35.7	508	7	ADM35239	Adm35239 Human LY1
733	5	35.7	451	3	AAU43024	Aag43024 Arabidops	806	5	35.7	508	7	ADM35264	Adm35264 Human LY1
734	5	35.7	451	5	ABM79400	Abm79400 Taxane sy	807	5	35.7	508	8	ADR89715	Adr89715 Human can
735	5	35.7	451	6	ABU40758	Abu40758 Protein e	808	5	35.7	508	8	ADL06539	Adl06539 Human tum
736	5	35.7	453	4	ABM59823	Abm59823 Drosophil	809	5	35.7	509	2	AAU43215	Aay43215 Bacillus
737	5	35.7	455	7	ADU31345	Adu31345 Human nov	810	5	35.7	509	2	AAU14138	Aay14138 Zea may
738	5	35.7	456	4	AAU35277	Aau35277 Enterooc	811	5	35.7	509	3	AAU44603	Aay44603 Maize MLO
739	5	35.7	457	6	ABP80604	Abp80604 N. gonorr	812	5	35.7	509	5	ABP73880	Abp73880 Candida a
740	5	35.7	458	3	AAU41812	Aag41812 Arabidops	813	5	35.7	509	5	ABP73880	Abp73880 Candida a
741	5	35.7	459	6	ABM71447	Abm71447 Staphyloc	814	5	35.7	510	3	AAU17003	Aag17003 Arabidops
742	5	35.7	460	7	ADM35273	Adm35273 Human LY1	815	5	35.7	511	3	AAU52005	Aag52005 Arabidops
743	5	35.7	464	6	ABU20568	Abu20568 Protein e	816	5	35.7	511	4	AAU62624	Aag62624 Human cel
744	5	35.7	464	8	ADU28122	Adu28122 Bacterial	817	5	35.7	512	8	ABM83795	Abm83795 Human dia
745	5	35.7	465	5	ABG96348	Abg96348 Human ova	818	5	35.7	513	8	ADK13898	Adk13898 Human PSK
746	5	35.7	466	7	ABO61137	Abm61137 Klebsiell	819	5	35.7	518	7	ABO82898	Abm82898 Pseudomon
747	5	35.7	467	5	ABG96349	Abg96349 Human ova	820	5	35.7	520	8	ADR86188	Adr86188 Aspergill
748	5	35.7	468	6	ABU50430	Abu50430 Protein e	821	5	35.7	520	8	ADR86430	Adr86430 Aspergill
749	5	35.7	468	7	ADU39829	Adu39829 Protein s	822	5	35.7	527	2	AAU47207	Aau47207 Homo sapi
750	5	35.7	469	3	AAU48077	Aag48077 Arabidops	823	5	35.7	527	3	AAU29820	Aag29820 Arabidops
751	5	35.7	470	6	ABM69001	Abm69001 Phototrab	824	5	35.7	528	8	ADN37289	Adn37289 Barley st
752	5	35.7	470	8	ADJ37217	Adj37217 Human nuc	825	5	35.7	529	6	AAO23295	Aao23295 Chimpanze
753	5	35.7	471	8	ADN21925	Adn21925 Bacterial	826	5	35.7	530	6	AAO23292	Aao23292 Chimpanze
754	5	35.7	473	5	ABM47872	Abm47872 Listeria	827	5	35.7	531	6	AAO23298	Aao23298 Chimpanze
755	5	35.7	473	6	AAE32081	Aae32081 Human TRI	828	5	35.7	533	4	ABG25433	Abg25433 Novel hum

829	5	35.7	534	2	AAW46823	Aaw46823 Amino aci	902	5	35.7	651	8	ADO19010	Ado19010 P. falcip
830	5	35.7	534	2	AAW98948	Aaw98948 Streptoco	903	5	35.7	657	6	ABU24098	Abu24098 Protein e
831	5	35.7	534	2	ABP56647	Abp56647 Chimpanze	904	5	35.7	659	5	ABB92840	Abb92840 Herbicida
832	5	35.7	537	3	AAAG41863	Aag41863 Arabidops	905	5	35.7	659	8	ADM74209	Adm74209 Human NOV
833	5	35.7	537	3	ABU07374	Abu07374 Human pro	906	5	35.7	659	8	ADM74211	Adm74211 Human NOV
834	5	35.7	537	3	ADG39780	Adg39780 Human nov	907	5	35.7	660	3	RAY53006	Ray53006 Human sec
835	5	35.7	539	4	AGG92968	Agg92968 C glutami	908	5	35.7	664	3	AGG44071	Agg44071 Arabidops
836	5	35.7	541	2	AAW13827	Aaw13827 Yeast tra	909	5	35.7	666	8	ADN22473	Adn22473 Bacterial
837	5	35.7	555	6	ABRS5358	Abf53558 Protein s	910	5	35.7	667	6	ABU10028	Abu10028 Human fat
838	5	35.7	555	6	ADK64384	Adk64384 Disease t	911	5	35.7	671	8	ADJ76209	Adj76209 Marker ge
839	5	35.7	555	8	ADS44070	Ads44070 Bacterial	912	5	35.7	672	7	ADJ71022	Adj71022 Human hea
840	5	35.7	558	4	ABBS8367	Abbs8367 Drosophil	913	5	35.7	675	3	AGS54049	Agss54049 Arabidops
841	5	35.7	561	3	AGG48076	Agg48076 Arabidops	914	5	35.7	675	7	ADG48898	Adg48898 Rat Prote
842	5	35.7	566	6	ABRS5129	Abf51129 Protein s	915	5	35.7	677	4	ABB66295	Abb66295 Drosophil
843	5	35.7	566	7	ADK63560	Adk62560 Disease t	916	5	35.7	678	4	ABBS8061	Abbs8061 Drosophil
844	5	35.7	569	3	AAAG41862	Aag41862 Arabidops	917	5	35.7	683	7	ADB31865	Adb31865 Plant (A.
845	5	35.7	569	8	ADS43892	Ads43892 Bacterial	918	5	35.7	684	3	AGS54048	Agss54048 Arabidops
846	5	35.7	575	5	ADL28016	Adl28016 ECMCAD pr	919	5	35.7	684	7	ADC46645	Adc46645 Thalecres
847	5	35.7	575	7	ADG39828	Adg39828 Protein s	920	5	35.7	684	8	ADO02151	Ado02151 Thalecres
848	5	35.7	575	7	ADJ70095	Adj70095 Human hea	921	5	35.7	686	4	AAU35772	Aau35772 Helicobac
849	5	35.7	575	8	ABM81819	Abm81819 Tumour-as	922	5	35.7	690	2	AAAR04904	Aar04904 Residual
850	5	35.7	577	3	AAAG41861	Aag41861 Arabidops	923	5	35.7	690	2	AAW16337	Aaw16337 Bacillus
851	5	35.7	578	7	AAO23422	Aao23422 Human ade	924	5	35.7	690	2	AAW01787	Aaw01787 Residual
852	5	35.7	580	5	ABBS97845	Abbs97845 Human sec	925	5	35.7	692	8	ADN21871	Adn21871 Bacterial
853	5	35.7	582	3	ABP64785	Abp64785 Arabidops	926	5	35.7	702	7	ADC01364	Adc01364 Enterohaer
854	5	35.7	583	5	ABP65849	Abp65849 Bifidobac	927	5	35.7	704	2	AAW11843	Aaw11843 Full leng
855	5	35.7	585	5	ABP64785	Abp64785 Human pro	928	5	35.7	704	8	ADS42672	Ads42672 Bacterial
856	5	35.7	585	8	ADO66038	Ado66038 Novel hum	929	5	35.7	705	8	ADN24630	Adn24630 Bacterial
857	5	35.7	590	7	ABO64226	Abog64226 Klebsiell	930	5	35.7	708	4	ABBS93073	Abbs93073 Human pro
858	5	35.7	601	6	ADA47994	Ada47994 Rice prot	931	5	35.7	708	5	ADR41530	Adr41530 Human CD-
859	5	35.7	605	3	AGG39401	Agg39401 Arabidops	932	5	35.7	710	8	ADN73161	Adn73161 Thale cre
860	5	35.7	607	8	ADS21254	Ads21254 Bacterial	933	5	35.7	714	6	ABU28903	Abu28903 Protein e
861	5	35.7	610	2	AAAR84891	Aar84891 Peptide t	934	5	35.7	718	8	ADL05067	Adl05067 M. cattarr
862	5	35.7	614	6	ABU39093	Abu39093 Protein e	935	5	35.7	719	5	ABBS91485	Abbs91485 Herbicida
863	5	35.7	615	8	ADP30137	Adp30137 Human sec	936	5	35.7	723	7	ADC01430	Adc01430 Enterohaer
864	5	35.7	619	8	ADN17828	Adn17828 Bacterial	937	5	35.7	727	8	ADN22992	Adn22992 Bacterial
865	5	35.7	620	2	AAV08880	Aav08880 E. coli D	938	5	35.7	744	3	AAV71410	Aav71410 PDZ domai
866	5	35.7	620	2	AAV52832	Aav52832 Escherich	939	5	35.7	746	6	ADB09174	Adb09174 Alloioococ
867	5	35.7	620	3	AAV51613	Aav51613 E. coli D	940	5	35.7	749	8	ADL81892	Adl81892 P. aerugi
868	5	35.7	620	3	AAAB20544	Aab20544 Escherich	941	5	35.7	759	5	ABBP66048	Abbp66048 Bifidobac
869	5	35.7	620	4	AAU34475	Aau34475 E. coli c	942	5	35.7	761	6	ABU09176	Abu09176 Alloioococ
870	5	35.7	620	4	AAU38490	Aau38490 Salmonell	943	5	35.7	762	6	ABU45541	Abu45541 Protein e
871	5	35.7	620	5	AAU21860	Aau21860 Isoprenoi	944	5	35.7	765	5	ABP25599	Abp25599 Streptoco
872	5	35.7	620	6	ABU47495	Abu47495 Protein e	945	5	35.7	765	6	ABU44799	Abu44799 Protein e
873	5	35.7	620	6	ABU28526	Abu28526 Protein e	946	5	35.7	766	8	ADN48028	Adn48028 Thermococ
874	5	35.7	620	6	ABU28055	Abu28055 Protein e	947	5	35.7	769	5	ABP73280	Abp73280 Candida a
875	5	35.7	620	7	ADJ70006	Adj70006 Human hea	948	5	35.7	770	5	ABP66345	Abp66345 Bifidobac
876	5	35.7	620	8	ADS42744	Ads42744 Bacterial	949	5	35.7	776	8	ADN22830	Adn22830 Bacterial
877	5	35.7	620	8	ADN18078	Adn18078 Bacterial	950	5	35.7	777	7	ADI21291	Adi21291 Novel hum
878	5	35.7	621	3	AAAG54050	Aag54050 Arabidops	951	5	35.7	787	7	ABO77722	Abog77722 Pseudomon
879	5	35.7	622	6	ABM67144	Abm67144 Photorhab	952	5	35.7	793	6	ADB09178	Adb09178 Alloioococ
880	5	35.7	624	6	AAU41121	Aau41121 Protein e	953	5	35.7	793	7	ADM26691	Adm26691 Hyperther
881	5	35.7	625	5	AAO21862	Aao21862 Isoprenoi	954	5	35.7	793	8	ADS44026	Ads44026 Bacterial
882	5	35.7	625	6	ABU30592	Abu30592 Protein e	955	5	35.7	795	4	AAU34003	Aau34003 Staphyloc
883	5	35.7	625	6	ABP98825	Abp98825 Human str	956	5	35.7	804	5	ABBS91419	Abbs91419 Herbicida
884	5	35.7	626	6	ABU49247	Abu49247 Protein e	957	5	35.7	813	4	ABG08850	Abg08850 Novel hum
885	5	35.7	626	7	ABO66596	Abog66596 Klebsiell	958	5	35.7	818	6	ABU54627	Abu54627 Human NOV
886	5	35.7	628	7	ADP44509	Adp44509 Mouse kin	959	5	35.7	818	7	ADC37207	Adc37207 Nuclear f
887	5	35.7	629	8	ADN17945	Adn17945 Bacterial	960	5	35.7	819	6	ABU18425	Abu18425 Protein e
888	5	35.7	630	6	ABP81628	Abp81628 Streptoco	961	5	35.7	837	7	ADL22743	Adl22743 Human dis
889	5	35.7	631	4	ABBS5327	Abbs5327 R. ruber	962	5	35.7	840	7	ABO65205	Abog65205 Klebsiell
890	5	35.7	631	5	ABP26603	Abp26603 Streptoco	963	5	35.7	848	8	ADI40974	Adi40974 Goldfish
891	5	35.7	631	5	ABP26604	Abp26604 Streptoco	964	5	35.7	848	8	ADI41018	Adi41018 Goldfish
892	5	35.7	638	7	ADK64166	Adk64166 Disease t	965	5	35.7	858	8	ADJ49940	Adj49940 Oil-assoc
893	5	35.7	638	8	ADN19338	Adn19338 Bacterial	966	5	35.7	862	4	ABB60042	Abb60042 Drosophil
894	5	35.7	641	8	ADM74213	Adm74213 Human NOV	967	5	35.7	862	4	ABB60440	Abb60440 Drosophil
895	5	35.7	644	4	ABG06230	Abg06230 Novel hum	968	5	35.7	862	4	ABB60445	Abb60445 Drosophil
896	5	35.7	645	7	ADF05855	Adf05855 Bacterial	969	5	35.7	862	4	ABB60449	Abb60449 Drosophil
897	5	35.7	648	6	ADA36595	Ada36595 Acinetoba	970	5	35.7	862	8	ADQ89574	Adq89574 Antagonis
898	5	35.7	650	6	ASU02116	Asu02116 S. pneumo	971	5	35.7	876	6	ADA13336	Ada13336 Human int
899	5	35.7	650	8	ADK46706	Adk46706 Streptoco	972	5	35.7	878	6	ABM69030	Abm69030 Photorhab
900	5	35.7	650	8	ADR94880	Adr94880 Novel S.	973	5	35.7	878	6	ADR83889	Adr83889 Human WOC
901	5	35.7	651	8	ADO19012	Ado19012 Amino aci	974	5	35.7	878	8	ADQ80380	Adq80380 Mucin 3B

975 5 35.7 883 6 ABM69376 Photorhab
976 5 35.7 885 6 ABM69449 Photorhab
977 5 35.7 887 4 ABM39431 Human pol
978 5 35.7 887 6 ABU54626 Human NOV
979 5 35.7 887 6 ABU40971 Protein e
980 5 35.7 888 5 AAU83013 Human hom
981 5 35.7 888 8 ADO79411 KIAA0783
982 5 35.7 889 8 ADJ50234 Oil-assoc
983 5 35.7 891 4 AAU34554 E. coli c
984 5 35.7 891 6 ABU28609 Protein e
985 5 35.7 891 6 ABU49944 Protein e
986 5 35.7 892 4 AAU38250 Salmonell
987 5 35.7 892 6 ABU47096 Protein e
988 5 35.7 892 6 ABU48057 Protein e
989 5 35.7 894 6 ABU49454 Protein e
990 5 35.7 894 7 ADF04439 Bacterial
991 5 35.7 898 7 ABO63805 Klebsiell
992 5 35.7 901 4 AAU41217 Human pol
993 5 35.7 901 6 ABU15843 Protein e
994 5 35.7 904 4 AAU36814 Staphyloc
995 5 35.7 904 6 ABM71629 Staphyloc
996 5 35.7 906 7 ADC96823 E. faeciu
997 5 35.7 910 8 ADI45391 Rice isop
998 5 35.7 913 6 ABU54625 Human NOV
999 5 35.7 943 5 ABG91056 Neisseria
1000 5 35.7 943 8 ADP08381 Neisseria

ALIGNMENTS

RESULT 1
AAW21966
ID AAW21966 standard; protein; 14 AA.
AC AAW21966;
XX
XX
DT 02-DEC-1997 (first entry)
XX
DE Human cyclin I peptide fragment.
XX
KW human; cyclin I; antisense; probe; neurone; cancer; antibody.
XX
XX Homo sapiens.
XX
XX WO9712973-A1.
XX
XX 10-APR-1997.
XX
XX 07-OCT-1996; 96WO-JP002905.
XX
XX 05-OCT-1995; 95JP-00284663.
XX
XX (SUME) SUMITOMO ELECTRIC IND CO.
XX
XX Nakamura T;
XX
XX WPI; 1997-226217/20.
XX
XX Human cyclin I protein and related (anti:sense) DNA - used for neuron
PT labelling method and cancer cell detection.
XX
XX Claim 7; Page 30; 45pp; Japanese.
XX
XX This peptide is a fragment of human cyclin I which can be specifically
CC recognised by antibodies of the invention. The antibodies are used to
CC detect the presence of cyclin I. Antisense cyclin I polynucleotides are
CC useful for as probes and can be labelled and used for detection of
CC neurones by hybridisation with mRNA for cyclin I (contained in the
CC neurones and arising by the expression of the cyclin I gene in these
CC cells). The gene can be used for detection of cancer cells by detecting
CC the expression of the cyclin I gene in these cells

SQ Sequence 14 AA;
Query Match 100.0%; Score 14; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EDNVSENVGSVCCT 14
Db 1 EDNVSENVGSVCCT 14
|||||
RESULT 2
ADN01131
ID ADN01131 standard; protein; 300 AA.
XX
AC ADN01131;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human cell growth, differentiation, and death-associated protein #15.
XX
KW human; cell growth; cell differentiation; cell death; CGDD;
KW cell proliferative disorder; arteriosclerosis; atherosclerosis; bursitis;
KW cirrhosis; hepatitis; polycythaemia vera; psoriasis; cancer;
KW developmental disorder; Cushing's syndrome; hypothyroidism;
KW neurological disorder; epilepsy; stroke; Alzheimer's disease;
KW Pick's disease; Huntington's disease; Parkinson's disease;
KW multiple sclerosis; autoimmune disorder; inflammatory disorder; AIDS;
KW allergy; anaemia; asthma; contact dermatitis; diabetes mellitus;
KW reproductive disorder; infertility; endometriosis; uterine fibroid.
XX
XX Homo sapiens.
XX
XX WO2004031364-A2.
XX
XX 15-APR-2004.
XX
XX 03-OCT-2003; 2003WO-US031441.
XX
XX 03-OCT-2002; 2002US-0416205P.
XX
XX 25-OCT-2002; 2002US-0421521P.
XX
XX 21-NOV-2002; 2002US-0428376P.
XX
XX 23-DEC-2002; 2002US-0436258P.
XX
XX 10-JAN-2003; 2003US-0439292P.
XX
XX 13-FEB-2003; 2003US-0447578P.
XX
XX (INCY-) INCYTE CORP.
XX
XX (BURR/) BURRILL J D.
XX
XX Elliott VS, Swarnakar A, Tang YT, Yue H, Lu DAM, Khare R;
XX Chawla NK, Richardson TW, Marquis JP, Lal PG, Nguyen DB, Lee SY;
XX Tran UK, Bhatia UG, Lee S, Blake JJ, Ho A, Zheng W, Gao J, Tran B;
XX Yang YG, Gietzen KJ, Hafalia AJA;
XX
XX WPI; 2004-330172/30.
XX
XX N-PSDB; ADN01156.
XX
XX New isolated polypeptides associated with cell growth, differentiation
PT and death, useful for diagnosing, treating or preventing e.g.
PT atherosclerosis, psoriasis, cancers, Alzheimer's disease, AIDS, anemia,
PT diabetes mellitus or infertility.
XX
XX Claim 1; SEQ ID NO 15; 213pp; English.
XX
XX The invention comprises the amino acid and coding sequences of human
CC proteins that are associated with cell growth, differentiation, and death
CC (CGDD). The DNA and protein sequences of the invention are useful for
CC diagnosing, treating or preventing disorders associated with aberrant
CC expression of CGDD, such as: cell proliferative disorders (e.g.
CC arteriosclerosis, atherosclerosis, bursitis, cirrhosis, hepatitis,
CC polycythaemia vera, psoriasis and cancers), developmental disorders (e.g.
CC Cushing's syndrome and hypothyroidism), neurological disorders (e.g.
CC epilepsy, stroke, Alzheimer's disease, Pick's disease, Huntington's

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDNVSENVGVCVT 14
|||||
DB 343 EDNVSENVGVCVT 356

RESULT 5
ID AAY52185 standard; protein; 377 AA.
XX
AC AAY52185;
XX

DT 09-FEB-2000 (first entry)
XX

DE Human cyclin I amino acid sequence.
XX

KW Cyclin-dependent kinase 2; CDK2; hsReq; hsReq*-1; hsReq*-2; cyclin I;
KW ERH; cell cycle; proliferation; cancer; hyperproliferative disorder;
KW atherosclerosis; tumour.
XX

OS Homo sapiens.
XX

FN WO9925829-A2.
XX

PD 27-MAY-1999.
XX

PF 12-NOV-1998; 98WO-US024095.
XX

PR 13-NOV-1997; 97US-00969106.
XX

PA (CURA-) CURAGEN CORP.
XX

PI Yang M, Nandabalan K, Schulz VP;
XX

DR WPI; 2000-061923/05.
XX

PT N-PSDB; AAZ37836.
XX

XX New complexes of the cyclin-dependent kinase 2 protein with its
interacting proteins, used to treat, e.g. atherosclerosis.
PT

PS Example; Fig 2; 90pp; English.
XX

CC This is the human Cyclin I amino acid sequence. Cyclin I is expressed at
almost constant levels throughout the cell cycle, and is implicated in
controlling cell cycle progression and transcriptional control. Cyclins
form complexes with cyclin-dependent kinases. CDK2, cyclin-dependent
kinase 2, is used in the invention which relates to complexes of the CDK2
protein with other proteins, selected from cyclin I, ERH, hsReq, hsReq*-1
and hsReq*-2 (AAY52185-Y52188). CDK2 is expressed late in G1 or early in
S phase of the cell cycle, and is pivotal for G1/S transition.
CC Compositions containing a CDK2 complex, an antibody targeting the
complex, and nucleotide sequences encoding CDK2 or its derivatives can be
used therapeutically. The complexes and their nucleotide sequences can be
used to treat diseases or disorders associated with increased or
decreased levels of the complex. Screening the complex, or a derivative
or a modulator of the complex for neoplastic activity by measuring the
survival or proliferation of cells from a malignant cell line when in
contact with the complex can be used to indicate if the complex has
anti-neoplastic activity. Screening for molecules that modulate the
formation of the complexes can be used for treating or preventing
atherosclerosis or atherosclerosis-associated disease by contacting cells
or using a test animal, in which tumour growth or regression is measured
to test whether anti-neoplastic activity is displayed. Diseases which can
be treated or prevented by molecule/s which modulate the function of the
complex include cancer, hyperproliferative disorders and atherosclerosis
XX

XX Sequence 377 AA;

Query Match 100.0%; Score 14; DB 3; Length 377;
Best Local Similarity 100.0%; Pred. No. 1.8e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDNVSENVGVCVT 14
|||||
DB 343 EDNVSENVGVCVT 356

RESULT 6
ABR3934

ID ABR3934 standard; protein; 377 AA.
XX

AC ABR3934;
XX

DT 11-AUG-2003 (first entry)
XX

DE Human prostate selective polypeptide Pr325.
XX

KW Prostate; molecular marker; cancer; cytostatic; gene therapy; human.
XX

OS Homo sapiens.
XX

FN WO2003014298-A2.
XX

PD 20-FEB-2003.
XX

PF 02-AUG-2002; 2002WO-US024431.
XX

PR 03-AUG-2001; 2001US-0309470P.
XX

PR 30-OCT-2001; 2001US-0330747P.
XX

PA (ORIG-) ORIGENE TECHNOLOGIES INC.
XX

PI Sun Z, Li X, Jay G, Kovacs KF, Shu Y, Fan W;
XX

DR WPI; 2003-256562/25.
XX

PT N-PSDB; ACC47339.
XX

XX New polynucleotide, useful for preparing a composition for treating
prostate disease, e.g., cancer.
PT

PS Claim 5; Page 147-149; 212pp; English.
XX

CC The invention relates to prostate selective polynucleotides and
polypeptides. The polynucleotides are expressed in prostate and are
useful as molecular markers, as drug targets, and for detecting,
CC monitoring, preventing or treating diseases and conditions related to
prostate, such as prostate cancers. The present sequence represents a
prostate specific polypeptide
XX

SQ Sequence 377 AA;

Query Match 100.0%; Score 14; DB 6; Length 377;
Best Local Similarity 100.0%; Pred. No. 1.8e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDNVSENVGVCVT 14
|||||
DB 343 EDNVSENVGVCVT 356

RESULT 7
ADP12615

ID ADP12615 standard; protein; 377 AA.
XX

AC ADP12615;
XX

DT 12-AUG-2004 (first entry)
XX

DE Protein encoded by mRNA of the invention #225.
XX

XX transplant rejection; immune system; rheumatoid arthritis; lupus;
KW inflammatory bowel disease; multiple sclerosis; HIV; AIDS.
XX
OS Homo sapiens.
XX

PN WO2004042346-A2.
PD 21-MAY-2004.
XX
XX 24-APR-2003; 2003WO-US012946.
XX
XX 24-APR-2002; 2002US-00131831.
PR 20-DEC-2002; 2002US-00325899.
XX
XX (EXPR-) EXPRESSION DIAGNOSTICS INC.
XX
XX Wohlgenuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;
PI Rosenberg S;
PI
XX WPI; 2004-400724/37.
XX
XX Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,
PT pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
PT rejection, in an individual, comprises detecting the expression level of
PT the genes.
XX
XX Claim 65; SEQ ID NO 2624; 1762pp; English.
XX
XX The present invention relates to diagnosing or monitoring transplant
CC rejection, e.g. cardiac or kidney transplant rejection, in an individual
CC comprises detecting the expression level of one or more genes. The
CC methods, system and kits are useful in diagnosing or monitoring
CC transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
CC islet, lung, bone marrow or stem cell transplant rejection,
CC xenotransplant rejection or mechanical organ replacement rejection, in an
CC individual. The method is also useful in assessing the immune status of
CC an individual. The methods are also useful in diagnosing and monitoring
CC diseases that involve the immune system, e.g. rheumatoid arthritis,
CC lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
CC viral, bacterial or fungal infection. The present sequence represents a
CC protein that is encoded by the mRNA of the invention.
XX
XX Sequence 377 AA;
SQ
Query Match 100.0%; Score 14; DB 8; Length 377;
Best Local Similarity 100.0%; Pred. No. 1.8e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EDNVSENVGVCVGT 14
Db 343 EDNVSENVGVCVGT 356
|||||
RESULT 8
ABM80569
ID ABM80569 standard; protein; 377 AA.
XX
XX AC ABM80569;
XX
XX 18-NOV-2004 (first entry)
DT
XX
XX Tumour-associated antigenic target (TAT) polypeptide PRO4605, SEQ.1450.
DE
XX
XX Tumour-associated antigenic target; TAT; human; overexpression; cancer;
KW tumour; diagnosis; cell proliferative disorder; breast cancer;
KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;
KW central nervous system cancer; bladder cancer; pancreatic cancer;
KW cervical cancer; melanoma; leukaemia; hybridisation probe;
KW chromosome identification; chromosome mapping; gene mapping;
KW gene therapy; cytostatic.
XX
XX Homo sapiens.
OS
XX
XX WO2004030615-A2.
PN
XX
XX 15-APR-2004.
PD
XX
XX 29-SEP-2003; 2003WO-US028547.
PF

XX 02-OCT-2002; 2002US-0414971P.
PR
XX (GETH) GENENTECH INC.
XX
XX Wu TD, Zhang Z, Zhou Y;
PI
XX WPI; 2004-347921/32.
DR
XX N-PSDB; ACN38124.
XX
XX New tumor-associated antigenic target polypeptides and nucleic acids,
PT useful in preparing a medicament for treating or detecting a
PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or
PT prostate cancer or tumor.
XX
XX Claim 12; SEQ ID NO 1450; 7273pp; English.
XX
XX The invention relates to human tumour-associated antigenic target (TAT)
CC polypeptides, and their related nucleic acids. The TAT polypeptides are
CC overexpressed in cancer tissues compared to normal tissues, and may thus
CC serve as effective targets for the diagnosis and treatment of cancer in
CC mammals. The invention also relates to nucleic acid and polypeptide
CC sequences at least 80% identical to the TAT nucleic acids and
CC polypeptides; expression vectors and host cells comprising a TAT nucleic
CC acid; an antibody specific for a TAT polypeptide; a peptide or organic
CC molecule which binds to a TAT polypeptide; fusion proteins comprising a
CC TAT polypeptide; and methods and compositions for the treatment or
CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
CC antibodies, antagonists, binding molecules and compositions are useful
CC for diagnosing or treating a cell proliferative disorder associated with
CC increased TAT expression, particularly cancers such as breast cancer,
CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
CC cancer, pancreatic cancer, cervical cancer, cancers of the central
CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be
CC used as hybridisation probes, in chromosome and gene mapping, in
CC chromosome identification and in gene therapy. The present sequence
CC represents a TAT polypeptide of the invention
XX
XX Sequence 377 AA;
SQ
Query Match 100.0%; Score 14; DB 8; Length 377;
Best Local Similarity 100.0%; Pred. No. 1.8e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EDNVSENVGVCVGT 14
Db 343 EDNVSENVGVCVGT 356
|||||
RESULT 9
ABP35708
ID ABP35708 standard; protein; 446 AA.
XX
XX AC ABP35708;
XX
XX 24-JUL-2002 (first entry)
DT
XX
XX Fungal ZBC protein sequence #134.
DE
XX
XX Secondary metabolite; fungus; ZBC gene; zinc binuclear cluster protein;
KW antibacterial; beta-lactam; anti-hypercholesterolaemic; lovastatin;
KW mevastatin; immunosuppressant; cyclosporin A; ergot alkaloid; ergotamine;
KW angiogenesis inhibitor; ovalicin; glucan synthase inhibitor; gliotoxin;
KW fungal toxin; cell surface receptor; plant growth regulator; pigment;
KW insecticide; antineoplastic.
XX
XX Unidentified.
OS
XX
XX WO200224865-A2.
PN
XX
XX 28-MAR-2002.
PD
XX
XX 19-SEP-2001; 2001WO-US029288.
PF

CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB116176-AB130511), expressed DNA
 CC sequences (AB101840-AB116175) and the encoded proteins (AB157737-
 CC AB172072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 556 AA;

Query Match 50.0%; Score 7; DB 4; Length 556;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VGSVCGT 14
 |||||
 Db 131 VGSVCGT 137

RESULT 12
 ABP78187
 ID ABP78187 standard; protein; 1068 AA.
 XX
 AC ABP78187;
 XX
 XX 07-MAR-2003 (first entry)
 XX
 DE N. gonorrhoeae amino acid sequence SEQ ID 2904.
 XX
 KW Antibacterial; infection; vaccine; gene therapy.
 XX
 OS Neisseria gonorrhoeae.
 XX
 XX WO200279243-A2.
 PN
 XX 10-OCT-2002.
 PD
 XX 12-FEB-2002; 2002WO-IB002069.
 PP
 XX 12-FEB-2001; 2001GB-00003424.
 PR
 XX (CHIR-) CHIRON SPA.
 PA
 XX Fontana MR, Pizza M, Masignani V, Monaci E;
 PI
 XX WPI; 2003-058415/05.
 DR
 DR N-PSDB; ABZ39157.

XX New protein from Neisseria gonorrhoeae, useful for the manufacture of a
 PT medicament for treating or preventing N. gonorrhoeae infection.
 PT
 XX Disclosure; Page 401; 815pp; English.
 PS
 XX The present invention relates to proteins from Neisseria gonorrhoeae.
 CC Also disclosed are the nucleic acid molecules encoding the proteins and
 CC antibodies that specifically bind to the proteins. The composition
 CC comprising the protein, nucleic acid or antibody is useful for the
 CC manufacture of a medicament for treating or preventing N. gonorrhoeae
 CC infection, this may be in the form of a vaccine or gene therapy.
 CC Sequences given in records ABP76736-ABP81046 represent nucleic acid
 CC molecules of the invention
 XX

XX Sequence 1068 AA;
 SQ
 Query Match 50.0%; Score 7; DB 6; Length 1068;
 Best Local Similarity 100.0%; Pred. No. 61;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 SENVGSV 11
 |||||
 Db 317 SENVGSV 323

RESULT 13

ADS29513
 ID ADS29513 standard; protein; 1190 AA.

XX
 AC ADS29513;
 XX
 DT 02-DEC-2004 (first entry)
 XX
 DE Bacterial polypeptide #18546.

XX Recombinant DNA construct; transformed plant; improved plant property;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
 KW pathogen tolerance; pest tolerance; plant disease resistance;
 KW cell cycle pathway modification; plant growth regulator;
 KW homologous recombination; seed oil yield; protein yield; carbohydrate;
 KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
 KW bacterial polypeptide.
 XX
 OS Bacteria.

XX US2003233675-A1.
 PN
 XX 18-DEC-2003.
 PD
 XX 20-FEB-2003; 2003US-00369493.
 PP
 XX 21-FEB-2002; 2002US-0360039P.
 PR

XX (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.

XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
 PI WPI; 2004-061375/06.
 DR
 XX New recombinant DNA construct comprising a promoter positioned to provide
 PT for expression of a polynucleotide encoding a polypeptide from a
 PT microbial source, useful for producing plants with improved properties.
 XX
 PS Claim 1; SEQ ID NO 18546; 122pp; English.

XX The invention relates to a recombinant DNA construct comprising a
 CC promoter functional in a plant cell, where the promoter is positioned to
 CC provide for expression of a polynucleotide encoding a polypeptide from a
 CC microbial source. The invention also relates to a transformed plant
 CC comprising the recombinant DNA construct and a method of producing a
 CC transformed plant having an improved property. The plant is a crop plant
 CC such as maize or soybean. The method of producing a transformed plant
 CC having an improved property comprises transforming a plant with the
 CC recombinant DNA construct and growing the transformed plant, where the
 CC polynucleotide or polypeptide is useful for improving plant properties.
 CC The recombinant DNA construct is useful for producing plants with
 CC improved plant properties, e.g. improved cold, heat or drought tolerance,
 CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
 CC increased resistance to plant disease, better growth rate by modification
 CC of the cell cycle pathway with plant growth regulators, increased rate of
 CC homologous recombination, modified seed oil or protein yield and/or
 CC content, improved yield by modification of carbohydrate, nitrogen or
 CC phosphorus use and/or uptake, by modification of photosynthesis or by
 CC providing improved plant growth and development under at least one stress
 CC condition, improved lignin production or improved galactomannan
 CC production. This sequence represents a bacterial polypeptide used in the
 CC scope of the invention. Note: The sequence data for this patent did not
 CC form part of the printed specification but was obtained in electronic
 CC format from USPTO at seqdata.uspto.gov/sequence.html.

XX Sequence 1190 AA;
 SQ
 Query Match 50.0%; Score 7; DB 8; Length 1190;
 Best Local Similarity 100.0%; Pred. No. 67;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      5 SENVGSV 11
Db      106 SENVGSV 112

RESULT 14
AAR74214
ID AAR74214 standard; peptide; 13 AA.
AC AAR74214;
XX
XX 25-MAR-2003 (revised)
DT 25-OCT-1995 (first entry)
XX
XX Internal fragment of bryodin-2.
XX
XX Ribosome inactivating protein; cell death; proliferation; tumour; cancer;
KW virus; malaria; trypanosomiasis; inflammation; autoimmune; disease;
KW purging; bone marrow.
XX
XX Bryonia dioica.
OS
XX WO9511977-A2.
XX
XX 04-MAY-1995.
XX
XX 25-OCT-1994; 94WO-US012382.
XX
XX 25-OCT-1993; 93US-00141891.
PR 20-OCT-1994; 94US-00324301.
XX
XX (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
XX Siegall CB, Gawlak SL, Marquardt H;
XX WPI; 1995-178870/23.
XX
XX New ribosome inactivating protein bryodin-2 and related conjugates - for
PT killing target cells, e.g. in treatment of cancer, also related nucleic
PT acid, vectors and transformed cells.
XX
XX Claim 4; Page 61; 81pp; English.
XX
XX The sequence is that of a fragment of a ribosome inactivating protein
CC termed bryodin-2, isolated from Bryonia dioica. Conjugates of the protein
CC with a ligand may be used to kill target cells (i.e. those to which the
CC ligand component binds specifically) or to inhibit proliferation of
CC tumour cells. Typical applications include the treatment of cancer, viral
CC infections, malaria, trypanosomiasis, inflammatory or autoimmune
CC diseases, including in vitro purging of e.g. bone marrow. See also
CC AAR74210-7. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 13 AA;

Query Match 42.9%; Score 6; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 VSENVG 9
Db      6 VSENVG 11

RESULT 15
ABG23791
ID ABG23791 standard; protein; 63 AA.
XX
XX ABG23791;
AC
XX 18-FEB-2002 (first entry)
DT
XX
XX Novel human diagnostic protein #23782.
DE
```

```
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
XX Homo sapiens.
OS
XX WO200175067-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US008631.
XX
XX 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
XX (HYSE-) HYSEQ INC.
PA
XX
XX Dmanac RT, Liu C, Tang YT;
XX WPI; 2001-639362/73.
XX N-PSDB; AAS87978.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
XX Claim 20; SEQ ID NO 54150; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 63 AA;

Query Match 42.9%; Score 6; DB 4; Length 63;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      8 VGSVCG 13
Db      30 VGSVCG 35

Search completed: February 11, 2005, 03:16:41
Job time : 41.9386 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 11, 2005, 03:11:39 ; Search time 1.21739 Seconds
(without alignments)
858.464 Million cell updates/sec

Title: US-09-736-250-5

Perfect score: 14

Sequence: 1 EDVSNVSGVCGT 14

Scoring table:

OLIGO Gapop 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

Word size : 0

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

Issued Patents AA.*
1: /cgm2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgm2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgm2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgm2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgm2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgm2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	14	100.0	14	3	US-09-054-492B-5
2	14	100.0	377	2	US-08-969-106-6
3	14	100.0	377	3	US-09-054-492B-1
4	14	100.0	377	4	US-09-338-125-6
5	7	50.0	446	4	US-09-538-092-781
6	6	42.9	13	1	US-08-324-301-5
7	6	42.9	282	1	US-08-324-301-15
8	6	42.9	1033	4	US-08-834-309-1
9	6	42.9	1066	3	US-09-541-782-8
10	6	42.9	1066	4	US-09-723-820-8
11	6	42.9	1066	4	US-10-270-085-8
12	6	42.9	1415	4	US-09-252-991A-26438
13	6	42.9	2362	4	US-09-949-016-8985
14	6	42.9	4544	1	US-08-469-486-52
15	6	42.9	4544	2	US-08-469-658-52
16	5	35.7	61	4	US-09-540-236-3067
17	5	35.7	65	4	US-09-107-433-4947
18	5	35.7	66	4	US-09-673-395A-264
19	5	35.7	68	4	US-09-562-737-131
20	5	35.7	70	4	US-09-107-532A-4592
21	5	35.7	70	4	US-09-107-532A-4593
22	5	35.7	87	4	US-09-328-352-4143
23	5	35.7	88	2	US-08-391-916A-10
24	5	35.7	91	4	US-09-489-039A-14306
25	5	35.7	94	4	US-09-465-558-20
26	5	35.7	97	4	US-09-562-737-126
27	5	35.7	98	4	US-09-543-681A-7281

28	5	35.7	104	4	US-09-465-558-24	Sequence 24, Appl
29	5	35.7	108	4	US-09-270-767-46391	Sequence 46391, A
30	5	35.7	109	3	US-08-936-165A-440	Sequence 440, App
31	5	35.7	112	4	US-09-543-681A-7275	Sequence 7275, Ap
32	5	35.7	113	4	US-09-949-016-9318	Sequence 9318, Ap
33	5	35.7	116	4	US-09-513-999C-5472	Sequence 5472, Ap
34	5	35.7	117	4	US-08-198-452A-951	Sequence 951, App
35	5	35.7	118	1	US-08-300-903A-13	Sequence 13, Appl
36	5	35.7	118	4	US-08-988-197-13	Sequence 13, Appl
37	5	35.7	118	4	US-10-385-072-13	Sequence 13, Appl
38	5	35.7	119	4	US-09-107-433-4937	Sequence 4937, Ap
39	5	35.7	120	4	US-09-543-681A-7262	Sequence 7262, Ap
40	5	35.7	124	4	US-09-328-352-5287	Sequence 5287, Ap
41	5	35.7	127	4	US-09-270-767-39006	Sequence 39006, A
42	5	35.7	127	4	US-09-270-767-54223	Sequence 54223, A
43	5	35.7	127	4	US-09-513-999C-4224	Sequence 4224, Ap
44	5	35.7	132	4	US-09-489-039A-11744	Sequence 11744, A
45	5	35.7	137	4	US-09-328-352-7715	Sequence 7715, Ap
46	5	35.7	149	4	US-09-513-999C-4257	Sequence 4257, Ap
47	5	35.7	158	4	US-09-270-767-32974	Sequence 32974, A
48	5	35.7	158	4	US-09-270-767-48191	Sequence 48191, A
49	5	35.7	162	3	US-08-078-271B-6	Sequence 6, Appli
50	5	35.7	163	2	US-08-783-395-5	Sequence 5, Appli
51	5	35.7	163	3	US-08-600-430-2	Sequence 2, Appli
52	5	35.7	163	3	US-08-600-430-4	Sequence 4, Appli
53	5	35.7	163	4	US-09-461-912A-44	Sequence 44, Appl
54	5	35.7	163	4	US-09-949-016-6077	Sequence 6077, Ap
55	5	35.7	164	4	US-09-248-796A-19361	Sequence 19361, A
56	5	35.7	168	4	US-09-270-767-34036	Sequence 34036, A
57	5	35.7	168	4	US-09-270-767-49253	Sequence 49253, A
58	5	35.7	169	4	US-08-248-796A-27591	Sequence 27591, A
59	5	35.7	174	4	US-09-949-016-11208	Sequence 11208, A
60	5	35.7	175	4	US-09-418-710-65	Sequence 65, Appl
61	5	35.7	175	4	US-09-839-479-64	Sequence 64, Appl
62	5	35.7	176	4	US-09-418-710-66	Sequence 66, Appl
63	5	35.7	176	4	US-09-839-479-65	Sequence 65, Appl
64	5	35.7	183	4	US-09-270-767-47315	Sequence 47315, A
65	5	35.7	185	4	US-09-543-681A-6449	Sequence 6449, Ap
66	5	35.7	186	4	US-09-125-635-2	Sequence 2, Appli
67	5	35.7	192	1	US-08-440-103-45	Sequence 45, Appl
68	5	35.7	192	1	US-08-440-542-45	Sequence 45, Appl
69	5	35.7	192	1	US-08-231-368-45	Sequence 45, Appl
70	5	35.7	192	3	US-08-440-210-45	Sequence 45, Appl
71	5	35.7	192	3	US-08-444-818-166	Sequence 166, App
72	5	35.7	192	3	US-09-046-604-45	Sequence 45, Appl
73	5	35.7	203	4	US-09-902-540-11721	Sequence 11721, A
74	5	35.7	204	4	US-09-562-737-127	Sequence 127, App
75	5	35.7	205	3	US-09-134-001C-4766	Sequence 4766, Ap
76	5	35.7	207	3	US-08-652-877-13	Sequence 13, Appl
77	5	35.7	207	3	US-08-476-515A-13	Sequence 13, Appl
78	5	35.7	212	4	US-09-328-352-5832	Sequence 5832, Ap
79	5	35.7	212	4	US-09-270-767-32098	Sequence 32098, A
80	5	35.7	213	3	US-09-156-579C-2	Sequence 2, Appli
81	5	35.7	225	1	US-08-300-903A-14	Sequence 14, Appl
82	5	35.7	225	4	US-10-385-072-14	Sequence 14, Appl
83	5	35.7	225	4	US-09-988-197-14	Sequence 14, Appl
84	5	35.7	227	4	US-09-270-767-39404	Sequence 39404, A
85	5	35.7	227	4	US-09-270-767-54621	Sequence 54621, A
86	5	35.7	231	4	US-09-402-515A-16	Sequence 16, Appl
87	5	35.7	232	2	US-08-738-413B-11	Sequence 11, Appl
88	5	35.7	234	1	US-08-684-862-3	Sequence 3, Appli
89	5	35.7	236	2	US-08-738-413B-12	Sequence 12, Appl
90	5	35.7	236	2	US-08-684-862-4	Sequence 4, Appli
91	5	35.7	236	2	US-08-684-862-5	Sequence 5, Appli
92	5	35.7	236	2	US-08-738-413B-10	Sequence 10, Appl
93	5	35.7	236	4	US-09-248-796A-16587	Sequence 16587, A
94	5	35.7	239	4	US-09-465-558-58	Sequence 58, Appl
95	5	35.7	245	4	US-09-248-796A-14382	Sequence 14382, A
96	5	35.7	247	4	US-09-270-767-43996	Sequence 43996, A
97	5	35.7	251	2	US-08-665-647-7	Sequence 7, Appli
98	5	35.7	258	4	US-09-538-092-728	Sequence 728, App
99	5	35.7	261	4	US-09-107-433-5013	Sequence 5013, Ap
100	5	35.7	262	4	US-09-465-558-62	Sequence 62, Appl

101	5	35.7	266	4	US-09-248-796A-17576	Sequence 17576, A	174	5	35.7	428	4	US-09-182-625F-9	Sequence 9, Appl
102	5	35.7	270	4	US-09-270-767-44001	Sequence 44001, A	175	5	35.7	428	4	US-09-182-625F-16	Sequence 16, Appl
103	5	35.7	271	4	US-09-252-991A-17292	Sequence 17292, A	176	5	35.7	432	4	US-09-103-331-40	Sequence 40, Appl
104	5	35.7	278	4	US-09-107-532A-6673	Sequence 6673, Ap	177	5	35.7	432	4	US-09-631-594-49	Sequence 49, Appl
105	5	35.7	289	4	US-09-252-991A-20221	Sequence 20221, A	178	5	35.7	433	4	US-09-248-796A-19799	Sequence 19799, A
106	5	35.7	289	4	US-09-543-681A-7998	Sequence 7998, Ap	179	5	35.7	436	3	US-09-150-213-4	Sequence 4, Appl
107	5	35.7	289	4	US-09-270-767-42634	Sequence 42634, A	180	5	35.7	448	4	US-09-949-016-9083	Sequence 9083, Ap
108	5	35.7	294	4	US-09-103-664A-5	Sequence 5, Appl	181	5	35.7	466	4	US-09-489-039A-7654	Sequence 7654, Ap
109	5	35.7	297	4	US-09-465-558-56	Sequence 56, Appl	182	5	35.7	474	4	US-09-081-385-148	Sequence 148, App
110	5	35.7	306	4	US-09-248-796A-16022	Sequence 16022, A	183	5	35.7	479	4	US-09-543-681A-7331	Sequence 7331, Ap
111	5	35.7	310	1	US-08-123-456A-37	Sequence 37, Appl	184	5	35.7	488	3	US-09-134-001C-4246	Sequence 4246, Ap
112	5	35.7	312	3	US-08-360-821B-36	Sequence 36, Appl	185	5	35.7	490	4	US-09-949-016-6091	Sequence 6091, Ap
113	5	35.7	312	4	US-09-851-026-36	Sequence 36, Appl	186	5	35.7	509	1	US-10-095-946-8	Sequence 8, Appl
114	5	35.7	313	4	US-09-583-110-4236	Sequence 4236, Ap	187	5	35.7	509	3	US-09-198-955A-6	Sequence 6, Appl
115	5	35.7	315	4	US-09-107-433-3706	Sequence 3706, Ap	188	5	35.7	509	3	US-09-183-959-8	Sequence 8, Appl
116	5	35.7	316	4	US-09-538-032-397	Sequence 397, App	189	5	35.7	509	3	US-09-694-531-6	Sequence 6, Appl
117	5	35.7	319	4	US-08-835-279-2	Sequence 2, Appl	190	5	35.7	509	4	US-09-347-650-6	Sequence 6, Appl
118	5	35.7	320	3	US-09-166-205B-64	Sequence 64, Appl	191	5	35.7	509	4	US-10-072-152-6	Sequence 6, Appl
119	5	35.7	320	4	US-09-806-658-2	Sequence 2, Appl	192	5	35.7	509	4	US-09-535-315-8	Sequence 8, Appl
120	5	35.7	320	4	US-09-949-016-7144	Sequence 7144, Ap	193	5	35.7	509	4	US-09-949-016-7965	Sequence 7965, Ap
121	5	35.7	323	4	US-09-710-693-2	Sequence 2, Appl	194	5	35.7	518	4	US-09-252-991A-31644	Sequence 31644, A
122	5	35.7	323	2	US-08-784-651-4	Sequence 4, Appl	195	5	35.7	526	3	US-09-342-648-8	Sequence 8, Appl
123	5	35.7	339	3	US-08-444-818-150	Sequence 150, App	196	5	35.7	530	4	US-09-248-796A-15021	Sequence 15021, A
124	5	35.7	339	3	US-08-444-818-158	Sequence 158, App	197	5	35.7	534	4	US-09-103-664A-2	Sequence 2, Appl
125	5	35.7	340	4	US-09-543-681A-5967	Sequence 5967, Ap	198	5	35.7	541	2	US-08-540-804-16	Sequence 16, Appl
126	5	35.7	345	4	US-09-902-540-12122	Sequence 12122, A	199	5	35.7	541	2	US-08-218-265-16	Sequence 16, Appl
127	5	35.7	349	4	US-09-270-767-45401	Sequence 45401, A	200	5	35.7	541	3	US-08-521-872-16	Sequence 16, Appl
128	5	35.7	350	4	US-09-818-780-95	Sequence 95, Appl	201	5	35.7	541	3	US-08-590-399-16	Sequence 16, Appl
129	5	35.7	353	3	US-08-134-001C-5511	Sequence 5511, Ap	202	5	35.7	590	4	US-09-489-039A-10743	Sequence 10743, A
130	5	35.7	354	4	US-09-328-352-3635	Sequence 3535, Ap	203	5	35.7	610	1	US-08-212-188-2	Sequence 2, Appl
131	5	35.7	354	4	US-08-248-796A-19050	Sequence 19050, A	204	5	35.7	610	3	PCT-US95-02708-2	Sequence 2, Appl
132	5	35.7	359	3	US-08-809-103B-2	Sequence 2, Appl	205	5	35.7	610	5	US-09-543-681A-6140	Sequence 6140, Ap
133	5	35.7	359	3	US-08-809-103B-4	Sequence 4, Appl	206	5	35.7	620	4	US-09-328-352-7882	Sequence 7882, Ap
134	5	35.7	359	3	US-08-809-103B-6	Sequence 6, Appl	207	5	35.7	626	4	US-09-583-110-3221	Sequence 3221, Ap
135	5	35.7	359	3	US-08-809-103B-8	Sequence 8, Appl	208	5	35.7	630	4	US-09-107-433-3515	Sequence 3515, Ap
136	5	35.7	362	4	US-08-691-861A-4	Sequence 4, Appl	209	5	35.7	631	4	US-08-849-480A-4	Sequence 4, Appl
137	5	35.7	362	4	US-09-634-238-417	Sequence 417, App	210	5	35.7	631	4	US-09-732-615-8	Sequence 8, Appl
138	5	35.7	362	4	US-09-248-796A-14994	Sequence 14994, A	211	5	35.7	645	4	US-09-543-681A-6140	Sequence 6140, Ap
139	5	35.7	366	4	US-09-248-796A-14679	Sequence 14679, A	212	5	35.7	648	4	US-09-328-352-7882	Sequence 7882, Ap
140	5	35.7	376	4	US-09-252-991A-19927	Sequence 19927, A	213	5	35.7	650	4	US-09-583-110-3221	Sequence 3221, Ap
141	5	35.7	376	4	US-09-252-991A-29172	Sequence 29172, A	214	5	35.7	650	4	US-09-107-433-3515	Sequence 3515, Ap
142	5	35.7	381	4	US-10-052-032-29	Sequence 29, Appl	215	5	35.7	686	2	US-08-849-480A-4	Sequence 4, Appl
143	5	35.7	382	2	US-08-555-268A-13	Sequence 13, Appl	216	5	35.7	704	3	US-08-792-832A-2	Sequence 2, Appl
144	5	35.7	395	3	US-08-991-426-2	Sequence 2, Appl	217	5	35.7	718	4	US-09-540-236-2753	Sequence 2753, Ap
145	5	35.7	395	3	US-09-143-470-2	Sequence 2, Appl	218	5	35.7	733	4	US-09-270-767-44442	Sequence 44442, A
146	5	35.7	395	4	US-09-771-023-8	Sequence 8, Appl	219	5	35.7	750	4	US-09-248-796A-14886	Sequence 14886, A
147	5	35.7	397	4	US-09-006-428A-2	Sequence 2, Appl	220	5	35.7	787	4	US-09-252-991A-26468	Sequence 26468, A
148	5	35.7	397	4	US-09-006-428A-19	Sequence 19, Appl	221	5	35.7	840	4	US-09-489-039A-11722	Sequence 11722, A
149	5	35.7	397	4	US-09-615-387C-2	Sequence 2, Appl	222	5	35.7	894	4	US-09-543-681A-4724	Sequence 4724, Ap
150	5	35.7	397	4	US-09-615-387C-19	Sequence 19, Appl	223	5	35.7	896	4	US-09-043-016A-13	Sequence 13, Appl
151	5	35.7	400	3	US-08-938-830-29	Sequence 29, Appl	224	5	35.7	898	4	US-09-489-039A-10322	Sequence 10322, A
152	5	35.7	404	4	US-09-182-625F-14	Sequence 14, Appl	225	5	35.7	906	4	US-09-107-532A-6450	Sequence 6450, Ap
153	5	35.7	404	4	US-09-182-625F-15	Sequence 15, Appl	226	5	35.7	941	3	US-09-074-658-75	Sequence 75, Appl
154	5	35.7	407	4	US-09-431-577-78	Sequence 78, Appl	227	5	35.7	941	3	US-08-476-515A-12	Sequence 12, Appl
155	5	35.7	408	2	US-08-924-847A-2	Sequence 2, Appl	228	5	35.7	944	2	US-08-867-941-23	Sequence 23, Appl
156	5	35.7	408	3	US-09-120-052-2	Sequence 2, Appl	229	5	35.7	944	2	US-08-867-941-24	Sequence 24, Appl
157	5	35.7	413	4	US-09-328-352-4227	Sequence 4227, Ap	230	5	35.7	944	3	US-09-074-658-23	Sequence 23, Appl
158	5	35.7	415	3	US-08-938-830-1	Sequence 1, Appl	231	5	35.7	944	3	US-09-074-658-24	Sequence 24, Appl
159	5	35.7	415	3	US-09-020-222-1	Sequence 1, Appl	232	5	35.7	944	3	US-08-652-877-12	Sequence 12, Appl
160	5	35.7	416	3	US-09-457-040B-10	Sequence 10, Appl	233	5	35.7	945	4	US-09-543-681A-4200	Sequence 4200, Ap
161	5	35.7	416	4	US-09-006-428A-1	Sequence 1, Appl	234	5	35.7	1034	4	US-09-562-737-43	Sequence 43, Appl
162	5	35.7	416	4	US-09-006-428A-17	Sequence 17, Appl	235	5	35.7	1036	4	US-09-248-796A-16128	Sequence 16128, A
163	5	35.7	416	4	US-09-710-693-1	Sequence 1, Appl	236	5	35.7	1147	3	US-08-470-260-5	Sequence 5, Appl
164	5	35.7	416	4	US-09-710-693-19	Sequence 19, Appl	237	5	35.7	1147	3	US-08-471-491-5	Sequence 5, Appl
165	5	35.7	416	4	US-09-615-387C-1	Sequence 1, Appl	238	5	35.7	1147	3	US-08-466-662-5	Sequence 5, Appl
166	5	35.7	416	4	US-09-615-387C-17	Sequence 17, Appl	239	5	35.7	1181	1	US-08-053-614-4	Sequence 4, Appl
167	5	35.7	424	2	US-08-532-214A-16	Sequence 16, Appl	240	5	35.7	1181	1	US-08-316-397B-4	Sequence 4, Appl
168	5	35.7	424	3	US-08-659-188-16	Sequence 16, Appl	241	5	35.7	1181	2	US-09-034-306-4	Sequence 4, Appl
169	5	35.7	424	3	US-08-655-227-16	Sequence 16, Appl	242	5	35.7	1181	3	US-09-259-437-4	Sequence 4, Appl
170	5	35.7	424	3	US-08-655-241-16	Sequence 16, Appl	243	5	35.7	1181	5	PCT-US93-09782-4	Sequence 4, Appl
171	5	35.7	424	3	US-09-149-976-16	Sequence 16, Appl	244	5	35.7	1222	4	US-09-206-942-37	Sequence 37, Appl
172	5	35.7	424	3	US-09-398-326-16	Sequence 16, Appl	245	5	35.7	1228	4	US-09-206-942-34	Sequence 34, Appl
173	5	35.7	424	4	US-09-853-450-16	Sequence 16, Appl	246	5	35.7	1302	4	US-09-949-016-10852	Sequence 10852, A

247	5	35.7	1311	2	US-08-540-406-4	Sequence 4, Appli	320	4	28.6	13	2	US-08-482-142-68	Sequence 68, Appli
248	5	35.7	1311	3	US-08-656-055-4	Sequence 4, Appli	321	4	28.6	13	2	US-08-478-572-68	Sequence 68, Appli
249	5	35.7	1311	3	US-08-954-668-4	Sequence 4, Appli	322	4	28.6	13	3	US-08-448-194-36	Sequence 36, Appli
250	5	35.7	1311	4	US-08-918-658-4	Sequence 4, Appli	323	4	28.6	13	3	US-08-484-296-68	Sequence 36, Appli
251	5	35.7	1311	4	US-08-724-631-4	Sequence 4, Appli	324	4	28.6	13	3	US-08-867-921-36	Sequence 36, Appli
252	5	35.7	1311	4	US-08-954-701A-4	Sequence 4, Appli	325	4	28.6	13	4	US-09-878-281A-249	Sequence 249, App
253	5	35.7	1311	5	PCT-US95-13233-4	Sequence 4, Appli	326	4	28.6	14	1	US-07-794-288D-21	Sequence 21, Appli
254	5	35.7	1402	4	US-09-125-635-12	Sequence 12, Appli	327	4	28.6	14	1	US-07-794-288D-42	Sequence 42, Appli
255	5	35.7	1402	4	US-09-445-335E-2	Sequence 2, Appli	328	4	28.6	14	1	US-08-487-890A-49	Sequence 49, Appli
256	5	35.7	1420	4	US-09-125-635-4	Sequence 4, Appli	329	4	28.6	14	2	US-08-478-435-49	Sequence 49, Appli
257	5	35.7	1447	3	US-09-376-330-17	Sequence 17, Appli	330	4	28.6	14	2	US-08-337-483-49	Sequence 49, Appli
258	5	35.7	1463	4	US-09-949-016-11696	Sequence 11696, A	331	4	28.6	14	2	US-08-478-373-49	Sequence 49, Appli
259	5	35.7	1464	3	US-08-891-640-2	Sequence 2, Appli	332	4	28.6	14	3	US-08-474-671-49	Sequence 49, Appli
260	5	35.7	1464	4	US-09-949-016-6738	Sequence 6738, Ap	333	4	28.6	14	3	US-08-483-577A-49	Sequence 49, Appli
261	5	35.7	1507	4	US-09-944-259-37	Sequence 37, Appli	334	4	28.6	14	3	US-08-897-438-49	Sequence 49, Appli
262	5	35.7	1512	3	US-09-443-184-48	Sequence 48, Appli	335	4	28.6	14	3	US-08-637-654-49	Sequence 49, Appli
263	5	35.7	1786	3	US-08-973-462-8	Sequence 8, Appli	336	4	28.6	14	3	US-08-649-518-49	Sequence 49, Appli
264	5	35.7	1876	4	US-09-418-710-71	Sequence 71, Appli	337	4	28.6	15	1	US-07-720-189-9	Sequence 9, Appli
265	5	35.7	1876	4	US-09-839-479-70	Sequence 70, Appli	338	4	28.6	15	1	US-08-036-555B-49	Sequence 49, Appli
266	5	35.7	1878	4	US-09-418-710-13	Sequence 13, Appli	339	4	28.6	15	1	US-07-794-288D-20	Sequence 20, Appli
267	5	35.7	1878	4	US-09-839-479-13	Sequence 13, Appli	340	4	28.6	15	1	US-07-794-288D-41	Sequence 41, Appli
268	5	35.7	1969	4	US-09-418-710-72	Sequence 72, Appli	341	4	28.6	15	1	US-07-794-288D-210	Sequence 210, App
269	5	35.7	1969	4	US-09-839-479-71	Sequence 71, Appli	342	4	28.6	15	1	US-08-469-569-49	Sequence 49, Appli
270	5	35.7	1972	4	US-09-418-710-21	Sequence 21, Appli	343	4	28.6	15	1	US-08-222-619-9	Sequence 9, Appli
271	5	35.7	1972	4	US-09-839-479-21	Sequence 21, Appli	344	4	28.6	15	1	US-08-249-322A-49	Sequence 49, Appli
272	5	35.7	2048	3	US-08-268-347-48	Sequence 48, Appli	345	4	28.6	15	1	US-08-665-220-41	Sequence 41, Appli
273	5	35.7	2600	4	US-09-949-016-7309	Sequence 7309, Ap	346	4	28.6	15	1	US-08-665-220-46	Sequence 46, Appli
274	5	35.7	2697	4	US-10-144-198-12	Sequence 12, Appli	347	4	28.6	15	1	US-08-469-526A-49	Sequence 49, Appli
275	5	35.7	3135	1	US-08-323-170B-2	Sequence 2, Appli	348	4	28.6	15	2	US-08-618-408B-46	Sequence 46, Appli
276	5	35.7	3135	3	US-08-954-441-2	Sequence 2, Appli	349	4	28.6	15	2	US-08-734-591A-49	Sequence 49, Appli
277	5	35.7	3259	4	US-09-949-016-6507	Sequence 6507, Ap	350	4	28.6	15	2	US-08-469-660-49	Sequence 49, Appli
278	5	35.7	3289	2	US-08-477-451-2	Sequence 2, Appli	351	4	28.6	15	2	US-08-553-257A-3	Sequence 3, Appli
279	5	35.7	4654	3	US-08-476-515A-84	Sequence 84, Appli	352	4	28.6	15	3	US-09-091-001-2	Sequence 2, Appli
280	5	35.7	4655	3	US-08-652-877-84	Sequence 84, Appli	353	4	28.6	15	3	US-08-341-018-82	Sequence 82, Appli
281	5	35.7	4655	3	US-08-652-877-86	Sequence 86, Appli	354	4	28.6	15	3	US-08-470-335-49	Sequence 49, Appli
282	5	35.7	4655	3	US-08-652-877-88	Sequence 88, Appli	355	4	28.6	15	3	US-08-735-021-49	Sequence 49, Appli
283	5	35.7	4655	3	US-08-652-877-90	Sequence 90, Appli	356	4	28.6	15	3	US-08-734-664A-49	Sequence 49, Appli
284	4	28.6	4	2	US-08-667-001-8	Sequence 8, Appli	357	4	28.6	15	3	US-08-470-339-49	Sequence 49, Appli
285	4	28.6	6	5	PCT-US93-12679-13	Sequence 13, Appli	358	4	28.6	15	3	US-09-257-218-59	Sequence 59, Appli
286	4	28.6	8	1	US-08-477-727A-66	Sequence 66, Appli	359	4	28.6	15	3	US-09-311-760-59	Sequence 59, Appli
287	4	28.6	8	1	US-08-477-727A-68	Sequence 68, Appli	360	4	28.6	15	3	US-09-291-692-41	Sequence 41, Appli
288	4	28.6	8	3	US-08-444-818-335	Sequence 335, App	361	4	28.6	15	3	US-09-291-692-46	Sequence 46, Appli
289	4	28.6	8	3	US-08-444-818-336	Sequence 336, App	362	4	28.6	15	3	US-09-561-756-97	Sequence 97, Appli
290	4	28.6	8	3	US-09-139-802-157	Sequence 157, App	363	4	28.6	15	3	US-09-227-721-97	Sequence 97, Appli
291	4	28.6	8	4	US-09-659-786-157	Sequence 157, App	364	4	28.6	15	4	US-09-009-953-67	Sequence 67, Appli
292	4	28.6	8	4	US-08-926-914-157	Sequence 157, App	365	4	28.6	15	4	US-08-467-602-49	Sequence 49, Appli
293	4	28.6	9	2	US-08-177-109A-53	Sequence 53, Appli	366	4	28.6	15	4	US-08-865-579-59	Sequence 59, Appli
294	4	28.6	9	2	US-08-687-706-53	Sequence 53, Appli	367	4	28.6	15	4	US-09-441-992-3	Sequence 3, Appli
295	4	28.6	9	4	US-09-311-784A-440	Sequence 440, App	368	4	28.6	15	4	US-10-059-749-59	Sequence 59, Appli
296	4	28.6	10	1	US-07-794-288D-25	Sequence 25, Appli	369	4	28.6	15	4	US-09-954-697-97	Sequence 97, Appli
297	4	28.6	10	1	US-07-794-288D-46	Sequence 46, Appli	370	4	28.6	15	4	US-09-952-768-41	Sequence 41, Appli
298	4	28.6	10	1	US-07-794-288D-211	Sequence 211, App	371	4	28.6	15	4	US-09-952-768-46	Sequence 46, Appli
299	4	28.6	10	3	US-08-939-853A-20	Sequence 20, Appli	372	4	28.6	15	4	US-08-411-295F-113	Sequence 113, App
300	4	28.6	11	1	US-07-794-288D-24	Sequence 24, Appli	373	4	28.6	15	4	US-10-378-707-3	Sequence 3, Appli
301	4	28.6	11	1	US-07-794-288D-45	Sequence 45, Appli	374	4	28.6	15	5	PCT-US94-05083C-46	Sequence 46, Appli
302	4	28.6	11	1	US-07-794-288D-212	Sequence 212, App	375	4	28.6	15	5	PCT-US95-04075-9	Sequence 9, Appli
303	4	28.6	11	1	US-07-794-288D-217	Sequence 217, App	376	4	28.6	15	5	PCT-US95-06846A-49	Sequence 49, Appli
304	4	28.6	11	1	US-07-794-288D-222	Sequence 222, App	377	4	28.6	16	1	US-08-036-555B-37	Sequence 37, Appli
305	4	28.6	11	1	US-08-408-604A-104	Sequence 104, App	378	4	28.6	16	1	US-07-794-288D-19	Sequence 19, Appli
306	4	28.6	11	6	5260275-5	Patent No. 5260275	379	4	28.6	16	1	US-07-794-288D-40	Sequence 40, Appli
307	4	28.6	11	6	5260275-5	Patent No. 5260275	380	4	28.6	16	1	US-08-469-569-37	Sequence 37, Appli
308	4	28.6	12	1	US-07-794-288D-23	Sequence 23, Appli	381	4	28.6	16	1	US-08-222-619-30	Sequence 30, Appli
309	4	28.6	12	1	US-07-794-288D-44	Sequence 44, Appli	382	4	28.6	16	1	US-08-249-322A-37	Sequence 37, Appli
310	4	28.6	12	1	US-08-260-582-32	Sequence 32, Appli	383	4	28.6	16	1	US-08-307-724B-25	Sequence 25, Appli
311	4	28.6	12	2	US-08-406-330-40	Sequence 40, Appli	384	4	28.6	16	1	US-08-307-724B-25	Sequence 25, Appli
312	4	28.6	12	2	US-08-406-330-50	Sequence 50, Appli	385	4	28.6	16	1	US-08-469-526A-37	Sequence 37, Appli
313	4	28.6	12	2	US-08-556-597-50	Sequence 50, Appli	386	4	28.6	16	2	US-08-734-591A-37	Sequence 37, Appli
314	4	28.6	12	5	PCT-US95-05471-32	Sequence 32, Appli	387	4	28.6	16	2	US-08-469-660-37	Sequence 37, Appli
315	4	28.6	12	6	5378464-28	Patent No. 5378464	388	4	28.6	16	2	US-07-971-723-1	Sequence 1, Appli
316	4	28.6	12	6	5378464-28	Patent No. 5378464	389	4	28.6	16	3	US-08-470-335-37	Sequence 37, Appli
317	4	28.6	13	1	US-07-794-288D-22	Sequence 22, Appli	390	4	28.6	16	3	US-08-735-021-37	Sequence 37, Appli
318	4	28.6	13	1	US-07-794-288D-43	Sequence 43, Appli	391	4	28.6	16	3	US-08-734-664A-37	Sequence 37, Appli
319	4	28.6	13	1	US-08-681-812-4	Sequence 4, Appli	392	4	28.6	16	3	US-08-810-009-47	Sequence 47, Appli

333	4	28.6	16	3	US-08-470-339-37	Sequence 37, Appl	466	4	28.6	24	1	US-08-096-172A-17	Sequence 17, Appl
334	4	28.6	16	4	US-08-467-602-37	Sequence 37, Appl	467	4	28.6	24	1	US-08-096-172A-18	Sequence 18, Appl
335	4	28.6	16	4	US-09-776-490-47	Sequence 47, Appl	468	4	28.6	24	1	US-08-484-635-107	Sequence 107, Appl
336	4	28.6	16	5	PCT-US94-05083C-37	Sequence 37, Appl	469	4	28.6	24	2	US-08-484-631-107	Sequence 107, Appl
337	4	28.6	16	5	PCT-US95-04075-30	Sequence 30, Appl	470	4	28.6	24	2	US-08-310-512A-70	Sequence 70, Appl
338	4	28.6	16	5	PCT-US95-06846A-37	Sequence 37, Appl	471	4	28.6	24	2	US-08-827-570-107	Sequence 107, Appl
339	4	28.6	17	1	US-07-798-776-34	Sequence 24, Appl	472	4	28.6	24	3	US-08-841-085-70	Sequence 70, Appl
400	4	28.6	17	1	US-07-794-288D-18	Sequence 18, Appl	473	4	28.6	24	3	US-09-301-089-70	Sequence 70, Appl
401	4	28.6	17	3	US-07-794-288D-39	Sequence 39, Appl	474	4	28.6	24	4	US-09-206-942-4	Sequence 4, Appl
402	4	28.6	17	3	US-08-251-288A-24	Sequence 24, Appl	475	4	28.6	24	5	PCT-US94-08380-10	Sequence 10, Appl
403	4	28.6	17	3	US-09-298-819A-24	Sequence 24, Appl	476	4	28.6	24	5	PCT-US94-08380-11	Sequence 11, Appl
404	4	28.6	17	4	US-09-586-563C-24	Sequence 24, Appl	477	4	28.6	24	5	PCT-US94-08380-12	Sequence 12, Appl
405	4	28.6	17	4	US-09-586-562C-24	Sequence 24, Appl	478	4	28.6	24	5	PCT-US94-08380-13	Sequence 13, Appl
406	4	28.6	17	6	5223424-4	Patent No. 5223424	479	4	28.6	24	5	PCT-US94-08380-14	Sequence 14, Appl
407	4	28.6	17	6	5223424-4	Patent No. 5223424	480	4	28.6	24	5	PCT-US94-08380-15	Sequence 15, Appl
408	4	28.6	18	1	US-07-794-288D-17	Sequence 17, Appl	481	4	28.6	24	5	PCT-US94-08380-16	Sequence 16, Appl
409	4	28.6	18	1	US-07-794-288D-38	Sequence 38, Appl	482	4	28.6	24	5	PCT-US94-08380-17	Sequence 17, Appl
410	4	28.6	18	1	US-07-794-288D-214	Sequence 214, App	483	4	28.6	24	5	PCT-US94-08380-18	Sequence 18, Appl
411	4	28.6	19	1	US-07-794-288D-16	Sequence 16, Appl	484	4	28.6	24	5	PCT-US95-04570-70	Sequence 70, Appl
412	4	28.6	19	1	US-07-794-288D-37	Sequence 37, Appl	485	4	28.6	24	5	PCT-US95-04589-70	Sequence 70, Appl
413	4	28.6	19	1	US-07-794-288D-95	Sequence 95, Appl	486	4	28.6	25	1	US-07-794-288D-10	Sequence 10, Appl
414	4	28.6	19	1	US-07-794-288D-226	Sequence 226, App	487	4	28.6	25	1	US-07-794-288D-31	Sequence 31, Appl
415	4	28.6	19	1	US-08-446-692-68	Sequence 68, Appl	488	4	28.6	25	1	US-07-794-288D-113	Sequence 113, App
416	4	28.6	19	2	US-08-488-351A-68	Sequence 68, Appl	489	4	28.6	25	1	US-07-794-288D-120	Sequence 120, App
417	4	28.6	19	2	US-08-729-152-16	Sequence 16, Appl	490	4	28.6	25	1	US-07-794-288D-137	Sequence 137, App
418	4	28.6	19	3	US-09-329-350-29	Sequence 29, Appl	491	4	28.6	25	1	US-07-794-288D-144	Sequence 144, App
419	4	28.6	19	3	US-09-524-435-11	Sequence 11, Appl	492	4	28.6	25	1	US-07-794-288D-206	Sequence 206, App
420	4	28.6	19	4	US-09-441-502B-77	Sequence 77, Appl	493	4	28.6	25	1	US-08-096-172A-28	Sequence 28, Appl
421	4	28.6	19	4	US-08-841-636A-29	Sequence 29, Appl	494	4	28.6	25	1	US-08-096-172A-30	Sequence 30, Appl
422	4	28.6	20	1	US-07-794-288D-15	Sequence 15, Appl	495	4	28.6	25	1	US-08-096-172A-31	Sequence 31, Appl
423	4	28.6	20	1	US-07-794-288D-36	Sequence 36, Appl	496	4	28.6	25	1	US-08-096-172A-32	Sequence 32, Appl
424	4	28.6	20	1	US-07-794-288D-92	Sequence 92, Appl	497	4	28.6	25	1	US-08-096-172A-33	Sequence 33, Appl
425	4	28.6	20	1	US-07-794-288D-97	Sequence 97, Appl	498	4	28.6	25	1	US-08-096-172A-34	Sequence 34, Appl
426	4	28.6	20	1	US-07-794-288D-209	Sequence 209, App	499	4	28.6	25	1	US-08-096-172A-35	Sequence 35, Appl
427	4	28.6	20	2	US-08-934-915-13	Sequence 13, Appl	500	4	28.6	25	1	US-08-096-172A-36	Sequence 36, Appl
428	4	28.6	20	3	US-08-612-973-79	Sequence 79, Appl	501	4	28.6	25	1	US-08-096-172A-37	Sequence 37, Appl
429	4	28.6	20	3	US-08-612-973-80	Sequence 80, Appl	502	4	28.6	25	1	US-08-096-172A-38	Sequence 38, Appl
430	4	28.6	20	3	US-08-927-597-79	Sequence 79, Appl	503	4	28.6	25	1	US-08-096-172A-39	Sequence 39, Appl
431	4	28.6	20	3	US-08-927-597-80	Sequence 80, Appl	504	4	28.6	25	1	US-08-096-172A-40	Sequence 40, Appl
432	4	28.6	20	4	US-08-635-886C-35	Sequence 35, Appl	505	4	28.6	25	3	US-09-070-504-22	Sequence 22, Appl
433	4	28.6	20	4	US-08-635-886C-36	Sequence 36, Appl	506	4	28.6	25	3	US-08-552-749-3	Sequence 3, Appl
434	4	28.6	20	4	US-10-053-485-48	Sequence 48, Appl	507	4	28.6	25	3	US-08-552-749-4	Sequence 4, Appl
435	4	28.6	20	4	US-08-974-690C-35	Sequence 35, Appl	508	4	28.6	25	4	US-09-596-120-5	Sequence 5, Appl
436	4	28.6	20	4	US-08-974-690C-36	Sequence 36, Appl	509	4	28.6	25	4	PCT-US94-08380-22	Sequence 22, Appl
437	4	28.6	20	4	US-08-974-685-35	Sequence 35, Appl	510	4	28.6	25	5	PCT-US94-08380-28	Sequence 28, Appl
438	4	28.6	20	4	US-08-974-685-36	Sequence 36, Appl	511	4	28.6	25	5	PCT-US94-08380-29	Sequence 29, Appl
439	4	28.6	20	4	US-09-667-857-407	Sequence 407, App	512	4	28.6	25	5	PCT-US94-08380-30	Sequence 30, Appl
440	4	28.6	20	4	US-09-991-433-49	Sequence 49, Appl	513	4	28.6	25	5	PCT-US94-08380-31	Sequence 31, Appl
441	4	28.6	20	4	US-09-991-433-50	Sequence 50, Appl	514	4	28.6	25	5	PCT-US94-08380-32	Sequence 32, Appl
442	4	28.6	21	1	US-07-794-288D-14	Sequence 14, Appl	515	4	28.6	25	5	PCT-US94-08380-33	Sequence 33, Appl
443	4	28.6	21	1	US-07-794-288D-35	Sequence 35, Appl	516	4	28.6	25	5	PCT-US94-08380-34	Sequence 34, Appl
444	4	28.6	21	6	5171839-6	Patent No. 5171839	517	4	28.6	25	5	PCT-US94-08380-35	Sequence 35, Appl
445	4	28.6	21	6	5171839-6	Patent No. 5171839	518	4	28.6	25	5	PCT-US94-08380-36	Sequence 36, Appl
446	4	28.6	22	1	US-07-794-288D-13	Sequence 13, Appl	519	4	28.6	25	5	PCT-US94-08380-37	Sequence 37, Appl
447	4	28.6	22	1	US-07-794-288D-34	Sequence 34, Appl	520	4	28.6	25	5	PCT-US94-08380-38	Sequence 38, Appl
448	4	28.6	23	1	US-07-794-288D-12	Sequence 12, Appl	521	4	28.6	25	5	PCT-US94-08380-39	Sequence 39, Appl
449	4	28.6	23	1	US-07-794-288D-33	Sequence 33, Appl	522	4	28.6	25	5	PCT-US94-08380-40	Sequence 40, Appl
450	4	28.6	23	1	US-09-270-767-60883	Sequence 60883, A	523	4	28.6	26	1	US-07-794-288D-9	Sequence 9, Appl
451	4	28.6	24	1	US-07-794-288D-11	Sequence 11, Appl	524	4	28.6	26	1	US-07-794-288D-30	Sequence 30, Appl
452	4	28.6	24	1	US-07-794-288D-32	Sequence 32, Appl	525	4	28.6	26	1	US-07-794-288D-105	Sequence 105, App
453	4	28.6	24	1	US-07-794-288D-93	Sequence 93, Appl	526	4	28.6	26	1	US-07-794-288D-112	Sequence 112, App
454	4	28.6	24	1	US-07-794-288D-121	Sequence 121, App	527	4	28.6	26	1	US-07-794-288D-119	Sequence 119, App
455	4	28.6	24	1	US-07-794-288D-145	Sequence 145, App	528	4	28.6	26	1	US-07-794-288D-129	Sequence 129, App
456	4	28.6	24	1	US-07-794-288D-199	Sequence 199, App	529	4	28.6	26	1	US-07-794-288D-136	Sequence 136, App
457	4	28.6	24	1	US-07-794-288D-207	Sequence 207, App	530	4	28.6	26	1	US-07-794-288D-143	Sequence 143, App
458	4	28.6	24	1	US-07-794-288D-215	Sequence 215, App	531	4	28.6	26	1	US-07-942-245-222	Sequence 222, App
459	4	28.6	24	1	US-08-096-172A-10	Sequence 10, Appl	532	4	28.6	26	1	US-07-942-245-252	Sequence 252, App
460	4	28.6	24	1	US-08-096-172A-11	Sequence 11, Appl	533	4	28.6	26	1	US-08-362-037-37	Sequence 37, Appl
461	4	28.6	24	1	US-08-096-172A-12	Sequence 12, Appl	534	4	28.6	26	2	US-08-482-142-48	Sequence 48, Appl
462	4	28.6	24	1	US-08-096-172A-13	Sequence 13, Appl	535	4	28.6	26	2	US-08-482-142-66	Sequence 66, Appl
463	4	28.6	24	1	US-08-096-172A-14	Sequence 14, Appl	536	4	28.6	26	2	US-08-482-142-67	Sequence 67, Appl
464	4	28.6	24	1	US-08-096-172A-15	Sequence 15, Appl	537	4	28.6	26	2	US-08-482-142-112	Sequence 112, App
465	4	28.6	24	1	US-08-096-172A-16	Sequence 16, Appl	538	4	28.6	26	2		

539	4	28.6	26	2	US-08-478-572-48	Sequence 48, Appl	612	4	28.6	30	3	US-08-504-538A-15	Sequence 15, Appl
540	4	28.6	26	2	US-08-478-572-66	Sequence 66, Appl	613	4	28.6	30	3	US-09-070-504-2	Sequence 2, Appl
541	4	28.6	26	2	US-08-478-572-67	Sequence 67, Appl	614	4	28.6	30	3	US-09-070-504-19	Sequence 19, Appl
542	4	28.6	26	2	US-08-478-572-112	Sequence 112, App	615	4	28.6	30	3	US-09-227-357-662	Sequence 662, App
543	4	28.6	26	3	US-08-484-296-48	Sequence 48, Appl	616	4	28.6	30	3	US-08-630-052-15	Sequence 15, Appl
544	4	28.6	26	3	US-08-484-296-66	Sequence 66, Appl	617	4	28.6	30	4	US-09-537-226-11	Sequence 11, Appl
545	4	28.6	26	3	US-08-484-296-67	Sequence 67, Appl	618	4	28.6	30	4	US-09-813-345C-1	Sequence 1, Appl
546	4	28.6	26	3	US-08-484-296-112	Sequence 112, App	619	4	28.6	30	4	US-09-813-345C-2	Sequence 2, Appl
547	4	28.6	26	3	US-09-227-357-579	Sequence 579, App	620	4	28.6	30	4	US-09-813-345C-18	Sequence 18, Appl
548	4	28.6	26	5	PCT-US95-04481-25	Sequence 25, Appl	621	4	28.6	30	4	US-09-813-345C-19	Sequence 19, Appl
549	4	28.6	27	1	US-07-794-288D-8	Sequence 8, Appl	622	4	28.6	30	5	PCT-US95-09307-15	Sequence 15, Appl
550	4	28.6	27	1	US-07-794-288D-29	Sequence 29, Appl	623	4	28.6	30	6	5260275-4	Patent No. 5260275
551	4	28.6	27	1	US-07-794-288D-66	Sequence 66, Appl	624	4	28.6	30	6	5260275-4	Patent No. 5260275
552	4	28.6	27	1	US-07-794-288D-74	Sequence 74, Appl	625	4	28.6	31	3	US-08-504-538A-14	Sequence 14, Appl
553	4	28.6	27	1	US-07-794-288D-104	Sequence 104, App	626	4	28.6	31	3	US-09-070-504-18	Sequence 18, Appl
554	4	28.6	27	1	US-07-794-288D-111	Sequence 111, App	627	4	28.6	31	3	US-08-630-052-14	Sequence 14, Appl
555	4	28.6	27	1	US-07-794-288D-128	Sequence 128, App	628	4	28.6	31	5	PCT-US95-09307-14	Sequence 14, Appl
556	4	28.6	27	1	US-07-794-288D-135	Sequence 135, App	629	4	28.6	31	6	5256643-14	Patent No. 5256643
557	4	28.6	27	2	US-08-482-142-47	Sequence 47, Appl	630	4	28.6	31	6	5256643-14	Patent No. 5256643
558	4	28.6	27	2	US-08-482-142-111	Sequence 111, App	631	4	28.6	32	1	US-08-190-802A-110	Sequence 110, App
559	4	28.6	27	2	US-08-478-572-47	Sequence 47, Appl	632	4	28.6	32	1	US-08-190-802A-114	Sequence 114, App
560	4	28.6	27	2	US-08-478-572-111	Sequence 111, App	633	4	28.6	32	1	US-08-477-727A-76	Sequence 76, Appl
561	4	28.6	27	3	US-08-484-296-47	Sequence 47, Appl	634	4	28.6	32	1	US-08-477-727A-78	Sequence 78, Appl
562	4	28.6	27	3	US-08-484-296-111	Sequence 111, App	635	4	28.6	32	3	US-08-477-346-110	Sequence 110, App
563	4	28.6	27	4	US-09-205-258-702	Sequence 702, App	636	4	28.6	32	3	US-08-477-346-114	Sequence 114, App
564	4	28.6	27	4	US-09-084-303B-293	Sequence 293, App	637	4	28.6	32	3	US-08-473-089-110	Sequence 110, App
565	4	28.6	27	5	PCT-US95-04481-24	Sequence 24, Appl	638	4	28.6	32	3	US-08-473-089-114	Sequence 114, App
566	4	28.6	28	1	US-07-794-288D-7	Sequence 7, Appl	639	4	28.6	32	4	US-08-487-072A-110	Sequence 110, App
567	4	28.6	28	1	US-07-794-288D-28	Sequence 28, App	640	4	28.6	32	4	US-08-487-072A-114	Sequence 114, App
568	4	28.6	28	1	US-07-794-288D-65	Sequence 65, Appl	641	4	28.6	33	1	US-07-927-755A-4	Sequence 4, Appl
569	4	28.6	28	1	US-07-794-288D-73	Sequence 73, Appl	642	4	28.6	33	1	US-07-927-755A-5	Sequence 5, Appl
570	4	28.6	28	1	US-07-794-288D-103	Sequence 103, App	643	4	28.6	33	1	US-07-927-755A-6	Sequence 6, Appl
571	4	28.6	28	1	US-07-794-288D-127	Sequence 127, App	644	4	28.6	33	1	US-07-927-755A-7	Sequence 7, Appl
572	4	28.6	28	1	US-08-469-260A-456	Sequence 456, App	645	4	28.6	33	1	US-07-927-755A-8	Sequence 8, Appl
573	4	28.6	28	4	US-08-488-446-456	Sequence 456, App	646	4	28.6	33	2	US-08-461-990B-9	Sequence 9, Appl
574	4	28.6	28	4	US-08-467-344A-456	Sequence 456, App	647	4	28.6	33	3	US-09-433-428D-41	Sequence 41, Appl
575	4	28.6	28	4	US-09-302-626B-156	Sequence 156, App	648	4	28.6	33	3	US-09-433-428D-45	Sequence 45, Appl
576	4	28.6	28	4	US-08-424-550B-456	Sequence 456, App	649	4	28.6	34	1	US-07-927-755A-1	Sequence 1, Appl
577	4	28.6	28	6	5248606-12	Patent No. 5248606	650	4	28.6	34	1	US-07-927-755A-2	Sequence 2, Appl
578	4	28.6	28	6	5248606-12	Patent No. 5248606	651	4	28.6	34	1	US-07-927-755A-3	Sequence 3, Appl
579	4	28.6	29	1	US-07-794-288D-6	Sequence 6, Appl	652	4	28.6	34	1	US-08-262-037-38	Sequence 38, Appl
580	4	28.6	29	1	US-07-794-288D-27	Sequence 27, Appl	653	4	28.6	35	2	US-08-482-142-113	Sequence 113, App
581	4	28.6	29	1	US-07-794-288D-64	Sequence 64, Appl	654	4	28.6	35	2	US-08-478-572-113	Sequence 113, App
582	4	28.6	29	1	US-07-794-288D-72	Sequence 72, Appl	655	4	28.6	35	2	US-08-460-890A-45	Sequence 45, App
583	4	28.6	29	1	US-07-794-288D-90	Sequence 90, Appl	656	4	28.6	35	3	US-08-167-641C-45	Sequence 45, App
584	4	28.6	29	1	US-07-794-288D-91	Sequence 91, Appl	657	4	28.6	35	3	US-08-460-971A-45	Sequence 45, App
585	4	28.6	29	1	US-07-794-288D-94	Sequence 94, Appl	658	4	28.6	35	3	US-08-462-040-45	Sequence 45, App
586	4	28.6	29	1	US-07-794-288D-96	Sequence 96, Appl	659	4	28.6	35	3	US-08-484-296-113	Sequence 113, App
587	4	28.6	29	1	US-07-794-288D-183	Sequence 183, App	660	4	28.6	35	4	US-09-431-705-24	Sequence 24, Appl
588	4	28.6	29	1	US-07-794-288D-184	Sequence 184, App	661	4	28.6	35	4	US-09-374-958C-13	Sequence 13, Appl
589	4	28.6	29	1	US-07-794-288D-185	Sequence 185, App	662	4	28.6	36	1	US-08-117-080-2	Sequence 2, Appl
590	4	28.6	29	1	US-07-794-288D-186	Sequence 186, App	663	4	28.6	36	1	US-08-117-080-4	Sequence 4, Appl
591	4	28.6	29	1	US-07-794-288D-187	Sequence 187, App	664	4	28.6	36	1	US-08-471-329-2	Sequence 2, Appl
592	4	28.6	29	1	US-07-794-288D-188	Sequence 188, App	665	4	28.6	36	1	US-08-471-329-4	Sequence 4, Appl
593	4	28.6	29	1	US-08-378-761A-28	Sequence 28, Appl	666	4	28.6	36	1	US-08-477-727A-79	Sequence 79, Appl
594	4	28.6	29	1	US-08-485-286-28	Sequence 28, Appl	667	4	28.6	36	1	US-08-477-727A-83	Sequence 83, Appl
595	4	28.6	29	3	US-09-177-245A-1	Sequence 1, Appl	668	4	28.6	36	1	US-08-477-727A-86	Sequence 86, Appl
596	4	28.6	29	3	US-09-177-245A-189	Sequence 189, App	669	4	28.6	36	1	US-08-477-727A-88	Sequence 88, Appl
597	4	28.6	29	3	US-09-070-504-1	Sequence 1, Appl	670	4	28.6	36	1	US-08-477-727A-92	Sequence 92, Appl
598	4	28.6	29	4	US-09-812-283-189	Sequence 189, App	671	4	28.6	36	1	US-08-477-727A-98	Sequence 98, Appl
599	4	28.6	30	1	US-07-794-288D-5	Sequence 5, Appl	672	4	28.6	36	1	US-08-471-675A-5	Sequence 5, Appl
600	4	28.6	30	1	US-07-794-288D-26	Sequence 26, Appl	673	4	28.6	36	1	US-08-471-675A-7	Sequence 7, Appl
601	4	28.6	30	1	US-07-794-288D-175	Sequence 175, App	674	4	28.6	36	1	US-08-471-675A-10	Sequence 10, Appl
602	4	28.6	30	1	US-07-794-288D-176	Sequence 176, App	675	4	28.6	36	1	US-08-471-675A-11	Sequence 11, Appl
603	4	28.6	30	1	US-07-794-288D-177	Sequence 177, App	676	4	28.6	36	1	US-08-471-675A-14	Sequence 14, Appl
604	4	28.6	30	1	US-07-794-288D-178	Sequence 178, App	677	4	28.6	36	1	US-08-471-675A-20	Sequence 20, Appl
605	4	28.6	30	1	US-07-794-288D-179	Sequence 179, App	678	4	28.6	36	2	US-08-915-142-2	Sequence 2, Appl
606	4	28.6	30	1	US-07-794-288D-180	Sequence 180, App	679	4	28.6	36	2	US-08-915-142-4	Sequence 4, Appl
607	4	28.6	30	1	US-07-794-288D-195	Sequence 195, App	680	4	28.6	36	2	US-08-505-486-85	Sequence 85, Appl
608	4	28.6	30	1	US-07-794-288D-208	Sequence 208, App	681	4	28.6	36	2	US-08-892-549-7	Sequence 7, Appl
609	4	28.6	30	1	US-07-794-288D-218	Sequence 218, App	682	4	28.6	36	2	US-08-892-549-11	Sequence 11, Appl
610	4	28.6	30	1	US-07-794-288D-225	Sequence 225, App	683	4	28.6	36	2	US-08-892-549-14	Sequence 14, Appl
611	4	28.6	30	2	US-08-753-829A-8	Sequence 8, Appl	684	4	28.6	36	2	US-08-892-549-15	Sequence 15, Appl

685	4	28.6	36	2	US-08-892-549-18	Sequence 18, Appl	758	4	28.6	37	1	US-08-471-675A-12	Sequence 12, Appl
686	4	28.6	36	2	US-08-892-549-24	Sequence 24, Appl	759	4	28.6	37	1	US-08-471-675A-13	Sequence 13, Appl
687	4	28.6	36	2	US-08-892-549-39	Sequence 39, Appl	760	4	28.6	37	1	US-08-471-675A-15	Sequence 15, Appl
688	4	28.6	36	2	US-08-892-549-40	Sequence 40, Appl	761	4	28.6	37	1	US-08-471-675A-16	Sequence 16, Appl
689	4	28.6	36	3	US-08-801-028-85	Sequence 85, Appl	762	4	28.6	37	1	US-08-471-675A-17	Sequence 17, Appl
690	4	28.6	36	3	US-09-340-154-85	Sequence 85, Appl	763	4	28.6	37	1	US-08-471-675A-18	Sequence 18, Appl
691	4	28.6	36	3	US-08-302-069A-4	Sequence 4, Appl	764	4	28.6	37	1	US-08-471-675A-19	Sequence 19, Appl
692	4	28.6	36	3	US-08-302-069A-6	Sequence 6, Appl	765	4	28.6	37	1	US-08-471-675A-21	Sequence 21, Appl
693	4	28.6	36	3	US-08-302-069A-9	Sequence 9, Appl	766	4	28.6	37	1	US-08-471-675A-22	Sequence 22, Appl
694	4	28.6	36	3	US-08-302-069A-10	Sequence 10, Appl	767	4	28.6	37	1	US-08-471-675A-23	Sequence 23, Appl
695	4	28.6	36	3	US-08-302-069A-13	Sequence 13, Appl	768	4	28.6	37	2	US-08-259-762-1	Sequence 1, Appl
696	4	28.6	36	3	US-08-302-069A-19	Sequence 19, Appl	769	4	28.6	37	2	US-08-259-762-2	Sequence 2, Appl
697	4	28.6	36	4	US-09-482-611B-85	Sequence 85, Appl	770	4	28.6	37	2	US-08-259-762-3	Sequence 3, Appl
698	4	28.6	36	4	US-09-576-062A-4	Sequence 4, Appl	771	4	28.6	37	2	US-08-259-762-4	Sequence 4, Appl
699	4	28.6	36	4	US-09-576-062A-6	Sequence 6, Appl	772	4	28.6	37	2	US-08-259-762-5	Sequence 5, Appl
700	4	28.6	36	4	US-09-576-062A-9	Sequence 9, Appl	773	4	28.6	37	2	US-08-259-762-6	Sequence 6, Appl
701	4	28.6	36	4	US-09-576-062A-10	Sequence 10, Appl	774	4	28.6	37	2	US-08-259-762-7	Sequence 7, Appl
702	4	28.6	36	4	US-09-576-062A-13	Sequence 13, Appl	775	4	28.6	37	2	US-08-259-762-8	Sequence 8, Appl
703	4	28.6	36	4	US-09-576-062A-19	Sequence 19, Appl	776	4	28.6	37	2	US-08-259-762-9	Sequence 9, Appl
704	4	28.6	36	4	US-09-454-533-7	Sequence 7, Appl	777	4	28.6	37	2	US-08-801-863-8	Sequence 8, Appl
705	4	28.6	36	4	US-09-454-533-11	Sequence 11, Appl	778	4	28.6	37	2	US-08-801-863-9	Sequence 9, Appl
706	4	28.6	36	4	US-09-454-533-14	Sequence 14, Appl	779	4	28.6	37	2	US-08-801-863-10	Sequence 10, Appl
707	4	28.6	36	4	US-09-454-533-15	Sequence 15, Appl	780	4	28.6	37	2	US-08-486-596A-8	Sequence 8, Appl
708	4	28.6	36	4	US-09-454-533-18	Sequence 18, Appl	781	4	28.6	37	2	US-08-486-596A-9	Sequence 9, Appl
709	4	28.6	36	4	US-09-454-533-24	Sequence 24, Appl	782	4	28.6	37	2	US-08-486-596A-10	Sequence 10, Appl
710	4	28.6	36	4	US-09-454-533-39	Sequence 39, Appl	783	4	28.6	37	2	US-08-488-351A-66	Sequence 66, Appl
711	4	28.6	36	4	US-09-454-533-40	Sequence 40, Appl	784	4	28.6	37	2	US-08-313-185-3	Sequence 3, Appl
712	4	28.6	36	4	US-09-270-767-41321	Sequence 41321, A	785	4	28.6	37	2	US-08-459-499-6	Sequence 6, Appl
713	4	28.6	36	4	US-09-270-767-56537	Sequence 56537, A	786	4	28.6	37	2	US-08-459-499-6	Sequence 6, Appl
714	4	28.6	36	5	PCT-US95-09338-85	Sequence 85, Appl	787	4	28.6	37	2	US-09-004-713-9	Sequence 9, Appl
715	4	28.6	36	5	PCT-US95-09339-85	Sequence 85, Appl	788	4	28.6	37	2	US-09-004-713-10	Sequence 10, Appl
716	4	28.6	37	1	US-08-117-080-1	Sequence 1, Appl	789	4	28.6	37	2	US-08-619-841-1	Sequence 1, Appl
717	4	28.6	37	1	US-08-117-080-3	Sequence 3, Appl	790	4	28.6	37	2	US-08-619-841-2	Sequence 2, Appl
718	4	28.6	37	1	US-07-794-288D-1	Sequence 1, Appl	791	4	28.6	37	2	US-08-915-142-1	Sequence 1, Appl
719	4	28.6	37	1	US-07-794-288D-2	Sequence 2, Appl	792	4	28.6	37	2	US-08-315-142-3	Sequence 3, Appl
720	4	28.6	37	1	US-07-794-288D-3	Sequence 3, Appl	793	4	28.6	37	2	US-08-505-486-84	Sequence 84, Appl
721	4	28.6	37	1	US-07-929-206-6	Sequence 6, Appl	794	4	28.6	37	2	US-08-446-929A-1	Sequence 1, Appl
722	4	28.6	37	1	US-08-233-389C-8	Sequence 8, Appl	795	4	28.6	37	2	US-08-446-929A-2	Sequence 2, Appl
723	4	28.6	37	1	US-08-233-389C-9	Sequence 9, Appl	796	4	28.6	37	2	US-08-892-549-1	Sequence 1, Appl
724	4	28.6	37	1	US-08-233-389C-10	Sequence 10, Appl	797	4	28.6	37	2	US-08-892-549-2	Sequence 2, Appl
725	4	28.6	37	1	US-08-471-329-1	Sequence 1, Appl	798	4	28.6	37	2	US-08-892-549-3	Sequence 3, Appl
726	4	28.6	37	1	US-08-471-329-3	Sequence 3, Appl	799	4	28.6	37	2	US-08-892-549-4	Sequence 4, Appl
727	4	28.6	37	1	US-08-477-727A-5	Sequence 5, Appl	800	4	28.6	37	2	US-08-892-549-5	Sequence 5, Appl
728	4	28.6	37	1	US-08-477-727A-17	Sequence 17, Appl	801	4	28.6	37	2	US-08-892-549-8	Sequence 8, Appl
729	4	28.6	37	1	US-08-477-727A-29	Sequence 29, Appl	802	4	28.6	37	2	US-08-892-549-9	Sequence 9, Appl
730	4	28.6	37	1	US-08-477-727A-30	Sequence 30, Appl	803	4	28.6	37	2	US-08-892-549-10	Sequence 10, Appl
731	4	28.6	37	1	US-08-477-727A-42	Sequence 42, Appl	804	4	28.6	37	2	US-08-892-549-12	Sequence 12, Appl
732	4	28.6	37	1	US-08-477-727A-75	Sequence 75, Appl	805	4	28.6	37	2	US-08-892-549-13	Sequence 13, Appl
733	4	28.6	37	1	US-08-477-727A-87	Sequence 87, Appl	806	4	28.6	37	2	US-08-892-549-16	Sequence 16, Appl
734	4	28.6	37	1	US-08-477-727A-77	Sequence 77, Appl	807	4	28.6	37	2	US-08-892-549-17	Sequence 17, Appl
735	4	28.6	37	1	US-08-477-727A-80	Sequence 80, Appl	808	4	28.6	37	2	US-08-892-549-19	Sequence 19, Appl
736	4	28.6	37	1	US-08-477-727A-81	Sequence 81, Appl	809	4	28.6	37	2	US-08-892-549-20	Sequence 20, Appl
737	4	28.6	37	1	US-08-477-727A-82	Sequence 82, Appl	810	4	28.6	37	2	US-08-892-549-21	Sequence 21, Appl
738	4	28.6	37	1	US-08-477-727A-84	Sequence 84, Appl	811	4	28.6	37	2	US-08-892-549-22	Sequence 22, Appl
739	4	28.6	37	1	US-08-477-727A-85	Sequence 85, Appl	812	4	28.6	37	2	US-08-892-549-23	Sequence 23, Appl
740	4	28.6	37	1	US-08-477-727A-87	Sequence 87, Appl	813	4	28.6	37	2	US-08-892-549-25	Sequence 25, Appl
741	4	28.6	37	1	US-08-477-727A-89	Sequence 89, Appl	814	4	28.6	37	2	US-08-892-549-26	Sequence 26, Appl
742	4	28.6	37	1	US-08-477-727A-90	Sequence 90, Appl	815	4	28.6	37	2	US-08-892-549-27	Sequence 27, Appl
743	4	28.6	37	1	US-08-477-727A-91	Sequence 91, Appl	816	4	28.6	37	2	US-08-892-549-34	Sequence 34, Appl
744	4	28.6	37	1	US-08-477-727A-93	Sequence 93, Appl	817	4	28.6	37	2	US-08-892-549-35	Sequence 35, Appl
745	4	28.6	37	1	US-08-477-727A-94	Sequence 94, Appl	818	4	28.6	37	2	US-08-892-549-36	Sequence 36, Appl
746	4	28.6	37	1	US-08-477-727A-95	Sequence 95, Appl	819	4	28.6	37	2	US-08-892-549-37	Sequence 37, Appl
747	4	28.6	37	1	US-08-477-727A-96	Sequence 96, Appl	820	4	28.6	37	2	US-08-892-549-38	Sequence 38, Appl
748	4	28.6	37	1	US-08-477-727A-97	Sequence 97, Appl	821	4	28.6	37	2	US-08-892-549-41	Sequence 41, Appl
749	4	28.6	37	1	US-08-477-727A-99	Sequence 99, Appl	822	4	28.6	37	3	US-08-801-028-84	Sequence 84, Appl
750	4	28.6	37	1	US-08-477-727A-100	Sequence 100, App	823	4	28.6	37	3	US-09-053-197A-49	Sequence 49, Appl
751	4	28.6	37	1	US-08-477-727A-101	Sequence 101, App	824	4	28.6	37	3	US-09-340-154-84	Sequence 84, Appl
752	4	28.6	37	1	US-08-446-692-66	Sequence 66, Appl	825	4	28.6	37	3	US-08-784-582-51	Sequence 51, Appl
753	4	28.6	37	1	US-08-471-675A-2	Sequence 2, Appl	826	4	28.6	37	3	US-08-784-582-54	Sequence 54, Appl
754	4	28.6	37	1	US-08-471-675A-4	Sequence 4, Appl	827	4	28.6	37	3	US-08-302-069A-1	Sequence 1, Appl
755	4	28.6	37	1	US-08-471-675A-6	Sequence 6, Appl	828	4	28.6	37	3	US-08-302-069A-3	Sequence 3, Appl
756	4	28.6	37	1	US-08-471-675A-8	Sequence 8, Appl	829	4	28.6	37	3	US-08-302-069A-5	Sequence 5, Appl
757	4	28.6	37	1	US-08-471-675A-9	Sequence 9, Appl	830	4	28.6	37	3	US-08-302-069A-7	Sequence 7, Appl

831	4	28.6	37	3	US-08-302-069A-8	Sequence 8, Appli	Sequence 8, Appli	37	4	US-09-813-345C-8	Sequence 8, Appli
832	4	28.6	37	3	US-08-302-069A-11	Sequence 11, Appl	Sequence 11, Appl	37	4	US-09-813-345C-10	Sequence 10, Appl
833	4	28.6	37	3	US-08-302-069A-12	Sequence 12, Appl	Sequence 12, Appl	37	4	US-09-813-345C-11	Sequence 11, Appl
834	4	28.6	37	3	US-08-302-069A-14	Sequence 14, Appl	Sequence 14, Appl	37	4	US-09-813-345C-13	Sequence 13, Appl
835	4	28.6	37	3	US-08-302-069A-15	Sequence 15, Appl	Sequence 15, Appl	37	4	US-09-813-345C-16	Sequence 16, Appl
836	4	28.6	37	3	US-08-302-069A-16	Sequence 16, Appl	Sequence 16, Appl	37	4	US-09-813-345C-17	Sequence 17, Appl
837	4	28.6	37	3	US-08-302-069A-17	Sequence 17, Appl	Sequence 17, Appl	37	4	US-09-875-571A-1	Sequence 1, Appli
838	4	28.6	37	3	US-08-302-069A-18	Sequence 18, Appl	Sequence 18, Appl	37	4	PCT-US95-09338-84	Sequence 84, Appl
839	4	28.6	37	3	US-08-302-069A-20	Sequence 20, Appl	Sequence 20, Appl	37	5	PCT-US95-09339-84	Sequence 84, Appl
840	4	28.6	37	3	US-08-302-069A-21	Sequence 21, Appl	Sequence 21, Appl	37	6	5424221-1	Patent No. 5424221
841	4	28.6	37	3	US-08-302-069A-22	Sequence 22, Appl	Sequence 22, Appl	37	6	5424221-4	Patent No. 5424221
842	4	28.6	37	3	US-09-082-614A-3	Sequence 3, Appli	Sequence 3, Appli	37	6	5424221-5	Patent No. 5424221
843	4	28.6	37	3	US-09-070-504-3	Sequence 3, Appli	Sequence 3, Appli	37	6	5424221-6	Patent No. 5424221
844	4	28.6	37	3	US-09-070-504-4	Sequence 4, Appli	Sequence 4, Appli	37	6	5424221-6	Patent No. 5424221
845	4	28.6	37	3	US-09-070-504-5	Sequence 5, Appli	Sequence 5, Appli	37	6	5260275-1	Patent No. 5260275
846	4	28.6	37	3	US-09-070-504-6	Sequence 6, Appli	Sequence 6, Appli	37	6	5424221-1	Patent No. 5424221
847	4	28.6	37	3	US-09-070-504-7	Sequence 7, Appli	Sequence 7, Appli	37	6	5424221-4	Patent No. 5424221
848	4	28.6	37	3	US-09-070-504-8	Sequence 8, Appli	Sequence 8, Appli	37	6	5424221-5	Patent No. 5424221
849	4	28.6	37	3	US-09-070-504-10	Sequence 10, Appl	Sequence 10, Appl	37	6	5424221-6	Patent No. 5424221
850	4	28.6	37	3	US-09-070-504-11	Sequence 11, Appl	Sequence 11, Appl	38	1	US-07-776-272-19	Sequence 19, Appl
851	4	28.6	37	3	US-09-070-504-13	Sequence 13, Appl	Sequence 13, Appl	38	1	US-07-776-272-20	Sequence 20, Appl
852	4	28.6	37	3	US-09-070-504-16	Sequence 16, Appl	Sequence 16, Appl	38	1	US-07-776-272-21	Sequence 21, Appl
853	4	28.6	37	3	US-09-070-504-17	Sequence 17, Appl	Sequence 17, Appl	38	1	US-07-776-272-22	Sequence 22, Appl
854	4	28.6	37	3	US-09-085-761A-54	Sequence 54, Appl	Sequence 54, Appl	38	2	US-08-460-890A-44	Sequence 44, Appl
855	4	28.6	37	4	US-09-482-611B-84	Sequence 84, Appl	Sequence 84, Appl	38	3	US-08-167-641C-44	Sequence 44, Appl
856	4	28.6	37	4	US-09-576-062A-1	Sequence 1, Appli	Sequence 1, Appli	38	3	US-08-460-971A-44	Sequence 44, Appl
857	4	28.6	37	4	US-09-576-062A-3	Sequence 3, Appli	Sequence 3, Appli	38	3	US-08-462-040-A-4	Sequence 44, Appl
858	4	28.6	37	4	US-09-576-062A-5	Sequence 5, Appli	Sequence 5, Appli	38	4	US-09-902-540-16576	Sequence 16576, A
859	4	28.6	37	4	US-09-576-062A-8	Sequence 8, Appli	Sequence 8, Appli	39	1	US-08-477-727A-3	Sequence 3, Appli
860	4	28.6	37	4	US-09-576-062A-11	Sequence 11, Appl	Sequence 11, Appl	39	4	US-09-439-410A-94	Sequence 94, Appl
861	4	28.6	37	4	US-09-576-062A-12	Sequence 12, Appl	Sequence 12, Appl	39	4	US-09-509-559B-14	Sequence 14, Appl
862	4	28.6	37	4	US-09-576-062A-14	Sequence 14, Appl	Sequence 14, Appl	40	4	US-09-270-767-57494	Sequence 57494, A
863	4	28.6	37	4	US-09-576-062A-15	Sequence 15, Appl	Sequence 15, Appl	40	4	US-09-270-767-58306	Sequence 58306, A
864	4	28.6	37	4	US-09-576-062A-16	Sequence 16, Appl	Sequence 16, Appl	41	1	US-08-781-020-9	Sequence 9, Appli
865	4	28.6	37	4	US-09-576-062A-17	Sequence 17, Appl	Sequence 17, Appl	41	3	US-09-038-935-9	Sequence 9, Appli
866	4	28.6	37	4	US-09-576-062A-18	Sequence 18, Appl	Sequence 18, Appl	41	3	US-09-690-454-206	Sequence 206, App
867	4	28.6	37	4	US-09-576-062A-20	Sequence 20, Appl	Sequence 20, Appl	42	1	US-08-233-778-15	Sequence 15, Appl
868	4	28.6	37	4	US-09-576-062A-21	Sequence 21, Appl	Sequence 21, Appl	42	1	US-08-262-037-1	Sequence 1, Appli
869	4	28.6	37	4	US-09-576-062A-22	Sequence 22, Appl	Sequence 22, Appl	42	1	US-09-462-917A-128	Sequence 128, App
870	4	28.6	37	4	US-09-454-533-1	Sequence 1, Appli	Sequence 1, Appli	43	1	US-08-179-481-81	Sequence 81, Appl
871	4	28.6	37	4	US-09-454-533-2	Sequence 2, Appli	Sequence 2, Appli	43	2	US-08-488-161-80	Sequence 80, Appl
872	4	28.6	37	4	US-09-454-533-3	Sequence 3, Appli	Sequence 3, Appli	43	3	US-09-273-685-80	Sequence 80, Appl
873	4	28.6	37	4	US-09-454-533-4	Sequence 4, Appli	Sequence 4, Appli	43	4	US-07-757-022B-12	Sequence 12, Appl
874	4	28.6	37	4	US-09-454-533-5	Sequence 5, Appli	Sequence 5, Appli	43	4	US-09-057-363C-56	Sequence 56, Appl
875	4	28.6	37	4	US-09-454-533-8	Sequence 8, Appli	Sequence 8, Appli	43	4	US-09-057-363C-57	Sequence 57, Appl
876	4	28.6	37	4	US-09-454-533-9	Sequence 9, Appli	Sequence 9, Appli	43	4	US-09-057-363C-62	Sequence 62, Appl
877	4	28.6	37	4	US-09-454-533-10	Sequence 10, Appl	Sequence 10, Appl	43	4	US-09-057-363C-63	Sequence 63, Appl
878	4	28.6	37	4	US-09-454-533-12	Sequence 12, Appl	Sequence 12, Appl	43	4	US-09-057-363C-64	Sequence 64, Appl
879	4	28.6	37	4	US-09-454-533-21	Sequence 21, Appl	Sequence 21, Appl	43	4	US-09-265-107-56	Sequence 56, Appl
880	4	28.6	37	4	US-09-454-533-13	Sequence 13, Appl	Sequence 13, Appl	43	4	US-09-265-107-57	Sequence 57, Appl
881	4	28.6	37	4	US-09-454-533-16	Sequence 16, Appl	Sequence 16, Appl	43	4	US-09-265-107-62	Sequence 62, Appl
882	4	28.6	37	4	US-09-454-533-17	Sequence 17, Appl	Sequence 17, Appl	43	4	US-09-265-107-63	Sequence 63, Appl
883	4	28.6	37	4	US-09-454-533-19	Sequence 19, Appl	Sequence 19, Appl	43	4	US-09-265-107-64	Sequence 64, Appl
884	4	28.6	37	4	US-09-454-533-20	Sequence 20, Appl	Sequence 20, Appl	43	5	PCT-US95-11934-80	Sequence 80, Appl
885	4	28.6	37	4	US-09-454-533-22	Sequence 22, Appl	Sequence 22, Appl	44	1	US-08-421-661-4	Sequence 4, Appli
886	4	28.6	37	4	US-09-454-533-23	Sequence 23, Appl	Sequence 23, Appl	44	1	US-08-331-394-10	Sequence 10, Appl
887	4	28.6	37	4	US-09-454-533-25	Sequence 25, Appl	Sequence 25, Appl	45	1	US-08-250-858-10	Sequence 10, Appl
888	4	28.6	37	4	US-09-454-533-26	Sequence 26, Appl	Sequence 26, Appl	45	1	US-08-446-915-10	Sequence 10, Appl
889	4	28.6	37	4	US-09-454-533-27	Sequence 27, Appl	Sequence 27, Appl	45	2	US-08-744-139-10	Sequence 10, Appl
890	4	28.6	37	4	US-09-454-533-34	Sequence 34, Appl	Sequence 34, Appl	45	2	US-08-779-599-10	Sequence 10, Appl
891	4	28.6	37	4	US-09-454-533-36	Sequence 36, Appl	Sequence 36, Appl	45	5	PCT-US95-08639-10	Sequence 10, Appl
892	4	28.6	37	4	US-09-454-533-35	Sequence 35, Appl	Sequence 35, Appl	45	6	5424221-3	Patent No. 5424221
893	4	28.6	37	4	US-09-454-533-37	Sequence 37, Appl	Sequence 37, Appl	45	6	5424221-3	Patent No. 5424221
894	4	28.6	37	4	US-09-454-533-38	Sequence 38, Appl	Sequence 38, Appl	46	2	US-08-691-814B-16	Sequence 16, Appl
895	4	28.6	37	4	US-09-454-533-41	Sequence 41, Appl	Sequence 41, Appl	46	3	US-09-257-218-13	Sequence 13, Appl
896	4	28.6	37	4	US-09-084-303B-265	Sequence 265, App	Sequence 265, App	46	3	US-09-311-760-13	Sequence 13, Appl
897	4	28.6	37	4	US-09-084-303B-281	Sequence 281, App	Sequence 281, App	46	4	US-08-865-579-13	Sequence 13, Appl
898	4	28.6	37	4	US-09-813-345C-4	Sequence 4, Appli	Sequence 4, Appli	46	4	US-10-059-749-13	Sequence 13, Appl
899	4	28.6	37	4	US-09-813-345C-5	Sequence 5, Appli	Sequence 5, Appli	46	6	5240847-24	Patent No. 5240847
900	4	28.6	37	4	US-09-813-345C-8	Sequence 8, Appli	Sequence 8, Appli	46	6	5240847-24	Patent No. 5240847
901	4	28.6	37	4	US-09-813-345C-9	Sequence 9, Appli	Sequence 9, Appli	47	3	US-09-052-089A-14	Sequence 14, Appl
902	4	28.6	37	4	US-09-813-345C-5	Sequence 5, Appli	Sequence 5, Appli	47	3	US-07-736-361A-15	Sequence 15, Appl
903	4	28.6	37	4	US-09-813-345C-7	Sequence 7, Appli	Sequence 7, Appli	48	3	US-09-227-357-241	Sequence 241, App

977 4 28.6 49 2 US-08-456-647B-26
978 4 28.6 49 2 US-08-237-401A-26
979 4 28.6 49 3 US-09-284-819-4
980 4 28.6 49 4 US-09-369-247-114
981 4 28.6 50 1 US-08-262-037-39
982 4 28.6 50 2 US-08-142-551B-119
983 4 28.6 51 1 US-08-421-661-2
984 4 28.6 51 3 US-09-044-536A-7
985 4 28.6 51 4 US-10-002-818-3
986 4 28.6 51 4 US-09-621-976-6219
987 4 28.6 51 4 US-09-270-767-39632
988 4 28.6 51 4 US-09-270-767-54849
989 4 28.6 51 4 US-09-344-639D-3
990 4 28.6 51 4 US-10-067-422-24
991 4 28.6 51 4 US-09-851-873-47
992 4 28.6 52 4 US-09-621-976-7370
993 4 28.6 53 2 US-08-456-647B-40
994 4 28.6 53 2 US-08-237-401A-40
995 4 28.6 53 2 US-08-799-173A-9
996 4 28.6 53 4 US-09-170-042A-9
997 4 28.6 54 2 US-08-456-647B-46
998 4 28.6 54 2 US-08-237-401A-46
999 4 28.6 55 1 US-08-446-692-94
1000 4 28.6 55 2 US-08-488-351A-94

ALIGNMENTS

RESULT 1
US-09-054-492B-5
; Sequence 5, Application US/09054492B
; Patent No. 6218115
; GENERAL INFORMATION:
; APPLICANT: TAKESHI NAKAMURA
; TITLE OF INVENTION: HUMAN CYCLIN I AND GENES ENCODING SAME
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY, MADISON & SUTRO
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/054,492B
; FILING DATE: APRIL 3, 1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: PAUL E. WHITE, JR.
; REGISTRATION NUMBER: 32,011
; REFERENCE/DOCKET NUMBER: 7898/252159
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEX: 6714627CUSH
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-054-492B-5

Query Match 100.0%; Score 14; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 9.7e-08;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EDNVSENVGVCVT 14
Db 1 EDNVSENVGVCVT 14
RESULT 2
US-08-969-106-6
; Sequence 6, Application US/08969106
; Patent No. 5986055
; GENERAL INFORMATION:
; APPLICANT: Yang, M.
; APPLICANT: Nandabalan, K.
; APPLICANT: Schulz, V.
; TITLE OF INVENTION: CDK2 INTERACTIONS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/969,106
; FILING DATE: 13-NOV-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7934-057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 377 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-969-106-6

Query Match 100.0%; Score 14; DB 2; Length 377;
Best Local Similarity 100.0%; Pred. No. 1.4e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EDNVSENVGVCVT 14
Db 343 EDNVSENVGVCVT 356

RESULT 3
US-09-054-492B-1
; Sequence 1, Application US/09054492B
; Patent No. 6218115
; GENERAL INFORMATION:
; APPLICANT: TAKESHI NAKAMURA
; TITLE OF INVENTION: HUMAN CYCLIN I AND GENES ENCODING SAME
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY, MADISON & SUTRO
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/054,492B
FILING DATE: APRIL 3, 1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PAUL E. WHITE, JR.
REGISTRATION NUMBER: 32,011
REFERENCE/DOCKET NUMBER: 7898/252159
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEX: 6714627CUSH
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 377

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-054-492B-1

Query Match 100.0%; Score 14; DB 3; Length 377;
Best Local Similarity 100.0%; Pred. No. 1.4e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDNVSENVGVCVT 14
||| ||||| ||||| |||||
Db 343 EDNVSENVGVCVT 356

RESULT 4
US-09-338-125-6
Sequence 6, Application US/09338125
Patent No. 6521412
GENERAL INFORMATION:
APPLICANT: Yang, M.
APPLICANT: Nandabalan, K.
APPLICANT: Schulz, V.
TITLE OF INVENTION: CDK2 INTERACTIONS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/338,125
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/969,106
FILING DATE: 13-NOV-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mistock, S. Leelle
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7934-057
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 377 amino acids

TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-09-338-125-6

Query Match 100.0%; Score 14; DB 4; Length 377;
Best Local Similarity 100.0%; Pred. No. 1.4e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDNVSENVGVCVT 14
||| ||||| ||||| |||||
Db 343 EDNVSENVGVCVT 356

RESULT 5
US-09-538-092-781
Sequence 781, Application US/09538092
Patent No. 6753314
GENERAL INFORMATION:
APPLICANT: Giot, Loic
APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REFERENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CurapatSeqFormatter Version 0.9
SEQ ID NO 781
LENGTH: 446

TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
FEATURE:
NAME/KEY: misc feature
LOCATION: (0)...(0)
OTHER INFORMATION: Polypeptide Accession Number YPL133C
US-09-538-092-781

Query Match 50.0%; Score 7; DB 4; Length 446;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VSENVGS 10
||| |||||
Db 125 VSENVGS 131

RESULT 6
US-08-324-301-5
Sequence 5, Application US/08324301
Patent No. 5597569
GENERAL INFORMATION:
APPLICANT: Siegall, Clay B.
APPLICANT: Gawlak, Susan L.
APPLICANT: Marquardt, Hans
TITLE OF INVENTION: A NEW RIBOSOME-INACTIVATING PROTEIN
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bristol-Myers Squibb Company
STREET: 3005 First Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/324,301
;; FILING DATE:
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/141,891
;; FILING DATE: 25-OCT-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Poor, Brian W.
;; REGISTRATION NUMBER: 32,928
;; REFERENCE/DOCKET NUMBER: ONO109A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 206-728-4800
;; TELEFAX: 206-727-3601
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 13 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; FRAGMENT TYPE: internal
;; ORIGINAL SOURCE:
;; ORGANISM: Bryonica dioica
;; TISSUE TYPE: root
US-08-324-301-5

Query Match 42.9%; Score 6; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VSENVG 9
Db 6 VSENVG 11

RESULT 7
US-08-324-301-15
; Sequence 15, Application US/08324301
; Patent No. 5597569
; GENERAL INFORMATION:
; APPLICANT: Siegall, Clay B.
; APPLICANT: Gawlak, Susan L.
; APPLICANT: Marquardt, Hans
; TITLE OF INVENTION: A NEW RIBOSOME-INACTIVATING PROTEIN
; TITLE OF INVENTION: ISOLATED FROM THE PLANT BRYONICA DIOICA
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bristol-Myers Squibb Company
; STREET: 3005 First Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/324,301
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/141,891
; FILING DATE: 25-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Poor, Brian W.
; REGISTRATION NUMBER: 32,928
; REFERENCE/DOCKET NUMBER: ONO109A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-728-4800
; TELEFAX: 206-727-3601

;; INFORMATION FOR SEQ ID NO: 15:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 282 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; FRAGMENT TYPE: N-terminal
;; ORIGINAL SOURCE:
;; ORGANISM: Bryonia dioica
;; TISSUE TYPE: leaf
US-08-324-301-15

Query Match 42.9%; Score 6; DB 1; Length 282;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VSENVG 9
Db 194 VSENVG 199

RESULT 8
US-09-834-309-1
; Sequence 1, Application US/09834309
; Patent No. 6820011
; GENERAL INFORMATION:
; APPLICANT: Chen, Xiaojiang
; APPLICANT: Holers, V. Michael
; TITLE OF INVENTION: THREE-DIMENSIONAL STRUCTURE OF COMPLEMENT RECEPTOR TYPE 2 AND USE
; FILE REFERENCE: 2848-43
; CURRENT APPLICATION NUMBER: US/09/834,309
; CURRENT FILING DATE: 2001-04-11
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 1033
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-834-309-1

Query Match 42.9%; Score 6; DB 4; Length 1033;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 SENVGS 10
Db 167 SENVGS 172

RESULT 9
US-09-541-782-8
; Sequence 8, Application US/09541782
; Patent No. 6284480
; GENERAL INFORMATION:
; APPLICANT: Nislow, Corey
; APPLICANT: Sakowicz, Roman
; APPLICANT: Beraud, Christophe
; TITLE OF INVENTION: Antifungal Assay
; FILE REFERENCE: 1015
; CURRENT APPLICATION NUMBER: US/09/541,782
; CURRENT FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 1066
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-541-782-8

Query Match 42.9%; Score 6; DB 3; Length 1066;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


```
Qy      6  ENVGSV 11
Db      828  ENVGSV 833

RESULT 10
US-09-723-820-8
; Sequence 8, Application US/09723820
; Patent No. 6468760
; GENERAL INFORMATION:
; APPLICANT: Nislow, Corey
; APPLICANT: Sakowicz, Roman
; APPLICANT: Beraud, Christophe
; TITLE OF INVENTION: Antifungal Assay
; FILE REFERENCE: 1015
; CURRENT APPLICATION NUMBER: US/09/723,820
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/541,782
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 1066
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-723-820-8

Query Match      42.9%; Score 6; DB 4; Length 1066;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6  ENVGSV 11
Db      828  ENVGSV 833

RESULT 11
US-10-270-085-8
; Sequence 8, Application US/10270085
; Patent No. 6627408
; GENERAL INFORMATION:
; APPLICANT: Nislow, Corey
; APPLICANT: Sakowicz, Roman
; APPLICANT: Beraud, Christophe
; TITLE OF INVENTION: Antifungal Assay
; FILE REFERENCE: 1015
; CURRENT APPLICATION NUMBER: US/10/270,085
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: US/09/723,820
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/541,782
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 1066
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-10-270-085-8

Query Match      42.9%; Score 6; DB 4; Length 1066;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6  ENVGSV 11
Db      828  ENVGSV 833

RESULT 12
US-09-252-991A-26438
; Sequence 26438, Application US/09252991A
```

```
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 26438
; LENGTH: 1415
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26438

Query Match      42.9%; Score 6; DB 4; Length 1415;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5  ENVGSV 10
Db      616  ENVGSV 621

RESULT 13
US-09-949-016-8985
; Sequence 8985, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8985
; LENGTH: 2362
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8985

Query Match      42.9%; Score 6; DB 4; Length 2362;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6  ENVGSV 11
Db      2299  ENVGSV 2304

RESULT 14
US-08-469-486-52
; Sequence 52, Application US/08469486
; Patent No. 5739281
; GENERAL INFORMATION:
; APPLICANT: Thøgersen, Hans Christian
; APPLICANT: Holtet, Thor Las
; APPLICANT: Etzerodt, Michael
; TITLE OF INVENTION: Improved method for the refolding of
; TITLE OF INVENTION: proteins
; NUMBER OF SEQUENCES: 58
```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version
; SOFTWARE: #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,486
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/192,060
; FILING DATE: February 4, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul T. Clark
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 06363/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 542 5070
; TELEFAX: 617 542 8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4544 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-469-486-52

Query Match 42.9%; Score 6; DB 1; Length 4544;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ENVGSV 11
|||||
Db 2280 ENVGSV 2285

RESULT 15
US-08-469-658-52
; Sequence 52, Application US/08469658
; Patent No. 5917018
; GENERAL INFORMATION:
; APPLICANT: Th egersen, Hans Christian
; APPLICANT: Holtet, Thor Las
; APPLICANT: Etzerodt, Michael
; TITLE OF INVENTION: IMPROVED METHOD FOR THE REFOOLDING OF
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version
; SOFTWARE: #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,658
; FILING DATE: June 5, 1995

; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/192,060
; FILING DATE: February 4, 1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul T. Clark
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 06363/002002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 542 5070
; TELEFAX: 617 542 8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4544 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-469-658-52

Query Match 42.9%; Score 6; DB 2; Length 4544;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ENVGSV 11
|||||
Db 2280 ENVGSV 2285

Search completed: February 11, 2005, 03:18:39
Job time : 11.2174 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 11, 2005, 03:16:44 ; Search time 3.22251 Seconds
(without alignments)
1419.543 Million cell updates/sec

Title: US-09-736-250-5

Perfect score:

Sequence: 1 EDNVSENVGSVCGT 14

Scoring table: OLIGO

Scoring table:

Searched: 1376875 seqs. 326749119 residues

Word size : 0

Parameter	Value
Total number of hits satisfying chosen parameters.	1376875

Minimum no sea length: 0

Minimum DB seq	length: 0
Maximum DB seq	length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Published Announcements 22.4

- Published Applications AA:
- 1: /cgn2_6/pdata/2/pubpaa/US07_PUBCOMB.pcp.*
 - 2: /cgn2_6/pdata/2/pubpaa/PCT_NEW_PUB.pcp.*
 - 3: /cgn2_6/pdata/2/pubpaa/US05_NEW_PUB.pcp.*
 - 4: /cgn2_6/pdata/2/pubpaa/US06_PUBCOMB.pcp.*
 - 5: /cgn2_6/pdata/2/pubpaa/US07_NEW_PUB.pcp.*
 - 6: /cgn2_6/pdata/2/pubpaa/PCTUS_PUBCOMB.pcp.*
 - 7: /cgn2_6/pdata/2/pubpaa/US08_NEW_PUB.pcp.*
 - 8: /cgn2_6/pdata/2/pubpaa/US08_PUBCOMB.pcp.*
 - 9: /cgn2_6/pdata/2/pubpaa/US09A_PUBCOMB.pcp.*
 - 10: /cgn2_6/pdata/2/pubpaa/US09B_PUBCOMB.pcp.*
 - 11: /cgn2_6/pdata/2/pubpaa/US09C_PUBCOMB.pcp.*
 - 12: /cgn2_6/pdata/2/pubpaa/US09_NEW_PUB.pcp.*
 - 13: /cgn2_6/pdata/2/pubpaa/US10A_PUBCOMB.pcp.*
 - 14: /cgn2_6/pdata/2/pubpaa/US10B_PUBCOMB.pcp.*
 - 15: /cgn2_6/pdata/2/pubpaa/US10C_PUBCOMB.pcp.*
 - 16: /cgn2_6/pdata/2/pubpaa/US10D_PUBCOMB.pcp.*
 - 17: /cgn2_6/pdata/2/pubpaa/US10_NEW_PUB.pcp.*
 - 18: /cgn2_6/pdata/2/pubpaa/US11_NEW_PUB.pcp.*
 - 19: /cgn2_6/pdata/2/pubpaa/US60_NEW_PUB.pcp.*
 - 20: /cgn2_6/pdata/2/pubpaa/US60_PUBCOMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	14	100.0	14	12	US-09-736-250-5	Sequence 5, Appli
2	14	100.0	377	12	US-09-736-250-1	Sequence 1, Appli
3	7	50.0	446	15	US-10-149-310-280	Sequence 280, Appli
4	7	50.0	1190	15	US-10-359-493-18546	Sequence 18546, A
5	6	42.9	74	15	US-10-424-599-154932	Sequence 154932,
6	6	42.9	81	15	US-10-264-049-3886	Sequence 3886, Ap
7	6	42.9	95	16	US-10-437-963-179908	Sequence 179908,
8	6	42.9	98	15	US-10-424-599-244020	Sequence 244020,
9	6	42.9	100	16	US-10-437-963-113862	Sequence 113862,
10	6	42.9	169	15	US-10-359-493-17361	Sequence 17361, A
11	6	42.9	199	16	US-10-437-963-180011	Sequence 180011,
12	6	42.9	219	15	US-10-094-749-2381	Sequence 2381, Ap
13	6	42.9	220	16	US-10-437-963-197887	Sequence 197887,

87	5	35.7	11	14	US-10-160-506-32	Sequence 32, Appl	160	5	35.7	107	16	US-10-449-379-68	Sequence 68, Appl
88	5	35.7	11	16	US-10-449-379-32	Sequence 32, Appl	161	5	35.7	107	16	US-10-688-015-48	Sequence 48, Appl
89	5	35.7	11	16	US-10-688-015-32	Sequence 32, Appl	162	5	35.7	107	16	US-10-688-015-50	Sequence 50, Appl
90	5	35.7	16	14	US-10-040-862-10457	Sequence 10457, A	163	5	35.7	107	16	US-10-688-015-62	Sequence 62, Appl
91	5	35.7	16	15	US-10-057-4758-10457	Sequence 10457, A	164	5	35.7	107	16	US-10-688-015-63	Sequence 63, Appl
92	5	35.7	16	15	US-10-154-884B-10457	Sequence 10457, A	165	5	35.7	107	16	US-10-688-015-64	Sequence 64, Appl
93	5	35.7	16	16	US-10-764-324-10457	Sequence 10457, A	166	5	35.7	107	16	US-10-688-015-65	Sequence 65, Appl
94	5	35.7	30	14	US-10-040-862-10451	Sequence 10451, A	167	5	35.7	107	16	US-10-688-015-66	Sequence 66, Appl
95	5	35.7	30	15	US-10-040-862-10452	Sequence 10452, A	168	5	35.7	107	16	US-10-688-015-68	Sequence 68, Appl
96	5	35.7	30	15	US-10-057-4758-10451	Sequence 10451, A	169	5	35.7	108	16	US-09-930-169-2	Sequence 2, Appl
97	5	35.7	30	15	US-10-057-4758-10452	Sequence 10452, A	170	5	35.7	108	16	US-10-823-730-2	Sequence 2, Appl
98	5	35.7	30	15	US-10-154-884B-10451	Sequence 10451, A	171	5	35.7	109	9	US-09-939-980-440	Sequence 440, App
99	5	35.7	30	15	US-10-154-884B-10452	Sequence 10452, A	172	5	35.7	109	9	US-10-424-599-246648	Sequence 246648, A
100	5	35.7	30	16	US-10-764-324-10451	Sequence 10451, A	173	5	35.7	109	16	US-10-437-963-145674	Sequence 145674, A
101	5	35.7	30	16	US-10-764-324-10452	Sequence 10452, A	174	5	35.7	111	11	US-09-864-408A-3776	Sequence 3776, Ap
102	5	35.7	38	15	US-10-424-599-172545	Sequence 172545, A	175	5	35.7	112	15	US-10-424-599-223522	Sequence 223522, A
103	5	35.7	42	14	US-10-217-584-11	Sequence 11, Appl	176	5	35.7	114	9	US-09-860-670-130	Sequence 130, App
104	5	35.7	47	9	US-09-864-761-37914	Sequence 37914, A	177	5	35.7	114	15	US-10-227-646-130	Sequence 130, App
105	5	35.7	51	15	US-10-424-599-204691	Sequence 204691, A	178	5	35.7	114	15	US-10-242-355-471	Sequence 471, App
106	5	35.7	56	10	US-09-764-872-390	Sequence 390, App	179	5	35.7	115	16	US-10-767-701-39276	Sequence 39276, A
107	5	35.7	56	15	US-10-424-599-210228	Sequence 210228, A	180	5	35.7	117	15	US-10-289-762-951	Sequence 951, App
108	5	35.7	58	15	US-10-424-599-185026	Sequence 185026, A	181	5	35.7	117	15	US-10-425-114-50550	Sequence 50550, A
109	5	35.7	59	16	US-10-437-963-145005	Sequence 145005, A	182	5	35.7	118	14	US-10-385-072-13	Sequence 13, Appl
110	5	35.7	62	15	US-10-424-599-213579	Sequence 213579, A	183	5	35.7	119	15	US-10-424-599-147520	Sequence 147520, A
111	5	35.7	63	16	US-10-767-701-46618	Sequence 46618, A	184	5	35.7	120	16	US-10-437-963-198266	Sequence 198266, A
112	5	35.7	65	9	US-09-864-761-39828	Sequence 39828, A	185	5	35.7	121	15	US-10-424-599-147400	Sequence 147400, A
113	5	35.7	68	9	US-09-864-761-40776	Sequence 40776, A	186	5	35.7	123	15	US-10-415-253-9	Sequence 9, Appl
114	5	35.7	70	14	US-10-211-962-131	Sequence 131, App	187	5	35.7	123	16	US-10-437-963-116512	Sequence 116512, A
115	5	35.7	70	16	US-10-437-963-166821	Sequence 166821, A	188	5	35.7	124	15	US-10-108-260A-2942	Sequence 2942, Ap
116	5	35.7	72	15	US-10-424-599-269038	Sequence 269038, A	189	5	35.7	124	15	US-10-424-599-186845	Sequence 186845, A
117	5	35.7	75	15	US-10-424-599-205429	Sequence 205429, A	190	5	35.7	128	15	US-10-282-122A-45210	Sequence 45210, A
118	5	35.7	77	15	US-10-424-599-246869	Sequence 246869, A	191	5	35.7	128	15	US-10-282-122A-56639	Sequence 56639, A
119	5	35.7	78	15	US-10-424-599-227220	Sequence 227220, A	192	5	35.7	128	15	US-10-282-122A-60151	Sequence 60151, A
120	5	35.7	80	15	US-10-424-599-221946	Sequence 221946, A	193	5	35.7	129	15	US-10-424-599-176693	Sequence 176693, A
121	5	35.7	81	9	US-09-864-761-38603	Sequence 38603, A	194	5	35.7	129	16	US-10-437-963-190293	Sequence 190293, A
122	5	35.7	81	15	US-10-424-599-257131	Sequence 257131, A	195	5	35.7	131	15	US-10-425-114-65328	Sequence 65328, A
123	5	35.7	85	15	US-10-029-386-30284	Sequence 30284, A	196	5	35.7	135	16	US-10-767-701-53143	Sequence 53143, A
124	5	35.7	86	15	US-10-424-599-256032	Sequence 256032, A	197	5	35.7	137	15	US-10-424-599-203717	Sequence 203717, A
125	5	35.7	87	16	US-10-437-963-144219	Sequence 144219, A	198	5	35.7	137	15	US-10-424-599-213271	Sequence 213271, A
126	5	35.7	89	15	US-10-424-599-164077	Sequence 164077, A	199	5	35.7	139	15	US-10-424-599-245760	Sequence 245760, A
127	5	35.7	89	16	US-10-437-963-158060	Sequence 158060, A	200	5	35.7	140	15	US-10-087-080-3	Sequence 3, Appl
128	5	35.7	92	14	US-10-238-075-1351	Sequence 1351, Ap	201	5	35.7	140	15	US-10-087-080-5	Sequence 5, Appl
129	5	35.7	93	16	US-10-767-701-45629	Sequence 45629, A	202	5	35.7	142	15	US-10-282-122A-71612	Sequence 71612, A
130	5	35.7	93	15	US-10-424-599-283837	Sequence 283837, A	203	5	35.7	146	16	US-10-767-701-54271	Sequence 54271, A
131	5	35.7	94	14	US-10-238-075-1349	Sequence 1349, Ap	204	5	35.7	147	10	US-09-930-169-1	Sequence 1, Appl
132	5	35.7	94	14	US-10-180-158-20	Sequence 20, Appl	205	5	35.7	147	15	US-10-424-599-280916	Sequence 280916, A
133	5	35.7	94	15	US-10-424-599-272645	Sequence 272645, A	206	5	35.7	147	16	US-10-823-730-1	Sequence 1, Appl
134	5	35.7	94	16	US-10-437-963-106428	Sequence 106428, A	207	5	35.7	152	15	US-10-424-599-254995	Sequence 254995, A
135	5	35.7	97	15	US-10-335-977-6253	Sequence 6253, Ap	208	5	35.7	153	15	US-10-424-599-154112	Sequence 154112, A
136	5	35.7	97	15	US-10-106-698-7296	Sequence 7296, Ap	209	5	35.7	154	15	US-10-424-599-274304	Sequence 274304, A
137	5	35.7	98	14	US-10-106-698-7296	Sequence 150194, A	210	5	35.7	156	9	US-09-925-298-644	Sequence 644, App
138	5	35.7	99	16	US-10-437-963-150194	Sequence 150194, A	211	5	35.7	156	14	US-10-102-806-644	Sequence 644, App
139	5	35.7	102	16	US-10-437-963-123629	Sequence 123629, A	212	5	35.7	160	15	US-10-369-493-5550	Sequence 5550, Ap
140	5	35.7	104	14	US-10-180-158-24	Sequence 24, Appl	213	5	35.7	163	13	US-10-114-893-18	Sequence 18, Appl
141	5	35.7	104	15	US-10-424-599-144161	Sequence 144161, A	214	5	35.7	163	15	US-10-424-599-280377	Sequence 280377, A
142	5	35.7	105	14	US-10-106-698-7605	Sequence 7605, Ap	215	5	35.7	163	15	US-10-104-047-3796	Sequence 3796, Ap
143	5	35.7	105	16	US-10-437-963-204843	Sequence 204843, A	216	5	35.7	164	15	US-10-104-047-3796	Sequence 3796, Ap
144	5	35.7	106	15	US-10-424-599-204929	Sequence 204929, A	217	5	35.7	166	9	US-09-764-864-1562	Sequence 1562, Ap
145	5	35.7	107	14	US-10-160-506-40	Sequence 40, Appl	218	5	35.7	166	10	US-09-930-169-3	Sequence 3, Appl
146	5	35.7	107	14	US-10-160-506-50	Sequence 50, Appl	219	5	35.7	166	16	US-10-823-730-3	Sequence 3, Appl
147	5	35.7	107	14	US-10-160-506-62	Sequence 62, Appl	220	5	35.7	167	16	US-10-767-701-62632	Sequence 62632, A
148	5	35.7	107	14	US-10-160-506-63	Sequence 63, Appl	221	5	35.7	170	16	US-10-437-963-164507	Sequence 164507, A
149	5	35.7	107	14	US-10-160-506-64	Sequence 64, Appl	222	5	35.7	171	15	US-10-424-599-217933	Sequence 217933, A
150	5	35.7	107	14	US-10-160-506-65	Sequence 65, Appl	223	5	35.7	173	15	US-10-296-115-1286	Sequence 1286, Ap
151	5	35.7	107	14	US-10-160-506-66	Sequence 66, Appl	224	5	35.7	174	9	US-09-738-626-4599	Sequence 4599, Ap
152	5	35.7	107	14	US-10-160-506-68	Sequence 68, Appl	225	5	35.7	174	17	US-10-494-541-16	Sequence 16, Appl
153	5	35.7	107	16	US-10-449-379-48	Sequence 48, Appl	226	5	35.7	175	9	US-09-839-479-64	Sequence 64, Appl
154	5	35.7	107	16	US-10-449-379-50	Sequence 50, Appl	227	5	35.7	175	15	US-10-376-537-65	Sequence 65, Appl
155	5	35.7	107	16	US-10-449-379-62	Sequence 62, Appl	228	5	35.7	176	9	US-09-839-479-65	Sequence 65, Appl
156	5	35.7	107	16	US-10-449-379-63	Sequence 63, Appl	229	5	35.7	176	15	US-10-376-537-66	Sequence 66, Appl
157	5	35.7	107	16	US-10-449-379-64	Sequence 64, Appl	230	5	35.7	176	15	US-10-702-148-65	Sequence 65, Appl
158	5	35.7	107	16	US-10-449-379-65	Sequence 65, Appl	231	5	35.7	177	15	US-10-424-599-210963	Sequence 210963, A
159	5	35.7	107	16	US-10-449-379-66	Sequence 66, Appl	232	5	35.7	179	16	US-10-767-701-31951	Sequence 31951, A

233	5	35.7	186	14	US-10-379-616-2	Sequence 2, Appli	306	5	35.7	292	15	US-10-424-599-262410	Sequence 262410,
234	5	35.7	186	16	US-10-767-701-59551	Sequence 59551, A	307	5	35.7	294	16	US-10-437-599-163248	Sequence 163248,
235	5	35.7	190	14	US-10-029-386-32464	Sequence 32464, A	308	5	35.7	295	15	US-10-424-599-191991	Sequence 191991,
236	5	35.7	191	15	US-10-108-2608-2677	Sequence 2677, Ap	309	5	35.7	296	15	US-10-424-599-157290	Sequence 157290,
237	5	35.7	194	15	US-10-424-599-142883	Sequence 142883,	310	5	35.7	297	14	US-10-180-158-56	Sequence 56, Appl
238	5	35.7	194	16	US-10-767-701-59997	Sequence 59997, A	311	5	35.7	299	14	US-10-156-761-12105	Sequence 12105, A
239	5	35.7	195	15	US-10-425-114-68513	Sequence 68513, A	312	5	35.7	301	15	US-10-425-114-68293	Sequence 68293, A
240	5	35.7	199	16	US-10-437-963-179485	Sequence 179485,	313	5	35.7	303	16	US-10-437-963-129511	Sequence 129511,
241	5	35.7	204	14	US-10-211-962-127	Sequence 127, App	314	5	35.7	305	15	US-10-437-963-122481	Sequence 122481,
242	5	35.7	204	15	US-10-424-599-260913	Sequence 260913,	315	5	35.7	309	15	US-10-424-599-246147	Sequence 246147,
243	5	35.7	206	15	US-10-424-599-2678056	Sequence 2678056,	316	5	35.7	309	15	US-10-424-599-262432	Sequence 262432,
244	5	35.7	208	16	US-10-437-963-166056	Sequence 166056,	317	5	35.7	311	15	US-10-310-154-716	Sequence 716, App
245	5	35.7	210	15	US-10-425-114-68348	Sequence 68348, A	318	5	35.7	312	9	US-09-851-026-36	Sequence 36, Appl
246	5	35.7	216	15	US-10-424-599-253265	Sequence 253265,	319	5	35.7	313	15	US-10-424-599-219585	Sequence 219585,
247	5	35.7	217	15	US-10-369-493-4145	Sequence 4145, Ap	320	5	35.7	313	16	US-10-474-776-406	Sequence 406, App
248	5	35.7	218	15	US-10-424-599-274301	Sequence 274301,	321	5	35.7	313	17	US-10-472-928-4416	Sequence 4416, Ap
249	5	35.7	218	16	US-10-767-701-36133	Sequence 36133, A	322	5	35.7	316	16	US-10-437-963-113907	Sequence 113907,
250	5	35.7	220	15	US-10-424-599-161667	Sequence 161667,	323	5	35.7	318	14	US-10-156-761-8907	Sequence 8907, Ap
251	5	35.7	225	14	US-10-385-072-14	Sequence 14, Appl	324	5	35.7	319	15	US-10-721-692-2	Sequence 2, Appli
252	5	35.7	225	15	US-10-424-599-203671	Sequence 203671,	325	5	35.7	320	15	US-10-154-884B-11042	Sequence 11042, A
253	5	35.7	228	15	US-10-424-599-211967	Sequence 211967,	326	5	35.7	320	16	US-10-688-011-2	Sequence 1, Appli
254	5	35.7	232	15	US-10-424-599-259889	Sequence 259889,	327	5	35.7	323	14	US-10-067-076-2	Sequence 2, Appli
255	5	35.7	234	15	US-10-382-122A-74167	Sequence 74167, A	328	5	35.7	323	15	US-10-389-566-547	Sequence 547, App
256	5	35.7	234	15	US-10-424-599-261438	Sequence 261438,	329	5	35.7	325	15	US-10-369-493-14625	Sequence 14625, A
257	5	35.7	234	17	US-10-472-928-4066	Sequence 4066, Ap	330	5	35.7	325	15	US-10-369-493-15076	Sequence 15076, A
258	5	35.7	235	15	US-10-369-493-16629	Sequence 16629, A	331	5	35.7	325	15	US-10-425-114-38918	Sequence 38918, A
259	5	35.7	235	15	US-10-369-493-19336	Sequence 19336, A	332	5	35.7	325	15	US-10-425-114-46017	Sequence 46017, A
260	5	35.7	239	14	US-10-180-158-58	Sequence 58, Appl	333	5	35.7	329	15	US-10-424-599-268338	Sequence 268338,
261	5	35.7	239	15	US-10-424-599-239717	Sequence 239717,	334	5	35.7	331	15	US-10-369-493-2706	Sequence 2706, Ap
262	5	35.7	242	16	US-10-437-963-145776	Sequence 8377, Ap	335	5	35.7	331	16	US-10-437-963-146325	Sequence 146325, A
263	5	35.7	244	15	US-10-363-829-469	Sequence 145776,	336	5	35.7	332	15	US-10-369-493-18828	Sequence 18828, A
264	5	35.7	246	16	US-10-363-829-469	Sequence 469, App	337	5	35.7	332	15	US-10-282-122A-44291	Sequence 44291, A
265	5	35.7	248	15	US-10-282-122A-77374	Sequence 77374, A	338	5	35.7	337	9	US-09-815-242-5617	Sequence 5617, Ap
266	5	35.7	248	15	US-10-425-114-43770	Sequence 43770, A	339	5	35.7	337	9	US-09-815-242-12539	Sequence 12539, A
267	5	35.7	250	15	US-10-369-493-13580	Sequence 13580, A	340	5	35.7	337	9	US-09-815-242-12876	Sequence 12876, A
268	5	35.7	252	14	US-10-391-2538-9	Sequence 9, Appli	341	5	35.7	337	14	US-10-097-237-9	Sequence 9, Appli
269	5	35.7	252	15	US-10-369-493-16974	Sequence 16974, A	342	5	35.7	337	15	US-10-282-122A-43996	Sequence 43996, A
270	5	35.7	252	15	US-10-425-114-71061	Sequence 71061, A	343	5	35.7	337	15	US-10-282-122A-70889	Sequence 70889, A
271	5	35.7	254	15	US-10-369-493-15717	Sequence 15717, A	344	5	35.7	337	15	US-10-282-122A-71733	Sequence 71733, A
272	5	35.7	255	14	US-10-040-862-9612	Sequence 9612, Ap	345	5	35.7	340	15	US-10-264-213-225	Sequence 225, App
273	5	35.7	255	15	US-10-057-4758-9612	Sequence 9612, Ap	346	5	35.7	342	15	US-10-425-114-68594	Sequence 68594, A
274	5	35.7	255	15	US-10-154-884B-9612	Sequence 9612, Ap	347	5	35.7	343	15	US-10-282-122A-61435	Sequence 61435, A
275	5	35.7	255	15	US-10-154-884B-11057	Sequence 11057, A	348	5	35.7	345	15	US-10-424-599-167321	Sequence 167321,
276	5	35.7	255	15	US-10-424-599-161858	Sequence 161858,	349	5	35.7	346	15	US-10-424-599-262445	Sequence 262445,
277	5	35.7	255	16	US-10-764-324-9612	Sequence 9612, Ap	350	5	35.7	349	9	US-09-738-626-4437	Sequence 4437, Ap
278	5	35.7	257	15	US-10-369-493-14250	Sequence 14250, A	351	5	35.7	349	10	US-09-746-660A-70	Sequence 70, Appl
279	5	35.7	257	15	US-10-369-493-15350	Sequence 15350, A	352	5	35.7	350	10	US-09-906-179A-3	Sequence 3, Appli
280	5	35.7	258	15	US-10-369-493-22360	Sequence 22360, A	353	5	35.7	350	10	US-09-906-179A-213	Sequence 213, App
281	5	35.7	258	15	US-10-424-599-246340	Sequence 246340,	354	5	35.7	350	10	US-09-906-179A-226	Sequence 226, App
282	5	35.7	261	14	US-10-040-862-9611	Sequence 9611, Ap	355	5	35.7	350	15	US-10-671-403-124	Sequence 124, App
283	5	35.7	261	15	US-10-057-4758-9611	Sequence 9611, Ap	356	5	35.7	350	15	US-10-671-419-124	Sequence 124, App
284	5	35.7	261	15	US-10-154-884B-9611	Sequence 9611, Ap	357	5	35.7	350	15	US-10-670-844-124	Sequence 124, App
285	5	35.7	261	15	US-10-154-884B-11056	Sequence 11056, A	358	5	35.7	350	15	US-10-671-134-124	Sequence 124, App
286	5	35.7	261	15	US-10-424-599-156048	Sequence 156048,	359	5	35.7	350	15	US-10-673-098-124	Sequence 124, App
287	5	35.7	261	16	US-10-764-324-9611	Sequence 9611, Ap	360	5	35.7	350	15	US-10-673-127-124	Sequence 124, App
288	5	35.7	262	14	US-10-180-158-62	Sequence 62, Appl	361	5	35.7	350	15	US-10-673-127-124	Sequence 124, App
289	5	35.7	263	15	US-10-425-114-69724	Sequence 69724, A	362	5	35.7	350	16	US-10-670-817-124	Sequence 124, App
290	5	35.7	267	15	US-10-424-599-284438	Sequence 284438,	363	5	35.7	350	16	US-10-673-119-124	Sequence 124, App
291	5	35.7	267	16	US-10-767-701-44378	Sequence 44378, A	364	5	35.7	350	16	US-10-746-167-95	Sequence 95, Appl
292	5	35.7	271	15	US-10-369-493-18215	Sequence 18215, A	365	5	35.7	350	16	US-10-671-207-124	Sequence 124, App
293	5	35.7	272	15	US-10-154-884B-11049	Sequence 11049, A	366	5	35.7	352	15	US-10-369-493-20074	Sequence 20074, A
294	5	35.7	275	15	US-10-335-977-7679	Sequence 7679, Ap	367	5	35.7	355	14	US-10-029-386-32133	Sequence 32133, A
295	5	35.7	276	15	US-10-369-493-11582	Sequence 11582, A	368	5	35.7	359	14	US-10-361-460-11	Sequence 11, Appl
296	5	35.7	278	15	US-10-335-977-7680	Sequence 7680, Ap	369	5	35.7	360	14	US-10-087-714-22	Sequence 22, Appl
297	5	35.7	285	15	US-10-424-599-191038	Sequence 191038,	370	5	35.7	362	14	US-10-259-740-4	Sequence 4, Appli
298	5	35.7	287	15	US-10-425-114-67678	Sequence 67678, A	371	5	35.7	364	10	US-09-863-776-39	Sequence 39, Appl
299	5	35.7	288	9	US-09-895-913A-122	Sequence 122, App	372	5	35.7	365	15	US-10-154-884B-11047	Sequence 11047, A
300	5	35.7	288	15	US-10-320-797-3070	Sequence 3070, Ap	373	5	35.7	365	15	US-10-424-599-225609	Sequence 225609,
301	5	35.7	288	15	US-10-282-122A-58858	Sequence 58858, A	374	5	35.7	366	15	US-10-424-599-278238	Sequence 278238,
302	5	35.7	288	17	US-10-472-928-132	Sequence 132, App	375	5	35.7	367	15	US-10-154-884B-11050	Sequence 11050, A
303	5	35.7	290	15	US-10-369-493-20468	Sequence 20468, A	376	5	35.7	367	15	US-10-282-122A-63404	Sequence 63404, A
304	5	35.7	291	15	US-10-369-493-18458	Sequence 18458, A	377	5	35.7	367	16	US-10-437-963-156275	Sequence 156275,
305	5	35.7	291	16	US-10-767-701-42245	Sequence 42245, A	378	5	35.7	371	14	US-10-032-585-7445	Sequence 7445, Ap

379	5	35.7	371	15	US-10-369-493-3828	Sequence 3828, Ap	452	5	35.7	481	16	US-10-437-963-183222	Sequence 183222,
380	5	35.7	374	15	US-10-425-114-40569	Sequence 40569, A	453	5	35.7	482	15	US-10-282-122A-59920	Sequence 59920, A
381	5	35.7	377	9	US-09-881-752A-92	Sequence 92, Appl	454	5	35.7	483	15	US-10-369-493-22491	Sequence 22491, A
382	5	35.7	377	15	US-10-335-977-6255	Sequence 6255, Ap	455	5	35.7	485	15	US-10-282-122A-65246	Sequence 65246, A
383	5	35.7	379	15	US-10-225-066A-188	Sequence 188, App	456	5	35.7	485	15	US-10-282-122A-65859	Sequence 65859, A
384	5	35.7	379	15	US-10-225-067-104	Sequence 104, App	457	5	35.7	487	17	US-10-866-527-6	Sequence 6, Appli
385	5	35.7	379	15	US-10-374-780A-416	Sequence 416, App	458	5	35.7	490	16	US-10-648-593-196	Sequence 196, App
386	5	35.7	381	14	US-10-052-092-29	Sequence 29, Appl	459	5	35.7	490	16	US-10-755-889-256	Sequence 256, App
387	5	35.7	381	14	US-10-437-107-29	Sequence 29, Appl	460	5	35.7	493	15	US-10-417-476-5	Sequence 5, Appli
388	5	35.7	382	9	US-09-771-956-3	Sequence 3, Appli	461	5	35.7	493	15	US-10-767-701-0483	Sequence 4083, A
389	5	35.7	382	15	US-10-282-122A-73650	Sequence 73650, A	462	5	35.7	502	15	US-10-369-493-20870	Sequence 20870, A
390	5	35.7	382	15	US-10-424-599-185647	Sequence 185647, A	463	5	35.7	503	15	US-10-282-122A-56338	Sequence 56338, A
391	5	35.7	382	17	US-10-926-225-3	Sequence 3, Appli	464	5	35.7	503	16	US-10-739-096-25	Sequence 25, Appl
392	5	35.7	384	16	US-10-437-963-180472	Sequence 180472, A	465	5	35.7	503	16	US-10-739-096-35	Sequence 35, Appl
393	5	35.7	384	15	US-10-369-493-16754	Sequence 16754, A	466	5	35.7	505	14	US-10-156-761-14471	Sequence 14471, A
394	5	35.7	386	15	US-10-369-493-13152	Sequence 13152, A	467	5	35.7	505	16	US-10-739-096-30	Sequence 30, Appl
395	5	35.7	387	16	US-10-437-963-103157	Sequence 103157, A	468	5	35.7	506	14	US-10-205-823-168	Sequence 168, App
396	5	35.7	387	16	US-10-437-963-184671	Sequence 184671, A	469	5	35.7	506	15	US-10-369-493-13139	Sequence 13139, A
397	5	35.7	389	15	US-10-074-978A-219	Sequence 219, App	470	5	35.7	506	16	US-10-755-889-580	Sequence 580, App
398	5	35.7	389	15	US-10-425-114-65684	Sequence 65684, A	471	5	35.7	508	9	US-09-771-161A-102	Sequence 102, App
399	5	35.7	389	15	US-10-037-417-131	Sequence 131, App	472	5	35.7	508	14	US-10-040-862-10464	Sequence 10464, A
400	5	35.7	391	15	US-10-094-749-3102	Sequence 3102, Ap	473	5	35.7	508	15	US-10-057-475B-10464	Sequence 10464, A
401	5	35.7	391	15	US-10-369-493-22565	Sequence 22565, A	474	5	35.7	508	15	US-10-154-884B-10464	Sequence 10464, A
402	5	35.7	392	15	US-10-282-122A-73649	Sequence 73649, A	475	5	35.7	508	15	US-10-154-884B-11039	Sequence 11039, A
403	5	35.7	394	16	US-10-437-963-129071	Sequence 129071, A	476	5	35.7	508	16	US-10-764-324-10464	Sequence 10464, A
404	5	35.7	394	16	US-10-437-963-162156	Sequence 162156, A	477	5	35.7	509	13	US-10-072-153-6	Sequence 6, Appli
405	5	35.7	395	9	US-09-728-401A-2	Sequence 2, Appli	478	5	35.7	509	14	US-10-032-585-7717	Sequence 7717, Ap
406	5	35.7	395	10	US-09-771-023-8	Sequence 8, Appli	479	5	35.7	509	15	US-10-655-433-6	Sequence 6, Appli
407	5	35.7	395	17	US-10-741-849-7050	Sequence 7050, Ap	480	5	35.7	514	15	US-10-425-114-54818	Sequence 54818, A
408	5	35.7	396	15	US-10-425-114-56117	Sequence 56117, A	481	5	35.7	515	15	US-10-425-114-70123	Sequence 70123, A
409	5	35.7	396	15	US-10-425-114-63135	Sequence 63135, A	482	5	35.7	515	15	US-10-425-114-73028	Sequence 73028, A
410	5	35.7	399	15	US-10-424-599-254992	Sequence 254992, A	483	5	35.7	516	14	US-10-156-761-10628	Sequence 10628, A
411	5	35.7	400	16	US-10-437-963-141040	Sequence 141040, A	484	5	35.7	527	15	US-10-425-114-39205	Sequence 39205, A
412	5	35.7	400	16	US-10-437-963-197136	Sequence 197136, A	485	5	35.7	527	15	US-10-425-114-39205	Sequence 39205, A
413	5	35.7	406	15	US-10-425-114-56149	Sequence 56149, A	486	5	35.7	529	16	US-10-739-096-6	Sequence 6, Appli
414	5	35.7	407	15	US-10-601-309-78	Sequence 78, Appl	487	5	35.7	530	16	US-10-739-096-2	Sequence 2, Appli
415	5	35.7	413	15	US-10-154-884B-11040	Sequence 11040, A	488	5	35.7	531	16	US-10-477-527-12	Sequence 12, Appl
416	5	35.7	415	15	US-10-154-884B-11041	Sequence 11041, A	489	5	35.7	535	15	US-10-424-599-199751	Sequence 199751, A
417	5	35.7	415	15	US-10-424-599-254998	Sequence 254998, A	490	5	35.7	535	15	US-10-120-801-12	Sequence 12, Appl
418	5	35.7	416	14	US-10-067-076-1	Sequence 1, Appli	491	5	35.7	539	9	US-09-738-626-6722	Sequence 6722, Ap
419	5	35.7	416	14	US-10-067-076-20	Sequence 20, Appl	492	5	35.7	540	15	US-10-424-599-227611	Sequence 227611, A
420	5	35.7	416	14	US-10-067-076-22	Sequence 22, Appl	493	5	35.7	541	16	US-10-437-963-133506	Sequence 133506, A
421	5	35.7	416	15	US-10-369-493-18612	Sequence 18612, A	494	5	35.7	542	15	US-10-424-599-146181	Sequence 146181, A
422	5	35.7	424	9	US-09-853-450-16	Sequence 16, Appl	495	5	35.7	545	15	US-10-424-599-219246	Sequence 219246, A
423	5	35.7	424	10	US-09-849-772-2	Sequence 2, Appli	496	5	35.7	548	15	US-10-424-599-229536	Sequence 229536, A
424	5	35.7	425	16	US-10-767-701-44784	Sequence 44784, A	497	5	35.7	555	9	US-09-801-368-350	Sequence 350, App
425	5	35.7	426	15	US-10-369-493-21051	Sequence 21051, A	498	5	35.7	555	15	US-10-369-493-22500	Sequence 22500, A
426	5	35.7	432	14	US-10-268-611-40	Sequence 40, Appl	499	5	35.7	560	15	US-10-425-114-45686	Sequence 45686, A
427	5	35.7	432	14	US-10-205-219-48	Sequence 48, Appl	500	5	35.7	569	15	US-10-369-493-22322	Sequence 22322, A
428	5	35.7	437	15	US-10-369-493-6987	Sequence 6987, Ap	501	5	35.7	575	15	US-10-120-801-60	Sequence 60, Appli
429	5	35.7	440	15	US-10-425-114-59337	Sequence 59337, A	502	5	35.7	575	15	US-10-312-352-8	Sequence 8, Appli
430	5	35.7	444	16	US-10-437-963-113732	Sequence 113732, A	503	5	35.7	575	16	US-10-408-765A-1901	Sequence 1901, Ap
431	5	35.7	445	15	US-10-282-122A-57306	Sequence 57306, A	504	5	35.7	578	15	US-10-403-337-68	Sequence 68, Appl
432	5	35.7	448	15	US-10-369-493-12738	Sequence 12738, A	505	5	35.7	578	15	US-10-351-890-68	Sequence 68, Appl
433	5	35.7	451	15	US-10-282-122A-68682	Sequence 68682, A	506	5	35.7	583	16	US-10-437-963-180545	Sequence 180545, A
434	5	35.7	456	9	US-09-815-242-10870	Sequence 10870, A	507	5	35.7	589	16	US-10-437-963-160820	Sequence 160820, A
435	5	35.7	459	15	US-10-074-978A-246	Sequence 246, App	508	5	35.7	592	15	US-10-425-114-65930	Sequence 65930, A
436	5	35.7	460	15	US-10-154-884B-11048	Sequence 11048, A	509	5	35.7	592	15	US-10-425-114-70054	Sequence 70054, A
437	5	35.7	460	15	US-10-425-114-46265	Sequence 46265, A	510	5	35.7	604	15	US-10-425-114-58837	Sequence 58837, A
438	5	35.7	464	15	US-10-369-493-17155	Sequence 17155, A	511	5	35.7	607	15	US-10-369-493-10287	Sequence 10287, A
439	5	35.7	464	15	US-10-282-122A-48492	Sequence 48492, A	512	5	35.7	614	15	US-10-282-122A-67017	Sequence 67017, A
440	5	35.7	465	14	US-10-097-340-151	Sequence 151, App	513	5	35.7	617	16	US-10-437-963-107860	Sequence 107860, A
441	5	35.7	467	14	US-10-097-340-153	Sequence 153, App	514	5	35.7	619	15	US-10-369-493-481	Sequence 481, App
442	5	35.7	468	15	US-10-120-801-61	Sequence 61, Appl	515	5	35.7	620	9	US-09-815-242-10068	Sequence 10068, A
443	5	35.7	468	15	US-10-282-122A-78354	Sequence 78354, A	516	5	35.7	620	9	US-09-815-242-14083	Sequence 14083, A
444	5	35.7	469	16	US-10-437-963-186909	Sequence 186909, A	517	5	35.7	620	15	US-10-381-779-31	Sequence 31, Appl
445	5	35.7	471	15	US-10-369-493-4578	Sequence 4578, Ap	518	5	35.7	620	15	US-10-369-493-731	Sequence 731, App
446	5	35.7	473	15	US-10-369-493-3972	Sequence 3972, Ap	519	5	35.7	620	15	US-10-369-493-21174	Sequence 21174, A
447	5	35.7	474	9	US-09-752-639-148	Sequence 148, App	520	5	35.7	620	15	US-10-282-122A-55979	Sequence 55979, A
448	5	35.7	474	9	US-09-984-198-148	Sequence 148, App	521	5	35.7	620	15	US-10-282-122A-56450	Sequence 56450, A
449	5	35.7	475	15	US-10-282-122A-71103	Sequence 71103, A	522	5	35.7	620	15	US-10-282-122A-75419	Sequence 75419, A
450	5	35.7	479	14	US-10-238-075-1407	Sequence 1407, App	523	5	35.7	623	16	US-10-408-765A-1812	Sequence 1812, Ap
451	5	35.7	479	15	US-10-369-493-7335	Sequence 7335, Ap	524	5	35.7	623	16	US-10-437-963-144350	Sequence 144350, A

525	5	35.7	624	15	US-10-282-122A-69045	Sequence 69045, A	598	16	US-10-467-534-79	Sequence 79, Appl
526	5	35.7	625	15	US-10-381-779-33	Sequence 33, Appl	599	16	US-10-437-963-180520	Sequence 180520, A
527	5	35.7	626	15	US-10-282-122A-58516	Sequence 58516, A	600	15	US-10-267-503-385	Sequence 385, App
528	5	35.7	627	15	US-10-282-122A-77171	Sequence 77171, A	601	15	US-09-840-746-19	Sequence 19, Appl
529	5	35.7	628	15	US-10-369-493-598	Sequence 598, App	602	15	US-10-437-963-122331	Sequence 122331, A
530	5	35.7	629	15	US-09-742-096-5	Sequence 5, Appl	603	15	US-10-389-566-1458	Sequence 1458, Ap
531	5	35.7	630	15	US-10-474-776-706	Sequence 706, App	604	15	US-10-211-963-43	Sequence 43, Appl
532	5	35.7	631	14	US-10-273-051-8	Sequence 8, Appl	605	15	US-10-389-566-1945	Sequence 1945, Ap
533	5	35.7	632	15	US-10-129-518-8	Sequence 8, Appl	606	15	US-10-389-566-1238	Sequence 1238, Ap
534	5	35.7	633	15	US-10-369-493-1991	Sequence 1991, Ap	607	15	US-09-815-242-5573	Sequence 5573, Ap
535	5	35.7	634	15	US-10-156-761-8643	Sequence 8643, Ap	608	15	US-10-389-566-1237	Sequence 1237, Ap
536	5	35.7	635	14	US-10-437-963-174390	Sequence 174390, A	609	15	US-10-317-835-16	Sequence 16, Appl
537	5	35.7	636	15	US-10-472-928-3386	Sequence 3386, Ap	610	15	US-10-168-583-7	Sequence 7, Appl
538	5	35.7	637	15	US-10-437-963-158260	Sequence 158260, A	611	15	US-10-032-585-7652	Sequence 7652, Ap
539	5	35.7	638	15	US-10-282-122A-52022	Sequence 52022, A	612	15	US-09-815-242-12617	Sequence 12617, A
540	5	35.7	639	15	US-10-437-963-165912	Sequence 165912, A	613	15	US-10-282-122A-44343	Sequence 44343, A
541	5	35.7	640	15	US-10-437-963-197260	Sequence 197260, A	614	15	US-10-857-625-704	Sequence 704, App
542	5	35.7	641	15	US-10-369-493-5126	Sequence 5126, Ap	615	15	US-09-966-521-110	Sequence 110, App
543	5	35.7	642	15	US-09-358-635-2	Sequence 2, Appl	616	15	US-10-429-094-110	Sequence 110, App
544	5	35.7	643	15	US-10-408-765A-2828	Sequence 2828, Ap	617	15	US-10-437-963-157156	Sequence 157156, A
545	5	35.7	644	15	US-10-295-403-98	Sequence 98, Appl	618	15	US-10-437-963-191478	Sequence 191478, A
546	5	35.7	645	14	US-10-286-264-44	Sequence 44, Appl	619	15	US-10-437-963-181712	Sequence 181712, A
547	5	35.7	646	15	US-10-412-699B-564	Sequence 564, App	620	15	US-10-282-122A-71757	Sequence 71757, A
548	5	35.7	647	15	US-09-815-242-11365	Sequence 11365, A	621	15	US-09-921-157-5	Sequence 5, Appl
549	5	35.7	648	15	US-10-437-963-204806	Sequence 204806, A	622	15	US-10-437-963-120457	Sequence 120457, A
550	5	35.7	649	15	US-10-369-493-4524	Sequence 4524, Ap	623	15	US-10-437-963-149114	Sequence 149114, A
551	5	35.7	650	15	US-10-369-493-21102	Sequence 21102, A	624	15	US-10-017-161-720	Sequence 720, App
552	5	35.7	651	15	US-10-369-493-7283	Sequence 7283, Ap	625	15	US-10-282-122A-46577	Sequence 46577, A
553	5	35.7	652	15	US-10-282-122A-56827	Sequence 56827, A	626	15	US-10-437-963-129457	Sequence 129457, A
554	5	35.7	653	15	US-10-437-963-155290	Sequence 155290, A	627	15	US-10-734-564-122	Sequence 122, App
555	5	35.7	654	15	US-10-424-599-156721	Sequence 156721, A	628	15	US-10-193-764-37	Sequence 37, Appl
556	5	35.7	655	15	US-10-369-493-5645	Sequence 5645, Ap	629	15	US-10-193-764-34	Sequence 34, Appl
557	5	35.7	656	15	US-10-425-114-50080	Sequence 50080, A	630	15	US-10-282-122A-76279	Sequence 76279, A
558	5	35.7	657	15	US-09-862-179A-1	Sequence 1, Appl	631	15	US-10-032-585-7858	Sequence 7858, Ap
559	5	35.7	658	15	US-10-437-963-135565	Sequence 135565, A	632	15	US-10-437-963-118488	Sequence 118488, A
560	5	35.7	659	15	US-09-771-161A-101	Sequence 101, App	633	15	US-10-437-963-189422	Sequence 189422, A
561	5	35.7	660	15	US-10-282-122A-73465	Sequence 73465, A	634	15	US-10-282-122A-69692	Sequence 69692, A
562	5	35.7	661	15	US-10-282-122A-72723	Sequence 72723, A	635	15	US-10-437-963-142101	Sequence 142101, A
563	5	35.7	662	15	US-10-032-585-7117	Sequence 7117, Ap	636	15	US-09-754-032-4	Sequence 4, Appl
564	5	35.7	663	15	US-10-437-963-108295	Sequence 108295, A	637	15	US-10-421-446-4	Sequence 4, Appl
565	5	35.7	664	15	US-10-369-493-5483	Sequence 5483, Ap	638	15	US-09-402-100-4	Sequence 4, Appl
566	5	35.7	665	15	US-10-369-493-22456	Sequence 22456, A	639	15	US-10-282-122A-55213	Sequence 55213, A
567	5	35.7	666	15	US-10-425-114-57786	Sequence 57786, A	640	15	US-10-379-616-12	Sequence 12, Appl
568	5	35.7	667	15	US-09-815-242-5499	Sequence 5499, Ap	641	15	US-10-408-765A-2282	Sequence 2282, Ap
569	5	35.7	668	15	US-10-267-989-6	Sequence 6, Appl	642	15	US-10-282-122A-66678	Sequence 66678, A
570	5	35.7	669	15	US-10-114-270-172	Sequence 172, App	643	15	US-10-379-616-4	Sequence 4, Appl
571	5	35.7	670	15	US-10-437-963-113995	Sequence 46349, A	644	15	US-10-418-027-1	Sequence 1, Appl
572	5	35.7	671	15	US-10-282-122A-63439	Sequence 63439, A	645	15	US-10-170-682-3	Sequence 3, Appl
573	5	35.7	672	15	US-10-436-715-34	Sequence 115995, A	646	15	US-10-355-218-2	Sequence 2, Appl
574	5	35.7	673	15	US-10-436-715-78	Sequence 10, Appl	647	15	US-10-369-493-22554	Sequence 22554, A
575	5	35.7	674	15	US-10-389-566-1944	Sequence 78, Appl	648	15	US-10-437-963-131952	Sequence 131952, A
576	5	35.7	675	15	US-10-457-031-171	Sequence 171, App	649	15	US-10-497-692-13	Sequence 13, Appl
577	5	35.7	676	15	US-10-424-599-214353	Sequence 214353, A	650	15	US-09-842-256-2	Sequence 2, Appl
578	5	35.7	677	15	US-10-282-122A-68895	Sequence 68895, A	651	15	US-09-832-292-37	Sequence 37, Appl
579	5	35.7	678	15	US-10-114-270-170	Sequence 170, App	652	15	US-10-437-963-140834	Sequence 140834, A
580	5	35.7	679	15	US-09-893-519A-73	Sequence 73, Appl	653	15	US-10-753-901-18	Sequence 18, Appl
581	5	35.7	680	15	US-10-389-566-2238	Sequence 2238, Ap	654	15	US-10-080-608A-37	Sequence 37, Appl
582	5	35.7	681	15	US-09-815-242-10147	Sequence 10147, A	655	15	US-10-370-685-126	Sequence 126, App
583	5	35.7	682	15	US-10-267-989-10	Sequence 10, Appl	656	15	US-10-282-122A-68175	Sequence 68175, A
584	5	35.7	683	15	US-10-282-122A-56533	Sequence 56533, A	657	15	US-10-087-192-663	Sequence 663, App
585	5	35.7	684	15	US-10-282-122A-77868	Sequence 77868, A	658	15	US-10-437-963-188419	Sequence 188419, A
586	5	35.7	685	15	US-09-815-242-13843	Sequence 13843, A	659	15	US-09-820-843A-16	Sequence 8, Appl
587	5	35.7	686	15	US-10-282-122A-75020	Sequence 75020, A	660	15	US-10-282-122A-63593	Sequence 63593, A
588	5	35.7	687	15	US-10-437-963-75981	Sequence 75981, A	661	15	US-10-369-493-1564	Sequence 1564, Ap
589	5	35.7	688	15	US-10-437-963-201319	Sequence 201319, A	662	15	US-10-188-832-86	Sequence 86, Appl
590	5	35.7	689	15	US-10-282-122A-77378	Sequence 77378, A	663	15	US-09-742-096-3	Sequence 3, Appl
591	5	35.7	690	15	US-10-014-156-13	Sequence 13, Appl	664	15	US-10-415-253-2	Sequence 2, Appl
592	5	35.7	691	15	US-10-282-122A-43767	Sequence 43767, A	665	15	US-10-424-599-147146	Sequence 147146, A
593	5	35.7	692	15	US-09-815-242-12407	Sequence 12407, A	666	15	US-10-087-192-666	Sequence 666, App
594	5	35.7	693	15	US-10-259-194A-322	Sequence 322, App	667	15	US-09-839-479-70	Sequence 70, Appl
595	5	35.7	694	15	US-10-437-963-111792	Sequence 111792, A	668	15	US-10-376-537-71	Sequence 71, Appl
596	5	35.7	695	15	US-10-114-270-168	Sequence 168, App	669	15	US-10-702-148-70	Sequence 70, Appl
597	5	35.7	696	15	US-10-425-114-39886	Sequence 39886, A	670	15		

671	5	35.7	1878	9	US-09-839-479-13	Sequence 13, Appl	744	4	28.6	9	15	US-10-057-475B-10084	Sequence 10084, A
672	5	35.7	1878	15	US-10-376-537-13	Sequence 13, Appl	745	4	28.6	9	15	US-10-057-475B-10109	Sequence 10109, A
673	5	35.7	1878	15	US-10-702-148-13	Sequence 13, Appl	746	4	28.6	9	15	US-10-057-475B-10114	Sequence 10114, A
674	5	35.7	1946	15	US-10-282-122A-62947	Sequence 62947, A	747	4	28.6	9	15	US-10-057-475B-10122	Sequence 10122, A
675	5	35.7	1969	9	US-09-839-479-71	Sequence 71, Appl	748	4	28.6	9	15	US-10-057-475B-10138	Sequence 10138, A
676	5	35.7	1969	15	US-10-376-537-72	Sequence 72, Appl	749	4	28.6	9	15	US-10-057-475B-10306	Sequence 10306, A
677	5	35.7	1969	15	US-10-702-148-71	Sequence 71, Appl	750	4	28.6	9	15	US-10-154-884B-10084	Sequence 10084, A
678	5	35.7	1972	9	US-09-839-479-21	Sequence 21, Appl	751	4	28.6	9	15	US-10-154-884B-10109	Sequence 10109, A
679	5	35.7	1972	15	US-10-376-537-21	Sequence 21, Appl	752	4	28.6	9	15	US-10-154-884B-10114	Sequence 10114, A
680	5	35.7	1972	15	US-10-702-148-21	Sequence 21, Appl	753	4	28.6	9	15	US-10-154-884B-10122	Sequence 10122, A
681	5	35.7	1975	16	US-10-437-563-188418	Sequence 188418, A	754	4	28.6	9	15	US-10-154-884B-10138	Sequence 10138, A
682	5	35.7	2062	15	US-10-389-566-1082	Sequence 1082, Ap	755	4	28.6	9	15	US-10-154-884B-10306	Sequence 10306, A
683	5	35.7	2139	17	US-10-480-456-1	Sequence 1, Appli	756	4	28.6	9	15	US-10-398-104-95	Sequence 95, Appl
684	5	35.7	2192	16	US-10-437-963-201156	Sequence 201156, A	757	4	28.6	9	16	US-10-764-324-10084	Sequence 10084, A
685	5	35.7	2364	15	US-10-205-331-66	Sequence 66, Appl	758	4	28.6	9	16	US-10-764-324-10109	Sequence 10109, A
686	5	35.7	2697	15	US-10-144-198-12	Sequence 12, Appl	759	4	28.6	9	16	US-10-764-324-10114	Sequence 10114, A
687	5	35.7	4080	15	US-10-307-817-138	Sequence 138, App	760	4	28.6	9	16	US-10-764-324-10122	Sequence 10122, A
688	5	35.7	4264	15	US-10-187-975-114	Sequence 114, App	761	4	28.6	9	16	US-10-764-324-10138	Sequence 10138, A
689	5	35.7	4349	10	US-09-970-944-4	Sequence 4, Appli	762	4	28.6	9	16	US-10-764-324-10138	Sequence 10138, A
690	5	35.7	4349	10	US-09-970-944-18	Sequence 18, Appl	763	4	28.6	9	16	US-10-764-324-10306	Sequence 10306, A
691	5	35.7	4349	10	US-09-970-944-19	Sequence 19, Appl	764	4	28.6	10	10	US-09-778-026-20	Sequence 20, Appl
692	5	35.7	4349	14	US-10-160-758-15	Sequence 15, Appl	765	4	28.6	10	10	US-09-998-350-4	Sequence 4, Appli
693	5	35.7	4349	14	US-10-174-677-76	Sequence 76, Appl	766	4	28.6	10	10	US-09-998-350-5	Sequence 5, Appli
694	5	35.7	4349	15	US-10-187-975-112	Sequence 112, App	767	4	28.6	10	10	US-09-998-350-6	Sequence 6, Appli
695	5	35.7	4349	16	US-10-408-765A-1739	Sequence 1739, Ap	768	4	28.6	10	10	US-09-998-350-8	Sequence 8, Appli
696	5	35.7	4624	16	US-10-408-765A-2991	Sequence 2991, Ap	769	4	28.6	10	10	US-09-998-350-11	Sequence 11, Appl
697	5	35.7	4640	16	US-10-408-765A-2103	Sequence 2103, Ap	770	4	28.6	10	10	US-09-998-350-12	Sequence 12, Appl
698	5	35.7	4655	16	US-10-741-601-314	Sequence 314, App	771	4	28.6	10	10	US-09-998-350-13	Sequence 13, Appl
699	5	35.7	4655	16	US-10-479-875-3	Sequence 3, Appli	772	4	28.6	10	10	US-09-998-350-14	Sequence 14, Appl
700	5	35.7	4655	17	US-10-741-600-897	Sequence 897, App	773	4	28.6	10	10	US-09-572-404B-2021	Sequence 2021, Ap
701	4	28.6	6	9	US-09-956-625-17	Sequence 17, Appl	774	4	28.6	10	10	US-09-572-404B-4044	Sequence 4044, Ap
702	4	28.6	6	14	US-10-195-970-2	Sequence 2, Appli	775	4	28.6	10	10	US-09-572-404B-4045	Sequence 4045, Ap
703	4	28.6	6	14	US-10-453-620-2	Sequence 2, Appli	776	4	28.6	10	10	US-09-573-822C-43	Sequence 43, Appl
704	4	28.6	7	9	US-09-956-625-3	Sequence 3, Appli	777	4	28.6	10	14	US-10-062-109A-436	Sequence 436, App
705	4	28.6	7	14	US-10-145-415-79	Sequence 79, Appl	778	4	28.6	10	14	US-10-062-109A-537	Sequence 537, App
706	4	28.6	8	9	US-09-765-086-157	Sequence 157, App	779	4	28.6	10	14	US-10-062-109A-634	Sequence 634, App
707	4	28.6	8	9	US-09-904-117-5	Sequence 5, Appli	780	4	28.6	10	14	US-10-005-480A-436	Sequence 436, App
708	4	28.6	8	13	US-10-041-030-29	Sequence 29, Appl	781	4	28.6	10	14	US-10-005-480A-537	Sequence 537, App
709	4	28.6	8	13	US-10-101-812-5	Sequence 5, Appli	782	4	28.6	10	14	US-10-005-480A-634	Sequence 634, App
710	4	28.6	8	14	US-10-101-662A-5	Sequence 5, Appli	783	4	28.6	10	15	US-10-432-236-3	Sequence 3, Appli
711	4	28.6	8	14	US-10-040-862-10407	Sequence 10407, A	784	4	28.6	10	16	US-10-648-854-20	Sequence 20, Appl
712	4	28.6	8	14	US-10-264-374-157	Sequence 157, App	785	4	28.6	10	17	US-10-901-243-85	Sequence 85, Appl
713	4	28.6	8	14	US-10-287-670-5	Sequence 5, Appli	786	4	28.6	10	17	US-10-901-243-86	Sequence 86, Appl
714	4	28.6	8	14	US-10-375-992-157	Sequence 157, App	787	4	28.6	10	17	US-10-901-243-87	Sequence 87, Appl
715	4	28.6	8	15	US-10-057-475B-10407	Sequence 10407, A	788	4	28.6	10	17	US-10-901-243-88	Sequence 88, Appl
716	4	28.6	8	15	US-10-154-884B-10407	Sequence 10407, A	789	4	28.6	11	9	US-09-826-290-206	Sequence 206, App
717	4	28.6	8	15	US-10-464-302-53	Sequence 53, Appl	790	4	28.6	11	10	US-09-852-910-46	Sequence 46, Appl
718	4	28.6	8	15	US-10-257-384A-19	Sequence 19, Appl	791	4	28.6	11	10	US-09-852-910-94	Sequence 94, Appl
719	4	28.6	8	15	US-10-264-374-157	Sequence 157, App	792	4	28.6	11	11	US-09-979-275A-1	Sequence 1, Appli
720	4	28.6	8	16	US-10-375-992-157	Sequence 157, App	793	4	28.6	11	14	US-10-013-815-32	Sequence 32, Appl
721	4	28.6	8	16	US-10-764-324-10407	Sequence 10407, A	794	4	28.6	11	14	US-10-160-506-102	Sequence 102, App
722	4	28.6	9	9	US-09-803-126-22	Sequence 22, Appl	795	4	28.6	11	14	US-10-286-457-327	Sequence 327, App
723	4	28.6	9	9	US-09-894-018-242	Sequence 242, App	796	4	28.6	11	15	US-10-411-336A-46	Sequence 46, Appl
724	4	28.6	9	10	US-09-998-350-1	Sequence 1, Appli	797	4	28.6	11	15	US-10-411-336A-94	Sequence 94, Appl
725	4	28.6	9	10	US-09-998-350-3	Sequence 3, Appli	798	4	28.6	11	15	US-10-264-309-130	Sequence 130, App
726	4	28.6	9	10	US-09-998-350-7	Sequence 7, Appli	799	4	28.6	11	15	US-10-398-104-235	Sequence 235, App
727	4	28.6	9	14	US-10-040-862-10084	Sequence 10084, A	800	4	28.6	11	16	US-10-449-379-102	Sequence 102, App
728	4	28.6	9	14	US-10-040-862-10109	Sequence 10109, A	801	4	28.6	11	16	US-10-688-015-102	Sequence 102, App
729	4	28.6	9	14	US-10-040-862-10114	Sequence 10114, A	802	4	28.6	12	10	US-09-988-493-197	Sequence 197, App
730	4	28.6	9	14	US-10-040-862-10122	Sequence 10122, A	803	4	28.6	12	12	US-10-601-837-27	Sequence 27, Appl
731	4	28.6	9	14	US-10-040-862-10138	Sequence 10138, A	804	4	28.6	12	16	US-10-128-520-92	Sequence 92, Appl
732	4	28.6	9	14	US-10-040-862-10306	Sequence 10306, A	805	4	28.6	13	10	US-09-899-046-249	Sequence 249, App
733	4	28.6	9	14	US-10-062-109A-137	Sequence 137, App	806	4	28.6	13	10	US-09-878-281-249	Sequence 249, App
734	4	28.6	9	14	US-10-062-109A-466	Sequence 466, App	807	4	28.6	13	10	US-09-873-224-249	Sequence 249, App
735	4	28.6	9	14	US-10-062-109A-567	Sequence 567, App	808	4	28.6	13	14	US-10-104-943-13	Sequence 13, Appl
736	4	28.6	9	14	US-10-360-836-32	Sequence 32, Appl	809	4	28.6	13	14	US-10-104-943-58	Sequence 58, Appl
737	4	28.6	9	14	US-10-005-480A-137	Sequence 137, App	810	4	28.6	13	14	US-10-104-943-74	Sequence 74, Appl
738	4	28.6	9	14	US-10-005-480A-466	Sequence 466, App	811	4	28.6	13	14	US-10-105-232-309	Sequence 309, App
739	4	28.6	9	14	US-10-005-480A-567	Sequence 567, App	812	4	28.6	13	14	US-10-105-232-330	Sequence 330, App
740	4	28.6	9	15	US-10-371-525-440	Sequence 440, App	813	4	28.6	13	14	US-10-189-437-296	Sequence 296, App
741	4	28.6	9	15	US-10-371-069-440	Sequence 440, App	814	4	28.6	13	14	US-10-189-437-317	Sequence 317, App
742	4	28.6	9	15	US-10-371-645-440	Sequence 440, App	815	4	28.6	13	16	US-10-601-837-74	Sequence 74, Appl
743	4	28.6	9	15	US-10-371-260-440	Sequence 440, App	816	4	28.6	13	16	US-10-468-496-682	Sequence 682, App

817	4	28.6	13	16	US-10-468-496-683	Sequence 583, App	890	20	14	US-10-189-437-294	Sequence 294, App
818	4	28.6	13	16	US-10-468-496-684	Sequence 584, App	891	20	15	US-10-238-960-7	Sequence 7, Appli
819	4	28.6	13	16	US-10-468-496-685	Sequence 585, App	892	20	15	US-10-238-960-8	Sequence 8, Appli
820	4	28.6	13	16	US-10-468-496-686	Sequence 586, App	893	20	15	US-10-651-165-35	Sequence 35, Appl
821	4	28.6	13	16	US-10-468-496-687	Sequence 587, App	894	20	15	US-10-651-165-36	Sequence 36, Appl
822	4	28.6	14	14	US-10-104-344-49	Sequence 49, Appl	895	20	15	US-10-239-103-5	Sequence 5, Appli
823	4	28.6	14	14	US-10-104-343-24	Sequence 24, Appl	896	20	15	US-10-432-465-63	Sequence 63, Appl
824	4	28.6	14	14	US-10-104-343-48	Sequence 48, Appl	897	20	15	US-10-432-465-64	Sequence 64, Appl
825	4	28.6	14	14	US-10-104-343-68	Sequence 68, Appl	898	20	15	US-10-432-465-65	Sequence 65, Appl
826	4	28.6	14	16	US-10-327-598-594	Sequence 594, App	899	20	16	US-10-433-091-32	Sequence 32, Appl
827	4	28.6	15	8	US-08-865-579-59	Sequence 59, Appl	900	20	16	US-10-433-091-33	Sequence 33, Appl
828	4	28.6	15	8	US-08-736-019-49	Sequence 49, Appl	901	20	16	US-10-433-091-34	Sequence 34, Appl
829	4	28.6	15	9	US-09-746-731-59	Sequence 59, Appl	902	20	16	US-10-321-798-79	Sequence 79, Appl
830	4	28.6	15	9	US-09-952-768-11	Sequence 41, Appl	903	20	16	US-10-321-798-80	Sequence 80, Appl
831	4	28.6	15	9	US-09-952-768-46	Sequence 46, Appl	904	20	16	US-10-794-929-69	Sequence 69, Appl
832	4	28.6	15	9	US-09-954-697-97	Sequence 97, Appl	905	20	11	US-09-833-245-1066	Sequence 1066, Ap
833	4	28.6	15	13	US-10-103-395-67	Sequence 67, Appl	906	21	14	US-10-174-410-45	Sequence 45, Appl
834	4	28.6	15	13	US-10-029-413A-26	Sequence 26, Appl	907	21	14	US-10-057-789-159	Sequence 159, App
835	4	28.6	15	13	US-10-059-749-59	Sequence 59, Appl	908	21	14	US-10-212-628-159	Sequence 159, App
836	4	28.6	15	14	US-10-174-105A-115	Sequence 115, App	909	21	14	US-10-105-232-306	Sequence 306, App
837	4	28.6	15	14	US-10-174-105A-116	Sequence 116, App	910	21	14	US-10-189-437-293	Sequence 293, App
838	4	28.6	15	15	US-10-378-707-3	Sequence 3, Appli	911	21	15	US-10-651-563-43	Sequence 43, Appl
839	4	28.6	15	15	US-10-668-955-46	Sequence 46, Appl	912	21	15	US-10-097-065-356	Sequence 356, App
840	4	28.6	16	8	US-08-736-019-37	Sequence 37, Appl	913	23	15	US-10-372-876-356	Sequence 356, App
841	4	28.6	16	9	US-09-776-430-47	Sequence 47, Appl	914	24	9	US-09-857-852-70	Sequence 70, Appl
842	4	28.6	16	9	US-09-776-431-47	Sequence 47, Appl	915	24	14	US-10-193-764-4	Sequence 4, Appli
843	4	28.6	16	14	US-10-006-760-58	Sequence 58, Appl	916	24	15	US-10-613-472-70	Sequence 70, Appl
844	4	28.6	16	15	US-10-378-173-139	Sequence 139, App	917	24	16	US-10-613-765-70	Sequence 70, Appl
845	4	28.6	16	15	US-10-436-715-244	Sequence 244, App	918	24	16	US-09-813-345-22	Sequence 22, Appl
846	4	28.6	16	15	US-10-436-715-283	Sequence 283, App	919	25	10	US-09-197-945-252	Sequence 252, App
847	4	28.6	16	15	US-10-182-936A-179	Sequence 179, App	920	25	10	US-09-924-447C-3	Sequence 3, Appli
848	4	28.6	16	16	US-10-128-520-93	Sequence 93, Appl	921	25	10	US-09-924-447C-4	Sequence 4, Appli
849	4	28.6	17	9	US-09-864-761-37350	Sequence 37350, A	922	25	14	US-10-239-423-29	Sequence 29, Appl
850	4	28.6	17	14	US-10-225-567A-1107	Sequence 1107, Ap	923	25	15	US-10-653-595-252	Sequence 252, App
851	4	28.6	17	16	US-10-258-637-40	Sequence 40, Appl	924	25	16	US-10-416-249-330	Sequence 330, App
852	4	28.6	17	16	US-10-258-637-43	Sequence 43, Appl	925	26	9	US-09-864-761-44151	Sequence 44151, A
853	4	28.6	18	10	US-09-776-724A-244	Sequence 244, App	926	26	9	US-09-864-761-46880	Sequence 46880, A
854	4	28.6	18	14	US-10-084-813-16	Sequence 16, Appl	927	26	9	US-09-921-397-7	Sequence 7, Appli
855	4	28.6	18	14	US-10-084-813-157	Sequence 157, App	928	26	9	US-09-921-397-35	Sequence 35, Appl
856	4	28.6	18	14	US-10-084-813-158	Sequence 158, App	929	26	10	US-09-983-802-579	Sequence 579, App
857	4	28.6	18	14	US-10-084-813-159	Sequence 159, App	930	26	10	US-09-984-490-579	Sequence 579, App
858	4	28.6	18	14	US-10-225-567A-1440	Sequence 1440, Ap	931	26	10	US-09-998-350-18	Sequence 18, Appl
859	4	28.6	18	15	US-10-419-462-39	Sequence 39, Appl	932	26	10	US-09-998-350-19	Sequence 19, Appl
860	4	28.6	19	8	US-08-841-636A-29	Sequence 29, Appl	933	26	11	US-09-973-278-607	Sequence 607, App
861	4	28.6	19	14	US-10-105-232-308	Sequence 308, App	934	26	11	US-10-029-386-30581	Sequence 30581, A
862	4	28.6	19	14	US-10-189-437-295	Sequence 295, App	935	27	9	US-09-864-761-34056	Sequence 34056, A
863	4	28.6	19	16	US-10-412-964-69	Sequence 69, Appl	936	27	10	US-09-933-767-702	Sequence 702, App
864	4	28.6	19	16	US-10-782-002-29	Sequence 29, Appl	937	27	14	US-10-004-860-702	Sequence 702, App
865	4	28.6	19	16	US-10-825-378-29	Sequence 29, Appl	938	27	14	US-10-057-789-275	Sequence 275, App
866	4	28.6	20	9	US-09-884-441-407	Sequence 407, App	939	27	14	US-10-212-628-275	Sequence 275, App
867	4	28.6	20	9	US-09-813-333-5	Sequence 5, Appli	940	27	14	US-10-023-282-702	Sequence 702, App
868	4	28.6	20	9	US-09-973-025-79	Sequence 79, Appl	941	27	14	US-10-339-740-293	Sequence 293, App
869	4	28.6	20	9	US-09-973-025-80	Sequence 80, Appl	942	28	8	US-08-424-5508-456	Sequence 456, App
870	4	28.6	20	10	US-09-991-433-49	Sequence 49, Appl	943	28	14	US-10-105-232-329	Sequence 329, App
871	4	28.6	20	10	US-09-991-433-50	Sequence 50, Appl	944	28	14	US-10-189-437-316	Sequence 316, App
872	4	28.6	20	10	US-09-899-303-79	Sequence 79, Appl	945	28	15	US-10-424-599-251229	Sequence 251229, App
873	4	28.6	20	10	US-09-899-303-80	Sequence 80, Appl	946	28	16	US-10-695-499-156	Sequence 156, App
874	4	28.6	20	10	US-09-907-969-407	Sequence 407, App	947	28	16	US-09-864-761-43902	Sequence 43902, A
875	4	28.6	20	10	US-09-995-808-79	Sequence 79, Appl	948	29	9	US-09-813-345-1	Sequence 1, Appli
876	4	28.6	20	10	US-09-995-808-80	Sequence 80, Appl	949	29	9	US-09-813-345-2	Sequence 2, Appli
877	4	28.6	20	10	US-09-995-860-79	Sequence 79, Appl	950	29	9	US-09-921-397-24	Sequence 24, Appl
878	4	28.6	20	10	US-09-995-860-80	Sequence 80, Appl	951	29	14	US-09-071-838-189	Sequence 189, App
879	4	28.6	20	10	US-09-995-791-79	Sequence 79, Appl	952	29	14	US-10-213-513-189	Sequence 189, App
880	4	28.6	20	10	US-09-995-791-80	Sequence 79, Appl	953	30	9	US-09-864-761-48497	Sequence 48497, A
881	4	28.6	20	10	US-09-927-771-407	Sequence 407, App	954	30	9	US-09-813-345-2	Sequence 2, Appli
882	4	28.6	20	13	US-10-044-703-5	Sequence 5, Appli	955	30	9	US-09-983-802-662	Sequence 662, App
883	4	28.6	20	14	US-10-053-485-48	Sequence 48, Appl	956	30	10	US-09-984-490-662	Sequence 662, App
884	4	28.6	20	14	US-10-013-815-3	Sequence 3, Appli	957	30	11	US-09-973-278-443	Sequence 443, App
885	4	28.6	20	14	US-10-198-053-407	Sequence 407, App	958	30	14	US-10-162-538-15	Sequence 15, Appl
886	4	28.6	20	14	US-10-198-053-613	Sequence 613, App	959	30	14	US-10-299-043-11	Sequence 11, Appl
887	4	28.6	20	14	US-10-371-634-42	Sequence 42, Appl	960	30	15	US-10-411-544-52	Sequence 52, Appl
888	4	28.6	20	14	US-10-105-232-307	Sequence 307, App	961	30	15	US-10-296-734-472	Sequence 472, App
889	4	28.6	20	14	US-10-280-066-32	Sequence 32, Appl	962	30	15	US-10-296-734-474	Sequence 474, App

963 4 28.6 30 16 US-10-685-435-41 Sequence 41, Appl
964 4 28.6 30 16 US-10-481-180-740 Sequence 740, App
965 4 28.6 30 17 US-10-718-071-45 Sequence 45, Appl
966 4 28.6 30 17 US-10-850-055-6 Sequence 6, Appl
967 4 28.6 31 9 US-09-813-345-18 Sequence 18, Appl
968 4 28.6 31 14 US-10-162-538-14 Sequence 14, Appl
969 4 28.6 31 15 US-10-424-599-167284 Sequence 167284,
970 4 28.6 31 16 US-10-258-637-30 Sequence 30, Appl
971 4 28.6 31 16 US-10-682-675-7 Sequence 7, Appl
972 4 28.6 32 14 US-10-472-928-3764 Sequence 3764, App
973 4 28.6 32 14 US-10-029-386-32129 Sequence 32129, A
974 4 28.6 32 14 US-10-029-386-34183 Sequence 34183, A
975 4 28.6 32 15 US-10-398-449-25 Sequence 25, Appl
976 4 28.6 32 15 US-10-311-366-27 Sequence 27, Appl
977 4 28.6 33 9 US-09-864-761-42244 Sequence 42244, A
978 4 28.6 33 9 US-09-864-761-42551 Sequence 42551, A
979 4 28.6 33 9 US-09-921-397-14 Sequence 14, Appl
980 4 28.6 33 11 US-09-855-604-216 Sequence 216, App
981 4 28.6 33 14 US-10-289-135A-37 Sequence 37, Appl
982 4 28.6 34 10 US-09-910-082A-311 Sequence 311, App
983 4 28.6 34 10 US-09-910-082A-393 Sequence 393, App
984 4 28.6 34 15 US-10-424-599-173709 Sequence 173709,
985 4 28.6 34 15 US-10-424-599-252012 Sequence 252012,
986 4 28.6 34 15 US-10-424-599-274374 Sequence 274374,
987 4 28.6 34 16 US-10-765-926-311 Sequence 311, App
988 4 28.6 34 16 US-10-765-926-393 Sequence 393, App
989 4 28.6 35 9 US-09-925-302-457 Sequence 457, App
990 4 28.6 35 9 US-09-864-761-35392 Sequence 35392, A
991 4 28.6 35 14 US-09-925-302-457 Sequence 457, App
992 4 28.6 35 14 US-10-059-261-99 Sequence 99, Appl
993 4 28.6 35 14 US-10-059-261-207 Sequence 207, App
994 4 28.6 35 14 US-10-029-386-27626 Sequence 27626, A
995 4 28.6 35 15 US-10-424-599-171017 Sequence 171017,
996 4 28.6 35 15 US-10-424-599-180127 Sequence 180127,
997 4 28.6 35 15 US-10-424-599-195564 Sequence 195564,
998 4 28.6 35 16 US-10-437-963-162435 Sequence 162435,
999 4 28.6 36 8 US-08-851-965-2 Sequence 2, Appl
1000 4 28.6 36 8 US-08-851-965-5 Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-09-736-250-5
; Sequence 5, Application US/09736250
; Publication No. US20050014139A1
; GENERAL INFORMATION:
; APPLICANT: SUMITOMO ELECTRIC INDUSTRIES, LTD.
; APPLICANT: NAKAMURA, Takeshi
; TITLE OF INVENTION: HUMAN CYCLIN I AND GENES ENCODING THE SAME
; FILE REFERENCE: 050212-0278
; CURRENT APPLICATION NUMBER: US/09/736,250
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 09/054,492
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: PCT/JP96/02905
; PRIOR FILING DATE: 1996-10-07
; PRIOR APPLICATION NUMBER: 284663/1995
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 5
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically synthesized
US-09-736-250-5
Query Match 100.0%; Score 14; DB 12; Length 14;
Best Local Similarity 100.0%; Pred. No. 9.2e-08; Length 14;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2
US-09-736-250-1
; Sequence 1, Application US/09736250
; Publication No. US20050014139A1
; GENERAL INFORMATION:
; APPLICANT: SUMITOMO ELECTRIC INDUSTRIES, LTD.
; APPLICANT: NAKAMURA, Takeshi
; TITLE OF INVENTION: HUMAN CYCLIN I AND GENES ENCODING THE SAME
; FILE REFERENCE: 050212-0278
; CURRENT APPLICATION NUMBER: US/09/736,250
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 09/054,492
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: PCT/JP96/02905
; PRIOR FILING DATE: 1996-10-07
; PRIOR APPLICATION NUMBER: 284663/1995
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1
; LENGTH: 377
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-736-250-1
Query Match 100.0%; Score 14; DB 12; Length 377;
Best Local Similarity 100.0%; Pred. No. 1.5e-06; Length 377;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3
US-10-149-310-280
; Sequence 280, Application US/10149310
; Publication No. US2004007039A1
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas
; APPLICANT: Madden, Kevin T.
; APPLICANT: Maxon, Mary
; APPLICANT: Sherman, Amir
; TITLE OF INVENTION: Modulation of Secondary Metabolite Production by
; FILE REFERENCE: 14184-019US1
; CURRENT APPLICATION NUMBER: US/10/149,310
; CURRENT FILING DATE: 2003-02-19
; PRIOR APPLICATION NUMBER: PCT/US01/29288
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: US 60/233,564
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 280
; LENGTH: 446
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-149-310-280
Query Match 50.0%; Score 7; DB 15; Length 446;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 4
US-10-149-310-280
; Sequence 280, Application US/10149310
; Publication No. US2004007039A1
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas
; APPLICANT: Madden, Kevin T.
; APPLICANT: Maxon, Mary
; APPLICANT: Sherman, Amir
; TITLE OF INVENTION: Modulation of Secondary Metabolite Production by
; FILE REFERENCE: 14184-019US1
; CURRENT APPLICATION NUMBER: US/10/149,310
; CURRENT FILING DATE: 2003-02-19
; PRIOR APPLICATION NUMBER: PCT/US01/29288
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: US 60/233,564
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 280
; LENGTH: 446
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-149-310-280
Query Match 50.0%; Score 7; DB 15; Length 446;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
RESULT 4
US-10-369-493-18546
; Sequence 18546, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 18546
; LENGTH: 1190
; TYPE: PRT
; ORGANISM: Halobacterium sp. NRC-1
US-10-369-493-18546
Query Match 50.0%; Score 7; DB 15; Length 1190;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 SENVGSV 11
Db 106 SENVGSV 112
|||||

RESULT 5
US-10-424-599-154932
; Sequence 154932, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 154932
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_110925C.1.pep
US-10-424-599-154932
Query Match 42.9%; Score 6; DB 15; Length 74;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VGSVCG 13
Db 2 VGSVCG 7
|||||

RESULT 6
US-10-264-049-3886
; Sequence 3886, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
```

```
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133P1
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 3886
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (10)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (28)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-264-049-3886
Query Match 42.9%; Score 6; DB 15; Length 81;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ENVGSV 11
Db 71 ENVGSV 76
|||||

RESULT 7
US-10-437-963-179908
; Sequence 179908, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 179908
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_77324C.1.pep
US-10-437-963-179908
Query Match 42.9%; Score 6; DB 16; Length 95;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VGSVCG 13
Db 48 VGSVCG 53
|||||
```

RESULT 8

US-10-424-599-244020
; Sequence 244020, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:

; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53223)B

; CURRENT APPLICATION NUMBER: US/10/424,599

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 285684

; SEQ ID NO 244020

; LENGTH: 98

; TYPE: PRT

; ORGANISM: Glycine max

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT3847_62378C.1.pep

US-10-424-599-244020

Query Match 42.9%; Score 6; DB 15; Length 98;

Best Local Similarity 100.0%; Pred. No. 73;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 NVSENV 8

Db 52 NVSENV 57

RESULT 9

US-10-437-963-119862
; Sequence 119862, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei

; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 119862

; LENGTH: 100

; TYPE: PRT

; ORGANISM: Oryza sativa

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (1)-(100)

; OTHER INFORMATION: unsure at all Xaa locations

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT4530_23037C.1.pep

US-10-437-963-119862

Query Match 42.9%; Score 6; DB 16; Length 100;

Best Local Similarity 100.0%; Pred. No. 74;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GSVCGT 14

Db 93 GSVCGT 98

RESULT 10

US-10-369-493-17361
; Sequence 17361, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.

; APPLICANT: Chen, Xianfeng

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

; FILE REFERENCE: 38-10(52052)B

; CURRENT APPLICATION NUMBER: US/10/369,493

; CURRENT FILING DATE: 2003-02-28

; PRIOR APPLICATION NUMBER: US 60/360,039

; PRIOR FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 47374

; SEQ ID NO 17361

; LENGTH: 169

; TYPE: PRT

; ORGANISM: Bacillus halodurans

US-10-369-493-17361

Query Match 42.9%; Score 6; DB 15; Length 169;

Best Local Similarity 100.0%; Pred. No. 1.2e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DNVSSEN 7

Db 117 DNVSSEN 122

RESULT 11

US-10-437-963-180011
; Sequence 180011, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei

; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 180011

; LENGTH: 199

; TYPE: PRT

; ORGANISM: Oryza sativa

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT4530_77417C.1.pep

US-10-437-963-180011

Query Match 42.9%; Score 6; DB 16; Length 199;

Best Local Similarity 100.0%; Pred. No. 1.3e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VGSVCG 13

Db 138 VGSVCG 143

RESULT 12

US-10-094-749-2381
; Sequence 2381, Application US/10094749
; Publication No. US20030219741A1
; GENERAL INFORMATION:

APPLICANT: ISOGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: WAKAMATSU, AI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: YAMAMOTO, JUN-ICHI
APPLICANT: ISONO, YUKIO
APPLICANT: HIO, YURI
APPLICANT: OTSUKA, KAORU
APPLICANT: NAGAI, KEIICHI
APPLICANT: IRIE, KYOTARO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NAOHICO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: OTSUKA, MOTOKYU
APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILE REFERENCE: 084335/0160 US/10/094,749
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/350,435
PRIOR FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: JP 2001-328381
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2381
LENGTH: 219
TYPE: PRT
ORGANISM: Homo sapiens
US-10-094-749-2381

Query Match 42.9%; Score 6; DB 15; Length 219;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VGSVCG 13
Db 37 VGSVCG 42

RESULT 13
US-10-437-963-197887
Sequence 197887, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kowalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 197887
LENGTH: 220
TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_93601C.1.pep
US-10-437-963-197887

Query Match 42.9%; Score 6; DB 16; Length 220;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GSVCGT 14
Db 182 GSVCGT 187

RESULT 14
US-10-080-170-315
Sequence 315, Application US/10080170
Publication No. US20030129601A1
GENERAL INFORMATION:
APPLICANT: COLE, S.T.
TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR
IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR
TREATMENT OF MYCOBACTERIOSES
FILE REFERENCE: 03495.0218
CURRENT APPLICATION NUMBER: US/10/080,170
CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: 60/270,123
PRIOR FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 652
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 315
LENGTH: 224
TYPE: PRT
ORGANISM: Mycobacterium leprae
US-10-080-170-315

Query Match 42.9%; Score 6; DB 14; Length 224;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VSENVG 9
Db 189 VSENVG 194

RESULT 15
US-10-080-170-315
Sequence 315, Application US/10080170
Publication No. US20040121322A9
GENERAL INFORMATION:
APPLICANT: COLE, S.T.
TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR
IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR
TREATMENT OF MYCOBACTERIOSES
FILE REFERENCE: 03495.0218
CURRENT APPLICATION NUMBER: US/10/080,170
CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: 60/270,123
PRIOR FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 652
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 315
LENGTH: 224
TYPE: PRT
ORGANISM: Mycobacterium leprae
US-10-080-170-315

Query Match 42.9%; Score 6; DB 16; Length 224;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VSENVG 9
Db 189 VSENVG 194

Search completed: February 11, 2005, 03:25:36
Job time : 19.2225 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 11, 2005, 03:06:34 ; Search time 1.07417 Seconds
(without alignments)
1254.025 Million cell updates/sec

Title: US-09-736-250-5

Perfect score: 14

Sequence: 1 EDNVSENVGVCVT 14

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

PIR 79.*

1: Pirl.*

2: Pirl.*

3: Pirl.*

4: Pirl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	50.0	446	2 S69051	hypothetical prote
2	7	50.0	1069	2 D91826	exodeoxyribonuclea
3	7	50.0	1190	2 B84193	chromosome segrega
4	6	42.9	106	2 C86086	hypothetical prote
5	6	42.9	109	2 G82929	ATP synthase C cha
6	6	42.9	118	2 AE1214	hypothetical prote
7	6	42.9	169	2 D83998	acetyl-CoA carboxy
8	6	42.9	224	2 D87236	conserved membrane
9	6	42.9	231	2 T20304	hypothetical prote
10	6	42.9	233	2 A1367	16S pseudouridylat
11	6	42.9	269	1 WZBE24	gene 24 protein -
12	6	42.9	291	2 D82491	hypothetical prote
13	6	42.9	296	2 B75555	probable lipase/es
14	6	42.9	345	2 S51548	killer toxin K28 -
15	6	42.9	359	2 H65201	pts system, fructo
16	6	42.9	381	2 AC1432	DNA polymerase III
17	6	42.9	381	2 AC1433	DNA polymerase III
18	6	42.9	389	2 D64333	pyruvate synthase
19	6	42.9	396	2 A13554	xylose transport s
20	6	42.9	457	2 S39079	puff C-8 protein -
21	6	42.9	457	2 A46188	CAMP-activated Na+
22	6	42.9	862	1 A49346	aldehyde dehydroge
23	6	42.9	935	2 E36806	hypothetical prote
24	6	42.9	1066	1 A48669	kinesin-related pr
25	6	42.9	1091	1 P10009	complement C3d/Eps
26	6	42.9	1131	2 T14517	hypothetical prote
27	6	42.9	1776	2 G86280	protein TSE21.13 (
28	6	42.9	1844	2 T51890	related to Nup98-N
29	6	42.9	4543	1 A53102	alpha-2-macroglobu

30	42.9	4544	1	S02392	alpha-2-macroglobu
31	42.9	4545	1	S25111	hypothetical prote
32	42.9	5170	2	T15348	26k kidney and gal
33	35.7	16	2	D58501	gene GFAP gamma pr
34	35.7	43	2	I52659	hypothetical prote
35	35.7	50	2	T20498	hypothetical prote
36	35.7	72	2	B84462	hypothetical prote
37	35.7	74	2	S26001	conserved hypotnet
38	35.7	84	2	D75545	interleukin-beta
39	35.7	88	2	D56084	ig light chain v r
40	35.7	91	2	PH1071	ig light chain v r
41	35.7	96	2	PH1070	ribosomal protein
42	35.7	98	2	A69007	very hypothetical
43	35.7	99	2	T39208	hypothetical prote
44	35.7	103	2	D64034	ig kappa chain v r
45	35.7	107	2	PL0268	B. subtilis comG o
46	35.7	107	2	AE1605	hypothetical prote
47	35.7	108	2	C64455	ribosomal protein
48	35.7	121	2	T44408	hypothetical prote
49	35.7	122	2	G95504	hypothetical prote
50	35.7	123	2	T26709	hypothetical prote
51	35.7	128	2	C91053	Nifu-like protein
52	35.7	128	2	H65029	iron-sulfur cofact
53	35.7	128	2	G85897	Nifu-like protein
54	35.7	131	2	S45059	AC1 protein (clone
55	35.7	140	2	I38232	gene SMA3 protein
56	35.7	140	2	I38233	gene SMA4 protein
57	35.7	140	2	I38234	gene SMA5 protein
58	35.7	143	2	T04524	photosystem I chai
59	35.7	145	2	A84587	hypothetical prote
60	35.7	149	2	A71074	probable methyalm
61	35.7	154	2	A11231	hypothetical prote
62	35.7	154	2	AH1585	hypothetical prote
63	35.7	156	2	E90508	conserved hypotnet
64	35.7	160	2	A48975	Thy-1 glycoprotein
65	35.7	160	2	T27963	hypothetical prote
66	35.7	163	2	JC5045	epithelial membran
67	35.7	166	2	T46231	hypothetical prote
68	35.7	179	2	D84773	hypothetical prote
69	35.7	184	2	T00277	conserved hypotnet
70	35.7	185	2	T31939	hypothetical prote
71	35.7	186	2	T25346	hypothetical prote
72	35.7	193	2	T26581	hypothetical prote
73	35.7	194	2	H90912	hypothetical prote
74	35.7	200	2	G84066	hypothetical prote
75	35.7	201	2	C96634	hypothetical prote
76	35.7	203	2	E97022	hypothetical prote
77	35.7	205	2	S34919	ribosomal protein
78	35.7	209	2	E64416	polyferredoxin - M
79	35.7	217	2	J50492	adenylate kinase (
80	35.7	220	2	F90065	hypothetical prote
81	35.7	221	2	JC4722	toxin co-regulated
82	35.7	222	2	H89763	hypothetical prote
83	35.7	225	2	T44105	hypothetical prote
84	35.7	226	2	T22445	hypothetical prote
85	35.7	227	2	G69762	two-component resp
86	35.7	228	2	AC1263	two-component resp
87	35.7	228	2	AE1625	two-component resp
88	35.7	229	2	A81169	hypothetical prote
89	35.7	231	2	A60468	venombin A (EC 3.4
90	35.7	231	2	G81936	hypothetical prote
91	35.7	232	1	A54361	venombin A (EC 3.4
92	35.7	233	1	JG0169	venombin A (EC 3.4
93	35.7	234	2	B95228	conserved hypotnet
94	35.7	234	2	F98092	conserved hypotnet
95	35.7	235	1	S65621	venombin AB (EC 3.
96	35.7	236	1	A41456	venombin A (EC 3.4
97	35.7	236	2	T07260	sulfate transport
98	35.7	239	2	G81369	probable membrane
99	35.7	240	2	E70115	hypothetical prote
100	35.7	241	2	F81218	competence protein
101	35.7	244	1	LNRTMC	mannose-binding le
102	35.7	244	2	T12051	3-oxoacyl-l-acyl-ca

103	5	35.7	244	2	T30120	hypothetical prote	176	5	35.7	344	2	D69420	hydrogenase expres
104	5	35.7	247	2	S73076	hypothetical prote	177	5	35.7	344	2	S22796	probable portal pr
105	5	35.7	248	1	Q0BE4L	probable glycoprot	178	5	35.7	346	2	T01123	hypothetical prote
106	5	35.7	248	2	F82128	3-oxoacyl-(acyl-ca	179	5	35.7	349	2	S12863	G protein-coupled
107	5	35.7	252	2	A87535	probable short cha	180	5	35.7	350	2	B70395	hypothetical prote
108	5	35.7	252	2	T14964	phage lambda-relat	181	5	35.7	355	2	G84651	biotin holocarboxy
109	5	35.7	252	2	B70602	hypothetical prote	182	5	35.7	356	2	AG0370	probable ABC-trans
110	5	35.7	253	2	T04059	hypothetical prote	183	5	35.7	359	2	S19235	gene C1 protein -
111	5	35.7	255	1	A28169	venombin A [EC 3.4	184	5	35.7	359	2	S19211	gene C1 protein -
112	5	35.7	255	2	UC7593	SH2 domain-contain	185	5	35.7	359	2	S22593	hypothetical prote
113	5	35.7	256	1	WMIMU2	28.5K transport pr	186	5	35.7	360	2	S57777	cysteine proteinas
114	5	35.7	257	1	JC2479	venombin B [EC 3.4	187	5	35.7	367	2	G97649	glutamine syntheta
115	5	35.7	257	2	T52298	squamosa promoter	188	5	35.7	367	2	F64202	probable GTP-bindi
116	5	35.7	258	1	S36783	venombin A [EC 3.4	189	5	35.7	371	2	D84186	hypothetical prote
117	5	35.7	258	2	A57290	venom plasminogen	190	5	35.7	373	2	G83574	hypothetical prote
118	5	35.7	258	2	A54907	casein kinase II (191	5	35.7	374	2	T44945	hypothetical prote
119	5	35.7	259	2	S22898	hypothetical prote	192	5	35.7	377	2	B64703	conserved hypotchet
120	5	35.7	260	2	AH2158	hypothetical prote	193	5	35.7	377	2	A71818	hypothetical prote
121	5	35.7	262	1	JC4803	venombin A [EC 3.4	194	5	35.7	379	2	T46002	hypothetical prote
122	5	35.7	267	2	B55850	hypothetical prote	195	5	35.7	380	1	G64509	conserved hypotchet
123	5	35.7	270	2	AC1956	phosphoesterase-re	196	5	35.7	380	2	T48953	hypothetical prote
124	5	35.7	270	2	C97772	diaminopimelate ep	197	5	35.7	382	2	T46133	neuropeptide Y/pep
125	5	35.7	275	2	T28738	hypothetical prote	198	5	35.7	383	2	T26902	hypothetical prote
126	5	35.7	276	2	B83161	probable short-cha	199	5	35.7	385	2	C87250	dnaj protein [lmpo
127	5	35.7	276	2	A30392	conserved hypotchet	200	5	35.7	387	2	F96798	hypothetical prote
128	5	35.7	276	2	A82668	molybdopterin bios	201	5	35.7	388	2	H84079	L-arabinose ABC tr
129	5	35.7	287	2	B81161	phosphoribosylamin	202	5	35.7	391	2	T39992	ribonucleoside-dip
130	5	35.7	287	2	G81943	probable phosphori	203	5	35.7	391	2	S34808	conserved hypotchet
131	5	35.7	288	2	C71936	probable co-chaper	204	5	35.7	397	2	AB0148	cell division prot
132	5	35.7	288	2	H64647	co-chaperone-curve	205	5	35.7	399	2	B84955	probable ribose/ga
133	5	35.7	288	2	H95018	transcription regu	206	5	35.7	400	2	E71338	hypothetical prote
134	5	35.7	289	1	A37209	thiosulfate sulfur	207	5	35.7	402	2	B90519	hypothetical prote
135	5	35.7	289	2	D70440	DNA polymerase I 3	208	5	35.7	408	2	T44859	glycosyltransferas
136	5	35.7	289	2	E30397	dihydrodipicolinat	209	5	35.7	412	2	C38104	LFY floral meriste
137	5	35.7	290	2	A57394	hypothetical prote	210	5	35.7	415	2	S37340	fio protein nomolo
138	5	35.7	290	2	AC2612	conserved hypotchet	211	5	35.7	416	2	B84276	glutamate dehydrog
139	5	35.7	292	2	AD2133	ferric aerobactin	212	5	35.7	419	2	T24820	hypothetical prote
140	5	35.7	292	2	E91130	hypothetical prote	213	5	35.7	420	2	AF1239	B. subtilis Yluc p
141	5	35.7	292	2	E85975	hypothetical prote	214	5	35.7	420	2	B38104	LFY floral meriste
142	5	35.7	292	2	T16085	hypothetical prote	215	5	35.7	422	1	A69853	hexuronate transpo
143	5	35.7	292	2	A40993	H+/K+-exchanging A	216	5	35.7	424	2	AG1804	LFY floral meriste
144	5	35.7	296	2	AH3343	serine O-acetyltra	217	5	35.7	427	2	AG1855	hypothetical prote
145	5	35.7	298	2	AB3190	hypothetical prote	218	5	35.7	429	2	JC4986	site-specific DNA-
146	5	35.7	298	2	S69523	hypothetical prote	219	5	35.7	431	2	H70302	conserved hypotchet
147	5	35.7	305	2	A96593	unknown protein [i	220	5	35.7	432	2	T51020	chorismate synthas
148	5	35.7	310	2	B55053	endothelial monocy	221	5	35.7	432	2	T46725	hypothetical prote
149	5	35.7	310	2	G86490	probable biotin ho	222	5	35.7	433	2	S63447	hypothetical prote
150	5	35.7	313	2	C95247	conserved hypotchet	223	5	35.7	433	2	H84826	hypothetical prote
151	5	35.7	313	2	H98111	conserved hypotchet	224	5	35.7	437	2	T21518	kynurenine-oxoglut
152	5	35.7	316	1	A38743	loricrin - human	225	5	35.7	439	2	D86297	hypothetical prote
153	5	35.7	317	2	T10813	1-aminocyclopropan	226	5	35.7	451	2	C81059	conserved hypotchet
154	5	35.7	317	2	C82450	1-phosphofructokin	227	5	35.7	451	2	B81818	conserved hypotchet
155	5	35.7	317	2	A97684	hypothetical prote	228	5	35.7	453	2	T21528	hypothetical prote
156	5	35.7	317	2	AB2909	rhizobioicin [lmpor	229	5	35.7	456	2	T22347	hypothetical prote
157	5	35.7	318	2	C84212	immunogenic protei	230	5	35.7	459	2	G89980	aldehyde dehydroge
158	5	35.7	319	2	A53502	folistatin - Afri	231	5	35.7	460	2	G81327	probable glycolate
159	5	35.7	320	2	G96714	hypothetical prote	232	5	35.7	464	2	H83752	glutamate dehydrog
160	5	35.7	322	2	JN0265	genome polypotein	233	5	35.7	465	2	D84427	hypothetical prote
161	5	35.7	322	2	E30457	rieske iron-sulfur	234	5	35.7	466	2	H96591	secreted protein c
162	5	35.7	322	2	B84635	hypothetical prote	235	5	35.7	468	2	AB0040	replicative DNA he
163	5	35.7	322	2	T50494	hypothetical prote	236	5	35.7	470	2	T31049	hypothetical prote
164	5	35.7	329	2	E69054	cobalamin biosynth	237	5	35.7	471	2	T27856	hypothetical prote
165	5	35.7	331	2	S74810	probable succinate	238	5	35.7	473	2	I40368	H+-transporting tw
166	5	35.7	333	2	AF1924	succinate dehydrog	239	5	35.7	473	2	AI1390	H+-transporting AT
167	5	35.7	335	2	E90014	hypothetical prote	240	5	35.7	475	2	AC1766	bacteriophage tail
168	5	35.7	336	2	E36020	probable sugar upt	241	5	35.7	475	2	AF0687	bacteriophage tail
169	5	35.7	337	2	D89850	glycolytic operon	242	5	35.7	481	2	S49778	hypothetical prote
170	5	35.7	337	2	T18431	hypothetical prote	243	5	35.7	483	2	S61975	glutathione-disulf
171	5	35.7	339	2	A95937	hypothetical adeny	244	5	35.7	485	2	B81871	probable GTP-bindi
172	5	35.7	340	2	T13781	NADH2 dehydrogenas	245	5	35.7	485	2	G81149	essential GTPase N
173	5	35.7	341	2	T51897	related to sorbito	246	5	35.7	488	2	T32149	hypothetical prote
174	5	35.7	342	2	A53057	retinal-binding pr	247	5	35.7	490	2	AF0156	probable D-mannosa
175	5	35.7	344	2	AF2873	glutamine syntheta	248	5	35.7	491	2	T50346	hypothetical prote

249 5 35.7 492 2 AD3047 copper tolerance p
250 5 35.7 492 2 H98238 hypothetical prote
251 5 35.7 493 2 T05161 hypothetical prote
252 5 35.7 497 1 S41397 DNA damage inducib
253 5 35.7 497 1 S33938 penton protein (II
254 5 35.7 497 2 S57073 probable membrane
255 5 35.7 499 2 T03877 hypothetical prote
256 5 35.7 504 2 D71615 hypothetical prote
257 5 35.7 504 2 T34411 hypothetical prote
258 5 35.7 505 2 H85361 leucyl aminopeptid
259 5 35.7 506 2 T38915 histidyl-tRNA synt
260 5 35.7 507 2 D75029 protein-export mem
261 5 35.7 507 2 A71215 hypothetical prote
262 5 35.7 518 2 G70174 hypothetical prote
263 5 35.7 520 2 H64510 hypothetical prote
264 5 35.7 520 2 S54151 cwi B protein - Az
265 5 35.7 521 2 F86418 61.6K hypothetical
266 5 35.7 526 2 E71423 hypothetical prote
267 5 35.7 527 2 T04659 hypothetical prote
268 5 35.7 528 1 WNEVB8 58K protein - barl
269 5 35.7 528 2 F70331 2-isopropylmalate
270 5 35.7 529 2 T03879 hypothetical prote
271 5 35.7 532 2 AD2420 hypothetical prote
272 5 35.7 535 2 E96730 hypothetical prote
273 5 35.7 537 2 T19764 hypothetical prote
274 5 35.7 541 2 T37945 conserved hypothet
275 5 35.7 544 1 S41389 penton protein (II
276 5 35.7 549 2 T50295 hypothetical prote
277 5 35.7 550 2 T34220 hypothetical prote
278 5 35.7 553 2 B55514 dihydrolipoamide S
279 5 35.7 555 2 S50157 cyclin-dependent k
280 5 35.7 560 2 S41808 glucose-6-phosphat
281 5 35.7 560 2 C84632 hypothetical prote
282 5 35.7 564 2 T11548 probable zinc meta
283 5 35.7 565 2 S38399 glutamate/aspartat
284 5 35.7 566 2 S19063 hypothetical prote
285 5 35.7 569 2 S84957 aspergillopepsin I
286 5 35.7 570 2 A11828 flavoprotein [impo
287 5 35.7 571 1 XZAD32 penton protein (II
288 5 35.7 571 1 XZADH5 penton protein (II
289 5 35.7 586 2 T39769 trp-asp repeats co
290 5 35.7 591 2 B87361 flagellar hook pro
291 5 35.7 593 1 S52984 catechol oxidase (
292 5 35.7 599 2 T10798 pterophorin-S - Vo
293 5 35.7 601 2 T38258 coronin-like prote
294 5 35.7 603 2 AG2070 hypothetical prote
295 5 35.7 619 2 A10385 1-deoxy-D-xylulose
296 5 35.7 620 2 A70554 1-deoxyxylulose-5-
297 5 35.7 620 2 D84771 dxs protein - Esch
298 5 35.7 620 2 B85538 1-deoxy-D-xylulose
299 5 35.7 620 2 B90688 1-deoxy-D-xylulose
300 5 35.7 620 2 T50150 yeast nrd1-like pr
301 5 35.7 625 2 B64172 dxs protein - Haem
302 5 35.7 626 2 H82266 1-deoxyxylulose-5-
303 5 35.7 627 2 D84494 probable Tail-like
304 5 35.7 629 2 G75390 1-deoxy-D-xylulose
305 5 35.7 630 2 B95191 endopeptidase O [i
306 5 35.7 630 2 B98058 endopeptidase O (E
307 5 35.7 632 2 E81684 1-deoxyxylulose-5-
308 5 35.7 633 2 A25473 chorion E2 protein
309 5 35.7 634 2 C96541 10-formyltetrahydr
310 5 35.7 634 2 T27881 hypothetical prote
311 5 35.7 635 2 H81793 hypothetical prote
312 5 35.7 638 1 S62932 hypothetical prote
313 5 35.7 640 2 F71527 probable transketo
314 5 35.7 646 2 S38819 plasma protein S -
315 5 35.7 656 2 T38741 major facilitator
316 5 35.7 657 2 C97113 serine/threonine p
317 5 35.7 659 2 C85057 probable receptor-
318 5 35.7 663 2 T24881 hypothetical prote
319 5 35.7 666 2 A47650 SWE12 protein - ye
320 5 35.7 666 2 T24170 hypothetical prote
321 5 35.7 667 2 T157110 hypothetical prote

322 322 35.7 673 2 C86278
323 323 35.7 675 1 KXMS
324 324 35.7 675 1 KXMS
325 325 35.7 682 2 T10319
326 326 35.7 686 2 G64618
327 327 35.7 688 2 D72418
328 328 35.7 701 2 T15235
329 329 35.7 702 2 T41792
330 330 35.7 702 2 D90886
331 331 35.7 704 2 F72855
332 332 35.7 708 2 C86404
333 333 35.7 714 2 B85732
334 334 35.7 718 2 S74509
335 335 35.7 718 2 AD2355
336 336 35.7 719 2 T02154
337 337 35.7 720 2 F85572
338 338 35.7 722 2 T19772
339 339 35.7 727 2 G90721
340 340 35.7 727 2 T26096
341 341 35.7 728 2 S76968
342 342 35.7 733 2 A45301
343 343 35.7 735 2 T35778
344 344 35.7 736 2 T41629
345 345 35.7 738 2 I49295
346 346 35.7 739 2 F86337
347 347 35.7 747 2 T39879
348 348 35.7 756 2 S47656
349 349 35.7 758 2 T38811
350 350 35.7 759 2 T11631
351 351 35.7 776 2 T20896
352 352 35.7 778 2 T16111
353 353 35.7 783 2 T30413
354 354 35.7 790 2 I51638
355 355 35.7 793 2 S65240
356 356 35.7 801 2 A33630
357 357 35.7 807 2 T32463
358 358 35.7 827 2 S48455
359 359 35.7 829 2 S96640
360 360 35.7 852 2 S41886
361 361 35.7 856 2 D87515
362 362 35.7 858 2 E96602
363 363 35.7 863 2 C90482
364 364 35.7 891 1 DEEC
365 365 35.7 891 2 D85704
366 366 35.7 891 2 E90846
367 367 35.7 891 2 AG0265
368 368 35.7 892 2 AE0650
369 369 35.7 894 2 D82127
370 370 35.7 901 2 C89810
371 371 35.7 906 2 T47340
372 372 35.7 940 2 S49087
373 373 35.7 943 2 C81070
374 374 35.7 944 2 C81798
375 375 35.7 950 2 T44422
376 376 35.7 966 2 T30017
377 377 35.7 970 2 S01352
378 378 35.7 971 2 T03181
379 379 35.7 972 2 H84903
380 380 35.7 991 2 A99604
381 381 35.7 1007 2 F80156
382 382 35.7 1008 2 S28858
383 383 35.7 1008 2 T12532
384 384 35.7 1009 2 T16604
385 385 35.7 1017 2 T48452
386 386 35.7 1024 2 T05234
387 387 35.7 1029 2 F96602
388 388 35.7 1042 2 S43904
389 389 35.7 1051 2 A39712
390 390 35.7 1065 2 C89954
391 391 35.7 1085 2 S66149
392 392 35.7 1093 2 H84126
393 393 35.7 1111 2 T23047
394 394 35.7 1132 2 S37206

F14L17.15 protein
plasma protein S p
plasma protein S p
envelope protein E
cadmium-transporti
DNA ligase - Therm
hypothetical prote
ORV-E56 orf46 - Bo
VgrE protein [impo
occlusion-derived
probable protein A
Rhe element associ
polyribonucleotide
polyribonucleotide
protein kinase hom
probable outer mem
hypothetical prote
probable outer mem
hypothetical prote
hypothetical prote
microbulbule-associ
probable fusidic a
hypothetical prote
IL-12 receptor bet
F14O10.2 protein -
hypothetical prote
TMDC II protein -
Na+/H+-exchanging
hypothetical prote
hypothetical prote
viral enhancing fa
F-cadherin - Afri
probable membrane
zinc finger protei
hypothetical prote
6-phosphofructo-2-
hypothetical prote
DNA repair protein
TonB-dependent rec
hypothetical prote
ABC transporter, A
acetaldehyde dehyd
hypothetical prote
acetaldehyde dehyd
alcohol dehydrogen
alcohol dehydrogen
alcohol dehydrogen
conserved hypothet
hypothetical prote
lactoferrin bindin
lactoferrin-bindin
lactoferrin bindin
oxoglutarate dehyd
hypothetical prote
type III site-spec
hypothetical prote
hypothetical prote
hypothetical prote
glutamate receptor
glutamate receptor
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
hyaluronidase - Cl
kinase-like protei
DNA polymerase III
gene pipsaqueak pro
cation efflux syst
hypothetical prote
phytochrome - moss

395	5	35.7	1151	2	S03722	DNA-directed DNA p	468	4	28.6	42	2	C71343	hypothetical prote
396	5	35.7	1185	2	T19212	hypothetical prote	469	4	28.6	44	2	F82837	hypothetical prote
397	5	35.7	1186	2	C64588	cag pathogenicity	470	4	28.6	45	2	A35752	caltrin-like prote
398	5	35.7	1215	2	B48281	cytotoxin-associat	471	4	28.6	45	2	H83936	hypothetical prote
399	5	35.7	1249	2	AC1065	helicase related p	472	4	28.6	49	2	S72213	beta-fructofuranos
400	5	35.7	1261	2	T50065	hypothetical prote	473	4	28.6	50	2	I38970	fibroblast growth
401	5	35.7	1271	2	A45555	glutamate rich pro	474	4	28.6	50	2	G82540	hypothetical prote
402	5	35.7	1275	2	T38397	probable GTPase ac	475	4	28.6	51	2	C88470	protein C28H8.2 [i
403	5	35.7	1319	2	S49951	SM4 protein - yea	476	4	28.6	53	1	A27537	rubredoxin - Chlor
404	5	35.7	1326	2	AC3372	kinesin-like prote	477	4	28.6	53	1	RUPB	rubredoxin - Pepto
405	5	35.7	1338	2	T18442	hypothetical prote	478	4	28.6	54	2	S36814	fibroblast growth
406	5	35.7	1351	2	S44665	ZK370.4 protein -	479	4	28.6	54	2	S32360	SNAP receptor - bo
407	5	35.7	1396	2	F81686	DNA-directed RNA p	480	4	28.6	55	2	G43256	hypothetical prote
408	5	35.7	1397	2	T51292	Dna2p - fission ye	481	4	28.6	55	2	T03370	gene m4 protein -
409	5	35.7	1398	2	T39568	hypothetical helic	482	4	28.6	56	1	TIBOA	pancreatic secreto
410	5	35.7	1405	1	DJZPA	DNA-directed DNA p	483	4	28.6	56	1	TIPG	pancreatic secreto
411	5	35.7	1417	2	A83080	hypothetical prote	484	4	28.6	56	1	TISHA	pancreatic secreto
412	5	35.7	1424	2	T03851	thyroid hormone re	485	4	28.6	56	2	I37977	zinc finger protei
413	5	35.7	1429	2	T41699	C2-domain family p	486	4	28.6	56	2	H82667	hypothetical prote
414	5	35.7	1433	1	A36734	bacillopeptidase F	487	4	28.6	57	2	C84213	30S ribosomal prot
415	5	35.7	1447	2	S63669	unp glucosyl-glycopr	488	4	28.6	57	2	S74693	hypothetical prote
416	5	35.7	1462	2	T42639	glucocorticoid rec	489	4	28.6	59	2	T01278	hypothetical prote
417	5	35.7	1505	2	UC4851	hypoxia-inducible	490	4	28.6	60	2	B86682	prophage pil prote
418	5	35.7	1509	2	T19486	hypothetical prote	491	4	28.6	60	2	C69169	hypothetical prote
419	5	35.7	1522	2	H88380	protein T22F7.3 [i	492	4	28.6	61	1	TIEEH	proteinase inhibit
420	5	35.7	1557	2	D41214	protein-tyrosine-p	493	4	28.6	61	2	A90343	carboxy-end of fer
421	5	35.7	1558	2	B71603	RBSA-H3 antigen pP	494	4	28.6	61	2	S57815	antimicrobial pept
422	5	35.7	1616	2	G64242	cytadherence-acces	495	4	28.6	62	2	AB1042	hypothetical prote
423	5	35.7	1630	2	C41214	protein-tyrosine-p	496	4	28.6	62	2	A36891	transfer complex p
424	5	35.7	1630	2	T40217	hypothetical prote	497	4	28.6	62	2	S30239	hypothetical prote
425	5	35.7	1733	1	RNB52L	DNA-directed RNA p	498	4	28.6	63	2	B69333	4-oxalocrotonate t
426	5	35.7	1829	2	T24583	hypothetical prote	499	4	28.6	63	2	D86673	hypothetical prote
427	5	35.7	1848	2	A44140	cellulose-binding	500	4	28.6	63	2	S57816	antimicrobial pept
428	5	35.7	1854	2	T13576	hypothetical prote	501	4	28.6	64	2	B86800	prophage p13 prote
429	5	35.7	1964	2	A59282	nonmuscle myosin I	502	4	28.6	65	2	I79540	dnak-type molecula
430	5	35.7	2023	2	T13154	polycomb protein e	503	4	28.6	67	2	D83719	mercuric transport
431	5	35.7	2044	2	AB1180	probable peptidogl	504	4	28.6	67	2	T17537	hypothetical prote
432	5	35.7	2062	2	G96602	probable receptor	505	4	28.6	67	2	A12190	hypothetical prote
433	5	35.7	2090	2	T30075	hypothetical prote	506	4	28.6	68	2	D82027	hypothetical prote
434	5	35.7	2153	2	T30074	hypothetical prote	507	4	28.6	70	2	T14969	hypothetical prote
435	5	35.7	2163	2	T51397	hypothetical prote	508	4	28.6	70	2	S25190	pilin precursor -
436	5	35.7	2185	1	GNVYB3	genome polyprotein	509	4	28.6	70	2	S07731	hypothetical prote
437	5	35.7	2252	2	S06188	genome polyprotein	510	4	28.6	70	2	AD1995	hypothetical prote
438	5	35.7	2364	2	A56577	microtubule-associ	511	4	28.6	71	2	T50483	glucose-repressibl
439	5	35.7	2396	2	T13714	kakapo gene protei	512	4	28.6	72	2	I37232	calcitonin gene-re
440	5	35.7	2478	2	AH2140	polyketide synthas	513	4	28.6	72	2	B35523	hypothetical prote
441	5	35.7	2523	2	F70846	probable PPG prote	514	4	28.6	72	2	T07370	ubiquinol-cytochro
442	5	35.7	2664	2	T28626	variant-specific s	515	4	28.6	72	2	D98143	hypothetical prote
443	5	35.7	2802	2	F97686	cyclic beta-(1-2)	516	4	28.6	73	1	S61830	subtilisin/chymotr
444	5	35.7	2831	2	A12911	beta (1->2) glucan	517	4	28.6	73	2	AI2727	hypothetical prote
445	5	35.7	2833	2	A43360	inositol 1,4,5-tri	518	4	28.6	74	2	S33831	hypothetical prote
446	5	35.7	2895	2	H85362	hypothetical prote	519	4	28.6	75	2	AD3131	hypothetical prote
447	5	35.7	2946	2	T15840	hypothetical prote	520	4	28.6	75	2	AG1917	hypothetical prote
448	5	35.7	3014	1	UC5620	genome polyprotein	521	4	28.6	76	1	B64700	carbon storage reg
449	5	35.7	3135	2	A48584	transmission block	522	4	28.6	76	2	I52570	glycophorin - huma
450	5	35.7	3259	1	A56539	giantin - human	523	4	28.6	76	2	E71820	probable carbon st
451	5	35.7	4767	2	T31345	hypothetical prote	524	4	28.6	76	2	T48276	hypothetical prote
452	5	35.7	4868	2	B54161	ryanodine-binding	525	4	28.6	76	2	S43590	M04D8.3 protein (C
453	4	28.6	14	2	B28018	very late antigen-	526	4	28.6	77	2	C69359	snRNP homolog - Ar
454	4	28.6	21	2	PC7043	ubiquitin carboxyl	527	4	28.6	77	2	A75048	hypothetical prote
455	4	28.6	23	2	A33105	dihydrofolate redu	528	4	28.6	77	2	E82612	hypothetical prote
456	4	28.6	31	2	D95212	hypothetical prote	529	4	28.6	77	2	AF1091	E. coli yjdi prote
457	4	28.6	32	2	S32971	dodecandrin - endo	530	4	28.6	77	2	AB1958	hypothetical prote
458	4	28.6	32	2	C26393	calelectrin - marb	531	4	28.6	78	2	A47243	T-cell receptor be
459	4	28.6	34	2	A43564	neurogenic protein	532	4	28.6	78	2	F72807	gp63 protein - Mgc
460	4	28.6	35	2	I52325	P2x purinoceptor s	533	4	28.6	78	2	S31008	gene 63 protein -
461	4	28.6	36	2	E84416	hypothetical prote	534	4	28.6	79	1	TIHUA	pancreatic secreto
462	4	28.6	37	2	JH0709	calcitonin gene-re	535	4	28.6	79	1	TIRT1	pancreatic secreto
463	4	28.6	37	2	S05037	insulinoma amyloid	536	4	28.6	79	1	TIRT2	pancreatic secreto
464	4	28.6	37	2	T11815	hypothetical prote	537	4	28.6	79	2	T17014	metallothionein-li
465	4	28.6	40	2	C82780	hypothetical prote	538	4	28.6	79	2	T06381	proteinase inhibit
466	4	28.6	41	2	D82458	hypothetical prote	539	4	28.6	79	2	AG1062	bacteriophage gene
467	4	28.6	42	2	T09597	probable LFY flora	540	4	28.6	79	2	D86945	hypothetical prote

541 4 28.6 79 2 S57905 hypothetical prote
542 4 28.6 79 2 T37512 hypothetical prote
543 4 28.6 79 2 G82863 conserved hypothet
544 4 28.6 79 2 B83671 hypothetical prote
545 4 28.6 80 1 S01498 pancreatic secreto
546 4 28.6 80 1 EGVZSF growth factor - ra
547 4 28.6 80 2 AG0150 probable stress re
548 4 28.6 81 1 S29820 acrosin/trypsin in
549 4 28.6 81 2 C86710 hypothetical prote
550 4 28.6 81 2 B82705 hypothetical prote
551 4 28.6 82 2 S77795 H+transporting tw
552 4 28.6 82 2 S28655 hypothetical prote
553 4 28.6 82 2 T17685 hypothetical prote
554 4 28.6 82 2 AC2753 conserved hypothet
555 4 28.6 82 2 AC2804 hypothetical prote
556 4 28.6 82 2 C97583 hypothetical prote
557 4 28.6 83 1 G5BPSV gene 5 protein - s
558 4 28.6 83 2 JN0400 hypothetical 8.8K
559 4 28.6 83 2 C94274 hypothetical prote
560 4 28.6 83 2 T19790 hypothetical prote
561 4 28.6 83 2 AG2771 hypothetical prote
562 4 28.6 84 2 B82599 hypothetical prote
563 4 28.6 85 2 S60856 M protein precurs
564 4 28.6 85 2 D70488 cytochrome-c oxida
565 4 28.6 86 1 A34427 peptide PEC-60 pre
566 4 28.6 86 2 S39579 DNA-directed RNA p
567 4 28.6 86 2 H64246 ribosomal protein
568 4 28.6 87 2 T47128 probable ribosomal
569 4 28.6 87 2 T47113 hypothetical prote
570 4 28.6 88 2 A37262 Ig kappa chain V r
571 4 28.6 88 2 B90584 30S ribosomal prot
572 4 28.6 88 2 D37914 homeotic protein C
573 4 28.6 89 1 TCHUIA islet amyloid poly
574 4 28.6 89 2 S22344 islet amyloid poly
575 4 28.6 89 2 A33542 islet amyloid poly
576 4 28.6 89 2 S32551 thionin variant Th
577 4 28.6 89 2 S55648 hypothetical prote
578 4 28.6 89 2 T26222 hypothetical prote
579 4 28.6 89 2 JQ1822 Salfa protein - va
580 4 28.6 89 2 AF0312 probable exported
581 4 28.6 89 2 T03072 probable zinc fing
582 4 28.6 90 2 A81313 probable membrane
583 4 28.6 90 2 A86968 hypothetical prote
584 4 28.6 90 2 T17562 hypothetical prote
585 4 28.6 90 2 T42196 transposase tras -
586 4 28.6 90 2 S23259 iro protein - Thio
587 4 28.6 91 2 G72088 ferredoxin [2Fe-2S
588 4 28.6 91 2 B86536 ferredoxin IV [imp
589 4 28.6 91 2 B81715 ferredoxin [2Fe-2S
590 4 28.6 91 2 G71562 ferredoxin [2Fe-2S
591 4 28.6 91 2 A71654 ribosomal protein
592 4 28.6 91 2 AG1980 hypothetical prote
593 4 28.6 92 2 T48895 glyA protein [imp
594 4 28.6 92 2 S13116 islet amyloid prot
595 4 28.6 92 2 S15688 seminal vesicle pr
596 4 28.6 92 2 T16884 hypothetical prote
597 4 28.6 93 1 C33542 islet amyloid poly
598 4 28.6 93 1 TCR71A islet amyloid poly
599 4 28.6 93 2 T47252 conidiation protei
600 4 28.6 94 1 C21895 ribosomal protein
601 4 28.6 94 1 RBP222 abci protein - pha
602 4 28.6 94 2 D89947 50S ribosomal prot
603 4 28.6 94 2 S62084 M-like protein enn
604 4 28.6 95 1 BORT3 prostatic steroid-
605 4 28.6 95 2 B82793 hypothetical prote
606 4 28.6 95 2 B37857 hypothetical prote
607 4 28.6 96 2 T11096 NADH2 dehydrogenas
608 4 28.6 96 2 S42410 protein translocat
609 4 28.6 96 2 S42409 protein translocat
610 4 28.6 96 2 E69790 hypothetical prote
611 4 28.6 96 2 T08761 hypothetical prote
612 4 28.6 97 2 S60846 M protein precurs
613 4 28.6 97 2 D64344 hypothetical prote

614 4 28.6 98 2 I50101
615 4 28.6 98 2 C84323
616 4 28.6 98 2 E81205 conserved hypothet
617 4 28.6 99 2 A42196 preprotein translo
618 4 28.6 99 2 AE1422 PTS, cellobiose-sp
619 4 28.6 99 2 G70931 probable PE protei
620 4 28.6 99 2 E90329 conserved hypothet
621 4 28.6 99 2 S22957 hypothetical prote
622 4 28.6 99 2 T02626 hypothetical prote
623 4 28.6 99 2 AD1454 hypothetical prote
624 4 28.6 99 2 AE1090 hypothetical prote
625 4 28.6 99 2 AC3260 hypothetical prote
626 4 28.6 100 2 F71725 glutamyl-tRNA amid
627 4 28.6 100 2 T40494 probable guanine n
628 4 28.6 100 2 G98295 hypothetical prote
629 4 28.6 101 2 T28661 hypothetical prote
630 4 28.6 101 2 AF0223 hypothetical prote
631 4 28.6 102 2 A23620 ribonuclease T1 (E
632 4 28.6 102 2 G69007 ribosomal protein
633 4 28.6 102 2 T17738 hypothetical prote
634 4 28.6 102 2 S09892 hypothetical prote
635 4 28.6 102 2 F82517 conserved hypothet
636 4 28.6 102 2 A97534 hypothetical prote
637 4 28.6 102 2 A82829 colicin V precurs
638 4 28.6 102 2 F81377 flagellar motor sw
639 4 28.6 103 1 W1BP22 gene 17 protein -
640 4 28.6 103 2 T34790 hypothetical prote
641 4 28.6 104 1 NRNCT1 ribonuclease T1 (E
642 4 28.6 104 2 S55728 chitin synthase (E
643 4 28.6 104 2 B72491 hypothetical prote
644 4 28.6 104 2 A75016 hypothetical prote
645 4 28.6 104 2 T39020 hypothetical prote
646 4 28.6 104 2 AD0289 probable lipoprote
647 4 28.6 105 2 H81136 hypothetical prote
648 4 28.6 105 2 A71249 hypothetical prote
649 4 28.6 105 2 C72631 hypothetical prote
650 4 28.6 106 1 R6D0P2 acidic ribosomal p
651 4 28.6 106 2 JC7175 Arpase inhibitor p
652 4 28.6 106 2 C69436 LSU ribosomal prot
653 4 28.6 106 2 AF1181 E. coli SugE prote
654 4 28.6 106 2 AG1538 E. coli SugE prote
655 4 28.6 106 2 AC0177 hypothetical prote
656 4 28.6 106 2 A12219 hypothetical prote
657 4 28.6 106 2 G95152 v-type sodium ATP
658 4 28.6 107 2 S38713 Ig kappa chain V r
659 4 28.6 107 2 S33132 ig light chain V r
660 4 28.6 107 2 A11242 B. subtilis comG o
661 4 28.6 108 2 E72426 transposase - Ther
662 4 28.6 108 2 T14991 hypothetical prote
663 4 28.6 108 2 T33901 hypothetical prote
664 4 28.6 108 2 G72624 hypothetical prote
665 4 28.6 108 2 T49731 hypothetical prote
666 4 28.6 108 2 S43582 insulin homolog 2
667 4 28.6 108 2 AD0715 conserved hypothet
668 4 28.6 108 2 AF1043 hypothetical prote
669 4 28.6 108 2 AG0853 hypothetical prote
670 4 28.6 109 1 A44275 nonstructural prot
671 4 28.6 109 1 MNIBH2 nonstructural prot
672 4 28.6 109 2 S58182 nonstructural prot
673 4 28.6 109 2 S29387 nif0 protein - Azo
674 4 28.6 109 2 S64313 probable membrane
675 4 28.6 109 2 F81953 hypothetical prote
676 4 28.6 109 2 D81012 hypothetical prote
677 4 28.6 109 2 A86104 probable regulator
678 4 28.6 110 1 R6SSP2 acidic ribosomal p
679 4 28.6 110 2 B72496 hypothetical prote
680 4 28.6 110 2 S09991 hypothetical prote
681 4 28.6 110 2 G81192 hypothetical prote
682 4 28.6 110 2 E82781 hypothetical prote
683 4 28.6 111 1 QQSABE hypothetical prote
684 4 28.6 111 2 JX0085 pancreatic ribonuc
685 4 28.6 111 2 D37286 ig kappa chain V r
686 4 28.6 111 2 A53221 acidic ribosomal p

neuromedin B recep
30S ribosomal prot
hypothetical prote
preprotein translo
PTS, cellobiose-sp
probable PE protei
conserved hypothet
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
glutamyl-tRNA amid
probable guanine n
hypothetical prote
hypothetical prote
hypothetical prote
ribonuclease T1 (E
ribosomal protein
hypothetical prote
hypothetical prote
conserved hypothet
hypothetical prote
colicin V precurs
flagellar motor sw
gene 17 protein -
hypothetical prote
ribonuclease T1 (E
chitin synthase (E
hypothetical prote
hypothetical prote
probable lipoprote
hypothetical prote
hypothetical prote
hypothetical prote
acidic ribosomal p
Arpase inhibitor p
LSU ribosomal prot
E. coli SugE prote
E. coli SugE prote
hypothetical prote
hypothetical prote
v-type sodium ATP
Ig kappa chain V r
ig light chain V r
B. subtilis comG o
transposase - Ther
hypothetical prote
hypothetical prote
hypothetical prote
nonstructural prot
nonstructural prot
nonstructural prot
nif0 protein - Azo
probable membrane
hypothetical prote
hypothetical prote
probable regulator
acidic ribosomal p
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
pancreatic ribonuc
ig kappa chain V r
acidic ribosomal p

687 4 28.6 111 2 S11128 genome polypeptide
688 4 28.6 111 2 A30918 hypothetical protein
689 4 28.6 111 2 A64917 probable membrane
690 4 28.6 111 2 F85766 hypothetical protein
691 4 28.6 111 2 C72514 hypothetical protein
692 4 28.6 111 2 S19475 hypothetical protein
693 4 28.6 111 2 C95414 hypothetical protein
694 4 28.6 112 1 L1HUMM Ig lambda chain V-
695 4 28.6 112 2 T44986 probable sulfate/t
696 4 28.6 112 2 A69451 conserved hypothet
697 4 28.6 112 2 A69451 omega-agatoxin IA
698 4 28.6 112 2 A45069 hypothetical protein
699 4 28.6 112 2 F49338 conserved hypothet
700 4 28.6 113 2 A10339 conserved hypothet
701 4 28.6 113 2 D84389 hypothetical protein
702 4 28.6 114 2 G11112 hypothetical protein
703 4 28.6 114 2 T11969 hypothetical protein
704 4 28.6 114 2 S11952 hypothetical protein
705 4 28.6 115 1 PTHU parathyroid hormone
706 4 28.6 115 1 PTHU parathyroid hormone
707 4 28.6 115 1 PTHG parathyroid hormone
708 4 28.6 115 2 J04202 parathyroid hormone
709 4 28.6 115 2 A29156 seminal fluid prot
710 4 28.6 115 2 T44712 acyl carrier prote
711 4 28.6 115 2 A33376 arsenate reductase
712 4 28.6 115 2 T40456 very hypothetical
713 4 28.6 115 2 S41118 hypothetical protein
714 4 28.6 116 2 T10080 lipid transfer pro
715 4 28.6 116 2 H86042 hypothetical protein
716 4 28.6 116 2 G31195 hypothetical protein
717 4 28.6 116 2 E72786 hypothetical protein
718 4 28.6 116 2 H97213 reductase/isomeras
719 4 28.6 117 2 B84604 probable glycine-r
720 4 28.6 117 2 A72310 hypothetical protein
721 4 28.6 117 2 S73025 hypothetical protein
722 4 28.6 117 2 T13210 minor capsid prote
723 4 28.6 117 2 T47990 hypothetical protein
724 4 28.6 117 2 A95381 hypothetical protein
725 4 28.6 117 2 AC3421 hypothetical expor
726 4 28.6 118 2 C96746 thionin, 63255-627
727 4 28.6 118 2 S25249 thionin variant Th
728 4 28.6 118 2 I33932 Ig kappa chain pre
729 4 28.6 118 2 A17139 PFS system, cellob
730 4 28.6 118 2 S55185 hypothetical protein
731 4 28.6 118 2 T15655 hypothetical protein
732 4 28.6 118 2 C81005 hypothetical protein
733 4 28.6 118 2 B82026 hypothetical protein
734 4 28.6 118 2 A81007 hypothetical protein
735 4 28.6 118 2 C82887 purine nucleoside
736 4 28.6 118 2 B71207 hypothetical protein
737 4 28.6 119 2 B45937 early chorion prot
738 4 28.6 119 2 S24292 chorion protein -
739 4 28.6 119 2 S24294 chorion protein -
740 4 28.6 119 2 S24231 chorion protein -
741 4 28.6 119 2 F49804 hypothetical protein
742 4 28.6 119 2 B72633 hypothetical protein
743 4 28.6 119 2 G86755 prophage p12 prote
744 4 28.6 119 2 E83106 hypothetical protein
745 4 28.6 119 2 T00294 transposase tras-
746 4 28.6 120 2 A50844 protein-Npi-phosph
747 4 28.6 120 2 H75483 aspartate 1-decarb
748 4 28.6 120 2 J01740 hypothetical 12.7K
749 4 28.6 120 2 I40821 regA protein - Clo
750 4 28.6 120 2 T03071 hypothetical protein
751 4 28.6 120 2 A11446 Protein gp9 (Bacte
752 4 28.6 120 2 F71005 hypothetical protein
753 4 28.6 121 1 LAKGAW alpha-lactalbumin
754 4 28.6 121 2 T51726 phosphotransferase
755 4 28.6 121 2 S24293 chorion class CA p
756 4 28.6 121 2 C75127 hypothetical protein
757 4 28.6 121 2 S27145 gene 30.7 protein
758 4 28.6 121 2 A9407 succinate dehydrog
759 4 28.6 121 2 A17130 hypothetical protein

760 4 28.6 121 2 AG2065
761 4 28.6 122 2 E71834 ribosomal protein
762 4 28.6 122 2 E64683 ribosomal protein
763 4 28.6 122 2 S29540 seminal vesicle se
764 4 28.6 122 2 T42844 endonuclease homol
765 4 28.6 122 2 S72337 hypothetical protein
766 4 28.6 122 2 T44906 hypothetical protein
767 4 28.6 122 2 B82271 hypothetical protein
768 4 28.6 122 2 E82519 hypothetical protein
769 4 28.6 122 2 A05304 hemoglobin beta-1
770 4 28.6 122 2 A11214 hypothetical protein
771 4 28.6 122 2 A12992 conserved hypothet
772 4 28.6 123 1 WQEC3S phosphotransferase
773 4 28.6 123 2 G85918 hypothetical protein
774 4 28.6 123 2 H91073 hypothetical protein
775 4 28.6 123 2 E90066 aspartate 1-decarb
776 4 28.6 123 2 S49906 HAE (highly acidic
777 4 28.6 123 2 S49907 HAE (highly acidic
778 4 28.6 123 2 S29714 guanine-nucleotide
779 4 28.6 123 2 S29714 guanine-nucleotide
780 4 28.6 123 2 A97333 fMN-binding protei
781 4 28.6 123 2 T38821 fMN-binding protei
782 4 28.6 123 2 T33456 hypothetical protein
783 4 28.6 123 2 F45891 hypothetical protein
784 4 28.6 124 2 H97720 hypothetical protein
785 4 28.6 124 2 C72206 conserved hypothet
786 4 28.6 124 2 D81810 hypothetical protein
787 4 28.6 124 2 S33081 G4L protein - vari
788 4 28.6 124 2 H72158 I4L protein - vari
789 4 28.6 124 2 T28504 hypothetical protein
790 4 28.6 124 2 T09126 protein CP12 precu
791 4 28.6 124 2 T48833 hypothetical protein
792 4 28.6 124 2 A95136 conserved hypothet
793 4 28.6 124 2 AG2789 conserved hypothet
794 4 28.6 124 2 S71888 S phase inhibitor
795 4 28.6 124 2 A11754 bacteriophage prot
796 4 28.6 125 1 TCCHRP calcitonin gene-re
797 4 28.6 125 1 F1SP4 photosystem I chai
798 4 28.6 125 2 T02490 hypothetical protein
799 4 28.6 125 2 T51037 hypothetical protein
800 4 28.6 125 2 T34695 hypothetical protein
801 4 28.6 125 2 AB1595 hypothetical protein
802 4 28.6 125 2 A97202 desulfoferrodoxin
803 4 28.6 125 2 A69354 rubredoxin-NAD+ re
804 4 28.6 125 2 S68837 rubredoxin-NAD+ re
805 4 28.6 125 2 A53627 fibroblast growth
806 4 28.6 125 2 RDVEX rubredoxin-NAD+ re
807 4 28.6 126 1 I46489 cysteine-rich hair
808 4 28.6 126 2 T34033 hypothetical protein
809 4 28.6 126 2 C72650 hypothetical protein
810 4 28.6 126 2 F91065 hypothetical protein
811 4 28.6 126 2 F90906 hypothetical protein
812 4 28.6 126 2 B90836 hypothetical protein
813 4 28.6 126 2 D90856 hypothetical protein
814 4 28.6 126 2 F90766 conserved hypothet
815 4 28.6 126 2 G90350 conserved hypothet
816 4 28.6 126 2 AH1334 hypothetical protein
817 4 28.6 126 2 AC1833 hypothetical protein
818 4 28.6 127 1 VCBP77 coat protein - pha
819 4 28.6 127 2 G84999 iron-sulfur cofact
820 4 28.6 127 2 H82285 calcitonin gene-re
821 4 28.6 127 2 A25864 crCB protein (impo
822 4 28.6 127 2 H87494 hypothetical protein
823 4 28.6 127 2 S76684 hypothetical protein
824 4 28.6 127 2 S40034 killer toxin KP4 p
825 4 28.6 127 2 E90038 hypothetical protein
826 4 28.6 128 1 TCCHUR calcitonin gene-re
827 4 28.6 128 1 TCCHUR calcitonin gene-re
828 4 28.6 128 2 AG0824 Nifu-like protein
829 4 28.6 128 2 AG0352 Nifu family protei
830 4 28.6 128 2 S10046 lysozyme (EC 3.2.1
831 4 28.6 128 2 B44173 calcitonin gene-re
832 4 28.6 128 2 AE1106 repressor (penicil

833	4	28.6	128	2	S33949	early E3B 14.7K pr	906	135	2	S52555	thionin variant Th
834	4	28.6	128	2	S46976	coat protein - pha	907	135	2	S52552	thionin variant Th
835	4	28.6	128	2	AH1816	hypothetical protein	908	28.6	2	JQ0472	T-cell receptor be
836	4	28.6	128	2	C48552	hypothetical protein	909	28.6	2	C64453	translation initia
837	4	28.6	128	2	T29978	hypothetical protein	910	28.6	2	S67160	hypothetical prote
838	4	28.6	128	2	T32502	hypothetical protein	911	28.6	2	C72315	hypothetical prote
839	4	28.6	128	2	S31009	gene 64 protein -	912	28.6	2	F72494	hypothetical prote
840	4	28.6	128	2	A71276	probable desulfote	913	28.6	2	S55647	hypothetical prote
841	4	28.6	128	2	T25200	hypothetical prote	914	28.6	2	C98128	hypothetical prote
842	4	28.6	129	2	C70022	3-oxoacyl- acyl-ca	915	28.6	2	AC3159	hypothetical prote
843	4	28.6	129	2	T08993	urease (EC 3.5.1.5	916	28.6	2	AF0734	hypothetical prote
844	4	28.6	129	2	T10175	acyl carrier prote	917	28.6	2	AF0734	probable bacteriop
845	4	28.6	129	2	A37798	mor protein - Esch	918	28.6	2	D82468	hypothetical prote
846	4	28.6	129	2	D72205	transposase - ther	919	28.6	2	S76237	hypothetical prote
847	4	28.6	129	2	JU0394	allergen Der f II	920	28.6	2	S67924	spore-wall fungal
848	4	28.6	129	2	A61501	allergen Der f II	921	28.6	2	T21733	hypothetical prote
849	4	28.6	129	2	T17710	hypothetical prote	922	28.6	1	KVMS21	hypothetical prote
850	4	28.6	129	2	T21290	hypothetical prote	923	28.6	1	S52545	thionin shared anti
851	4	28.6	129	2	A81933	hypothetical prote	924	28.6	2	T49013	hypothetical prote
852	4	28.6	129	2	E72777	hypothetical prote	925	28.6	2	H84485	hypothetical prote
853	4	28.6	130	2	H70010	polyribonucleotide	926	28.6	2	S46102	hypothetical prote
854	4	28.6	130	2	B34302	hypothetical prote	927	28.6	2	H70838	hypothetical prote
855	4	28.6	130	2	G70799	hypothetical prote	928	28.6	2	G95224	hypothetical prote
856	4	28.6	130	2	AH2876	conserved hypothet	929	28.6	2	B99089	hypothetical prote
857	4	28.6	130	2	B37653	hypothetical prote	930	28.6	2	T53300	interleukin-1-beta
858	4	28.6	131	2	H82909	DNA-binding protei	931	28.6	2	F87461	hypothetical prote
859	4	28.6	131	2	A37791	nfu protein [limpo	932	28.6	1	S38484	urease (EC 3.5.1.5
860	4	28.6	131	2	H1651	iron-sulfur cofact	933	28.6	2	S22515	thionin precursor,
861	4	28.6	131	2	S14390	tap2 protein - gar	934	28.6	2	B27586	hypothetical prote
862	4	28.6	131	2	C75117	hypothetical prote	935	28.6	2	D75148	hypothetical prote
863	4	28.6	131	2	T32405	hypothetical prote	936	28.6	2	T38500	hypothetical prote
864	4	28.6	131	2	T29455	hypothetical prote	937	28.6	2	D83882	hypothetical prote
865	4	28.6	131	2	B82451	hypothetical prote	938	28.6	2	AF3056	conserved hypothet
866	4	28.6	131	2	B83787	hypothetical prote	939	28.6	2	H98229	hypothetical prote
867	4	28.6	131	2	AH0348	probable membrane	940	28.6	2	H84345	inosine-5'-monopho
868	4	28.6	131	2	AG1361	protein gp8 (Bacte	941	28.6	2	H71348	conserved hypothet
869	4	28.6	131	2	AH1446	protein gp8 (Bacte	942	28.6	2	D72776	hypothetical prote
870	4	28.6	131	2	T28863	hypothetical prote	943	28.6	2	AB3085	conserved hypothet
871	4	28.6	131	2	E84540	hypothetical prote	944	28.6	2	G98201	hypothetical prote
872	4	28.6	131	2	H83156	hypothetical prote	945	28.6	1	C64005	hypothetical prote
873	4	28.6	131	2	S54573	hypothetical prote	946	28.6	2	D90164	hypothetical prote
874	4	28.6	132	1	MTONLK	melanin-concentrat	947	28.6	2	JC5742	membrane-bound pro
875	4	28.6	132	2	S34653	melanin-concentrat	948	28.6	2	G82915	ribosomal protein
876	4	28.6	132	2	B32910	melanin-concentrat	949	28.6	2	I51265	xCRABP - African c
877	4	28.6	132	2	F82916	ribosomal protein	950	28.6	2	S24081	envelope protein -
878	4	28.6	132	2	E90583	30S ribosomal prot	951	28.6	2	S24080	envelope protein -
879	4	28.6	132	2	S17928	acyl carrier prote	952	28.6	2	A87126	NrdI-family protei
880	4	28.6	132	2	T44951	flagella-related p	953	28.6	2	B61241	allergen Der f II
881	4	28.6	132	2	A02044	probable rhodanese	954	28.6	2	A61241	allergen Der f II
882	4	28.6	133	2	S52547	thionin variant Th	955	28.6	2	D83824	transcription regu
883	4	28.6	133	2	S52554	thionin variant Th	956	28.6	2	JC4597	signal transductio
884	4	28.6	133	2	C48776	polypeptide (E2/NS	957	28.6	2	T40987	hypothetical prote
885	4	28.6	133	2	E48776	polypeptide (E2/NS	958	28.6	2	A11156	hypothetical prote
886	4	28.6	133	2	G75061	hypothetical prote	959	28.6	2	A84482	hypothetical prote
887	4	28.6	133	2	S10038	hypothetical prote	960	28.6	2	S18587	hypothetical prote
888	4	28.6	133	2	E90792	hypothetical prote	961	28.6	1	S03579	probable transcrip
889	4	28.6	133	2	A98197	hypothetical prote	962	28.6	1	B70955	aspartate 1-decarb
890	4	28.6	133	2	C85824	unknown protein en	963	28.6	2	E97426	flagellar basal-bo
891	4	28.6	133	2	H30669	hypothetical prote	964	28.6	2	AE2644	flagellar basal-bo
892	4	28.6	133	2	E90977	hypothetical prote	965	28.6	2	F84415	hypothetical prote
893	4	28.6	133	2	B90260	conserved hypothet	966	28.6	2	A12536	hypothetical prote
894	4	28.6	133	2	T17609	hypothetical prote	967	28.6	2	A60394	cytokinin-induced
895	4	28.6	133	2	A12987	hypothetical prote	968	28.6	2	T10059	hypothetical prote
896	4	28.6	134	2	A44173	calcitonin gene-re	969	28.6	2	B81431	hypothetical prote
897	4	28.6	134	2	F96685	probable thionin F	970	28.6	2	F75335	probable transpos
898	4	28.6	134	2	S25446	thionin variant Th	971	28.6	2	S35275	probable flagellar
899	4	28.6	134	2	S25553	thionin variant Th	972	28.6	2	A11360	protein gp14 (Bact
900	4	28.6	134	2	A43589	mtp40 protein - My	973	28.6	2	AF1447	hypothetical prote
901	4	28.6	134	2	B83762	hypothetical prote	974	28.6	2	A13155	hypothetical prote
902	4	28.6	134	2	H69544	conserved hypothet	975	28.6	2	H98131	probable transcrip
903	4	28.6	134	2	T20928	hypothetical prote	976	28.6	2	T29914	hypothetical prote
904	4	28.6	134	2	D71188	hypothetical prote	977	28.6	2	AG3645	flagellar basal-bo
905	4	28.6	135	2	A56855	islet amyloid poly	978	28.6	1	HASN	hemoglobin alpha c

979 28.6 141 1 HZFG hemoglobin zeta ch
 980 28.6 141 2 C86845 H+-transporting tw
 981 28.6 141 2 S78354 ribosomal protein
 982 28.6 141 2 B70816 probable molybdopt
 983 28.6 141 2 D31263 probable phn opero
 984 28.6 141 2 T39554 very hypothetical
 985 28.6 141 2 E37811 hypothetical prote
 986 28.6 141 2 S15788 intermediate early
 987 28.6 141 2 PC1294 trophozoite surfac
 988 28.6 141 2 F95986 conserved hypothet
 989 28.6 141 2 AF0368 probable acetyltra
 990 28.6 142 2 S71361 actin-binding prot
 991 28.6 142 2 C48175 hypothetical plasm
 992 28.6 142 2 G86937 probable aspartate
 993 28.6 142 2 D71663 hypothetical prote
 994 28.6 142 2 C39610 BEF1 protein - yea
 995 28.6 142 2 AJ1521 hypothetical prote
 996 28.6 142 2 T67636 cystatin 1 - wheat
 997 28.6 142 2 T34136 hypothetical prote
 998 28.6 142 2 E84069 hypothetical prote
 999 28.6 142 2 D96983 CBS domains [impor
 1000 28.6 143 1 F64466 phosphopeptose iso

ALIGNMENTS

RESULT 1
 E89051
 C:Species: Saccharomyces cerevisiae
 C:Date: 22-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 16-Aug-2004
 C:Accession: S69051; S12795
 R:Hall, J.; DePaulo, T.; Ahmed, A.; Bussey, H.; Fortin, N.; Friesen, J.D.; Storms, R.K.;
 submitted to the EMBL Data Library, December 1995
 A:Description: The sequence of Saccharomyces cerevisiae chromosome XVI left arm.
 A:Reference number: S69040
 A:Accession: S69051
 A:Molecule type: DNA
 A:Residues: 1-446 <HAL>
 A:Cross-references: UNIPROT:P19541; EMBL:U43703; NID:G1244769; PIDN:AAB68226.1; PID:G124
 R:Rizgolofoff, A.; Capitanio, N.; Nobrega, M.P.; Gattli, D.
 EMBL J. 9, 2759-2764, 1990
 A:Title: Cytochrome oxidase assembly in yeast requires the product of COX11, a homolog o
 A:Reference number: S12795; MUID:90360986; PMID:2167832
 A:Accession: S12795
 A:Molecule type: DNA
 A:Residues: 1-95 <TZA>
 A:Cross-references: EMBL:X55731; NID:G3565; PIDN:CAA39262.1; PID:G3566
 A:Note: the authors translated the codon GAT for residue 84 as Glu
 C:Genetics:
 A:Cross-references: SGD:S0006054
 A:Map position: 16L
 A:Note: YPH133C
 C:Superfamily: GAL4 zinc binuclear cluster homology
 F:12-50/Domain: GAL4 zinc binuclear cluster homology <GAL4>

Query Match 50.0%; Score 7; DB 2; Length 446;
 Best Local Similarity 100.0%; Pred. No. 2.9; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 4 VSENVGS 10
 Db 125 VSENVGS 131
 |||||

RESULT 2
 D81826
 C:exodeoxyribonuclease V (EC 3.1.11.15) NMA1974 [imported] - Neisseria meningitidis (strain
 C:Species: Neisseria meningitidis
 C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
 C:Accession: D81826
 R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel

; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
 Nature 404, 502-506, 2000
 A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
 A:Reference number: A81775; MUID:20222556; PMID:10761919
 A:Accession: D81826
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1069 <PAR>
 A:Cross-references: UNIPROT:Q9JT46; GB:AL162757; GB:AL157959; NID:G7380371; PIDN:CAB8519
 A:Experimental source: serogroup A, strain Z2491
 C:Genetics:
 A:Gene: recC; NMA1974
 C:Superfamily: exodeoxyribonuclease V 125K chain
 C:Keywords: hydrolase

Query Match 50.0%; Score 7; DB 2; Length 1069;
 Best Local Similarity 100.0%; Pred. No. 6.1;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 5 SENVGSV 11
 Db 317 SENVGSV 323
 |||||

RESULT 3
 E84193
 C:chromosome segregation [imported] - Halobacterium sp. NRC-1
 C:Species: Halobacterium sp. NRC-1
 C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
 C:Accession: E84193
 R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.;
 Leithauer, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablo
 Jung, K.H.; Alam, M.; Freitas, T.
 Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
 A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li;
 A:Title: Genome sequence of Halobacterium species NRC-1.
 A:Reference number: A84160; MUID:20504483; PMID:11016950
 A:Accession: E84193
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1190 <STO>
 A:Cross-references: UNIPROT:Q9HS95; GB:AE004437; NID:G10579965; PIDN:AAG18913.1; GSPDB:G
 C:Genetics:
 A:Gene: smc1

Query Match 50.0%; Score 7; DB 2; Length 1190;
 Best Local Similarity 100.0%; Pred. No. 6.6;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 5 SENVGSV 11
 Db 106 SENVGSV 112
 |||||

RESULT 4
 C86086
 C:hypothetical protein frwC 2 [imported] - Escherichia coli (strain O157:H7, substrain EDL
 C:Species: Escherichia coli
 C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
 C:Accession: C86086
 R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
 iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
 Nature 409, 529-533, 2001
 A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A:Reference number: A85480; MUID:21074935; PMID:11206551
 A:Accession: C86086
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-106 <STO>
 A:Cross-references: UNIPROT:Q8X3P5; GB:AE005174; NID:G12518668; PIDN:AAG59151.1; GSPDB:G
 A:Experimental source: strain O157:H7, substrain EDL933
 C:Genetics:
 A:Gene: frwC_2

```
Query Match      42.9%; Score 6; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      8 VGSVCG 13
      |||||
Db      28 VGSVCG 33

RESULT 5
G82929
ATP synthase C chain UUI36 [imported] - Ureaplasma urealyticum
C;Species: Ureaplasma urealyticum
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: G82929
R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
submitted to GenBank, February 2000
A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a min
A;Reference number: A82870
A;Accession: G82929
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-109 <GLA>
A;Cross-references: GB:AE002114; GB:AF222894; NID:96899086; PIDN:AAF30542.1; GSPDB:GN001
A;Experimental source: serovar 3; biovar 1
C;Genetics:
A;Gene: atpE; UUI36
A;Genetic code: SGC3

Query Match      42.9%; Score 6; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 SENVGS 10
      |||||
Db      24 SENVGS 29

RESULT 6
AE1214
hypothetical protein lmo117 [imported] - Listeria monocytogenes (strain EGD-e)
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AE1214
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Feihi, H.
.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Krett, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AE1214
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-118 <GLA>
A;Cross-references: UNIPROT:Q8Y802; GB:NC_003210; PIDN:CAC99195.1; PID:gl6410519; GSPDB:
A;Experimental source: strain EGD-e
C;Genetics:
A;Gene: lmo117

Query Match      42.9%; Score 6; DB 2; Length 118;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 NVSENV 8
      |||||
Db      58 NVSENV 63

RESULT 7
D83998
acetyl-CoA carboxylase biotin carboxyl carrier subunit accB [imported] - Bacillus halodurans
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: D83998
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: D83998
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-169 <STO>
A;Cross-references: UNIPROT:Q9K962; GB:AF001516; GB:BA000004; NID:gi0175192; PIDN:BA8065
A;Experimental source: strain C-125
C;Genetics:
A;Gene: accB
C;Superfamily: biotin carboxyl carrier protein; lipoyl/biotin-binding homology

Query Match      42.9%; Score 6; DB 2; Length 169;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 DNVSSE 7
      |||||
Db      117 DNVSSE 122

RESULT 8
D87236
conserved membrane protein ML2614 [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: D87236
R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho
R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq
A;Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002
A;Accession: D87236
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-224 <STO>
A;Cross-references: UNIPROT:O06076; GB:AL450380; NID:gi13093840; PIDN:CAC32146.1; GSPDB:G
C;Genetics:
A;Gene: ML2614

Query Match      42.9%; Score 6; DB 2; Length 224;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 VSENVG 9
      |||||
Db      189 VSENVG 194

RESULT 9
T20304
hypothetical protein D1054.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T20304
R;Matthews, P.
submitted to the EMBL Data Library, June 1996
A;Reference number: Z19255
A;Accession: T20304
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-231 <WIL>
A;Cross-references: UNIPROT:Q27488; EMBL:Z74030; PIDN:CAA98441.1; GSPDB:GN00023; CESP:DI
A;Experimental source: clone D1054
C;Genetics:
```

A;Gene: CESP:D1054.2
 A;Map position: 5
 A;Introns: 13/2; 39/1; 121/2
 C;Superfamily: multicatalytic endopeptidase complex chain C9

Query Match 42.9%; Score 6; DB 2; Length 231;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ENVGSV 11
 |||||
 Db 48 ENVGSV 53

RESULT 10

AF1367
 16S pseudouridylylate synthase homolog lmo2342 [imported] - Listeria monocytogenes (strain
 C;Species: Listeria monocytogenes
 C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
 C;Accession: AF1367

R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker,
 D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
 D.; Jones, L.M.; Karet, U.
 Science 294, 849-852, 2001
 A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
 ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
 A;Title: Comparative genomics of Listeria species.
 A;Reference number: AB1077; MUID:21537279; PMID:11679669

A;Accession: AF1367

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-233 <GLA>

A;Cross-references: UNIPROT:Q8V4U0; GB:NC_003210; PIDN:CAD00420.1; PID:G16411830; GSPDB:
 A;Experimental source: strain EGD-e

C;Genetics:

A;Gene: lmo2342

C;Superfamily: conserved hypothetical protein HI1243

Query Match 42.9%; Score 6; DB 2; Length 233;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EDNVSE 6
 |||||
 Db 76 EDNVSE 81

RESULT 11

WZBE24

gene 24 protein - human herpesvirus 3

C;Species: human herpesvirus 3, varicella-zoster virus

C;Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 09-Jul-2004

C;Accession: F27343

R;Davison, A.J.; Scott, J.E.

J. Gen. Virol. 67, 1759-1816, 1986

A;Title: The complete DNA sequence of varicella-zoster virus.

A;Reference number: A27345; MUID:86306657; PMID:3018124

A;Accession: F27343

A;Molecule type: DNA

A;Residues: 1-269 <DAV>

A;Cross-references: UNIPROT:P09280; EMBL:X04370; NID:G59989; PIDN:CAA27907.1; PID:G60013

C;Genetics:

A;Gene: 24

C;Superfamily: varicella-zoster virus gene 24 protein

Query Match 42.9%; Score 6; DB 1; Length 269;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EDNVSE 6
 |||||
 Db 57 EDNVSE 62

RESULT 12

D82491

hypothetical protein VCA0181 [imported] - Vibrio cholerae (strain N16961 serogroup O1)

C;Species: Vibrio cholerae

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004

C;Accession: D82491

R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.;
 chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.
 l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000

A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A;Reference number: A82035; MUID:20406833; PMID:10952301

A;Accession: D82491

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-291 <HEI>

A;Cross-references: UNIPROT:Q9RMV5; GB:AE004358; GB:AE003853; NID:G9657566; PIDN:AAF9609

A;Experimental source: serogroup O1; strain N16961; biotype El Tor

C;Genetics:

A;Gene: VCA0181

A;Map position: 2

Query Match 42.9%; Score 6; DB 2; Length 291;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VGSVCG 13
 |||||
 Db 120 VGSVCG 125

RESULT 13

B75555

Probable lipase/esterase - Deinococcus radiodurans (strain R1)

C;Species: Deinococcus radiodurans

C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C;Accession: B75555

R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;

M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma

S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.

Science 286, 1571-1577, 1999

A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A;Reference number: A75250; MUID:20036896; PMID:10567266

A;Accession: B75555

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-296 <WHI>

A;Cross-references: UNIPROT:Q9RY19; GB:AE001876; GB:AE000513; NID:G6457800; PIDN:AAF0972

A;Experimental source: strain R1

C;Genetics:

A;Gene: DR0133

A;Map position: 1

C;Superfamily: probable lipolytic protein ybaC

Query Match 42.9%; Score 6; DB 2; Length 296;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VGSVCG 13
 |||||
 Db 173 VGSVCG 178

RESULT 14

S51548

killer toxin K28 - Saccharomyces cerevisiae killer particle M28

C;Species: Saccharomyces cerevisiae killer particle M28

C;Date: 15-Jul-1995 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004

C;Accession: S51548

R;Schmitt, M.J.

Mol. Gen. Genet. 246, 236-246, 1995

A;Title: Cloning and expression of a cDNA copy of the viral K(28) killer toxin gene in y;

A;Reference number: S51548; MUID:95166181; PMID:7862095

A;Accession: S51548

A;Molecule type: mRNA

A;Residues: 1-345 <SCH>

A;Cross-references: UNIPROT:Q7LZU3

C;Superfamily: Saccharomyces cerevisiae killer particle M28 killer toxin K28

Query Match 42.9%; Score 6; DB 2; Length 345;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 SENVGS 10

|||||

Db 268 SENVGS 273

RESULT 15

H65201

Dts system, fructose-like-2 IIC component - Escherichia coli (strain K-12)

C;Species: Escherichia coli

C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004

C;Accession: H65201

R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co

.A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A;Title: The complete genome sequence of Escherichia coli K-12.

A;Reference number: A64720; MUID:97426617; PMID:9278503

A;Accession: H65201

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-359 <BLAT>

A;Cross-references: UNIPROT:P32672; GB:AE000469; GB:U000096; MID:gl790385; PIDN:AAC76931.

A;Experimental source: strain K-12, substrain MG1655

C;Genetics:

A;Gene: frwC

Query Match

42.9%; Score 6; DB 2; Length 359;

Best Local Similarity 100.0%; Pred. No. 29;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VGSVCG 13

|||||

Db 281 VGSVCG 286

Search completed: February 11, 2005, 03:16:22

Job time : 12.0742 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 11, 2005, 03:11:19 ; Search time 3.72379 Seconds
(without alignments)
1925.221 Million cell updates/sec

Title: US-09-736-250-5

Perfect score: 14

Sequence: 1 EDNVSENVGVCVT 14

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1612378 seqs, 512079187 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14	100.0	377	1	Q14094 homo sapien
2	14	100.0	377	1	Q6fhh0 homo sapien
3	9	64.3	377	1	Q922v9 mus musculus
4	9	64.3	377	1	Q8c7e2 mus musculus
5	9	64.3	377	2	Q95lf2 mus musculus
6	8	57.1	600	2	Q8bxl7 debaryomyce
7	7	50.0	310	2	Q8syj3 drosophila
8	7	50.0	423	2	Q8gp73 streptococc
9	7	50.0	423	2	Q9ah92 streptococc
10	7	50.0	446	1	P19541 saccharomyc
11	7	50.0	462	2	Q6fjy2 candida gla
12	7	50.0	556	2	Q9vfg2 drosophila
13	7	50.0	1006	2	Q9u360 caenorhabdi
14	7	50.0	1069	2	Q9jt46 neisseria m
15	7	50.0	1190	2	Q9hs95 halobacteri
16	7	50.0	2153	2	Q6lfd0 plasmodium
17	6	42.9	106	2	Q8x3p5 escherichia
18	6	42.9	109	1	Q9pr08 ureaplasma
19	6	42.9	118	2	Q8y802 listeria mo
20	6	42.9	118	2	Q920w6 listeria mo
21	6	42.9	129	2	Q96zr1 sulfolobus
22	6	42.9	154	2	Q6m0u3 methanococc
23	6	42.9	154	2	Q8m8e1 pseudomonas
24	6	42.9	157	2	Q6l875 photobacter
25	6	42.9	161	2	Q92229 emericella
26	6	42.9	165	2	Q87y87 pseudomonas
27	6	42.9	169	2	Q9k962 bacillus ha
28	6	42.9	181	2	Q8tnh7 methanosarc
29	6	42.9	191	2	Q8jph9 hepatitis c
30	6	42.9	194	2	Q9vc16 drosophila
31	6	42.9	199	2	Q7f0b3 oryza sativ

32	6	42.9	200	2	Q8S290*
33	6	42.9	200	2	Q86BN8
34	6	42.9	205	2	Q6SHG0
35	6	42.9	211	2	Q9SH05
36	6	42.9	224	2	O06076
37	6	42.9	231	1	PSA2 CAEEL
38	6	42.9	233	2	Q8Y4U0
39	6	42.9	233	2	Q71X87
40	6	42.9	248	2	Q8LEE9
41	6	42.9	249	2	Q7R9T7
42	6	42.9	249	2	Q9FKJ8
43	6	42.9	269	1	UL34 VZVD
44	6	42.9	269	2	Q6QCN1
45	6	42.9	282	1	RIP2_BRYDI
46	6	42.9	291	2	Q9KMY5
47	6	42.9	296	2	Q9RY19
48	6	42.9	304	2	Q9N120
49	6	42.9	306	2	Q6J2C5
50	6	42.9	313	1	RBN_VIBVU
51	6	42.9	313	1	RBN_VIBVY
52	6	42.9	323	2	Q91XQ8
53	6	42.9	337	2	Q8PZT1
54	6	42.9	344	2	Q75E08
55	6	42.9	345	2	Q7LZU3
56	6	42.9	359	1	PTWC_ECOLI
57	6	42.9	359	2	Q7UB89
58	6	42.9	359	2	Q8FBA5
59	6	42.9	366	2	Q6C8N4
60	6	42.9	366	2	Q83PD2
61	6	42.9	373	2	O52987
62	6	42.9	373	2	Q6NYZ5
63	6	42.9	381	2	Q8YAW1
64	6	42.9	381	2	Q92FV1
65	6	42.9	381	2	Q725G9
66	6	42.9	383	2	Q8TZ57
67	6	42.9	389	1	PORA_METJA
68	6	42.9	396	2	Q8YDI5
69	6	42.9	396	2	Q937U1
70	6	42.9	401	2	Q6ACCO
71	6	42.9	413	2	Q7RIT0
72	6	42.9	425	2	Q8LQ73
73	6	42.9	448	2	Q8VUK5
74	6	42.9	450	2	Q27920
75	6	42.9	456	2	Q75BN2
76	6	42.9	457	2	Q26227
77	6	42.9	462	2	Q977P2
78	6	42.9	462	2	Q8L7L2
79	6	42.9	489	2	Q6BWU8
80	6	42.9	490	2	Q8MPG5
81	6	42.9	490	2	Q8MPG7
82	6	42.9	490	2	Q8MPG8
83	6	42.9	492	2	O6LXX3
84	6	42.9	492	2	O6QTA3
85	6	42.9	494	2	Q7RRV9
86	6	42.9	496	2	Q8BMR0
87	6	42.9	501	2	Q9N425
88	6	42.9	530	2	Q6FT30
89	6	42.9	530	2	Q8ES70
90	6	42.9	599	2	Q7QXX4
91	6	42.9	604	2	O6L4X6
92	6	42.9	605	2	Q7R9G1
93	6	42.9	622	1	DXS_THETN
94	6	42.9	634	2	Q64S11
95	6	42.9	634	2	Q64VM9
96	6	42.9	643	2	Q8KGZ8
97	6	42.9	701	2	Q8CB43
98	6	42.9	733	2	Q9Y6A6
99	6	42.9	758	2	Q7RRC8
100	6	42.9	759	1	NAHB_ONCMY
101	6	42.9	760	2	Q7OUX6
102	6	42.9	762	2	Q95W15
103	6	42.9	778	2	Q9NEW7
104	6	42.9	779	2	Q9NEW7

Q8ez90 drosophila	Q86bn8 drosophila	Q6shg0 uncultured	Q9sh05 arabidopsis	Q06076 mycobacteri	Q27488 caenorhabdi	Q8Y4U0 listeria mo	Q71X87 listeria mo	Q8LEE9 arabidopsis	Q7R9T7 plasmodium	Q9FKJ8 arabidopsis	Q09280 varicella-z	Q8GQNI human herpe	Q86M14 bryonia dio	Q8KMY5 vibrio chol	Q9RY19 deinococcus	Q9N120 oryctolagus	Q6J2C5 pseudomonas	Q8ddes2 vibrio vuln	Q8mq07 vibrio vuln	Q91xq8 mus musculu	Q9xtc1 methanosarc	Q75e08 ashbya gos	Q71zu3 m28 virus	P32672 escherichia	Q8ub89 shigella fl	Q8fba5 escherichia	Q6c8n4 yarrowia li	Q83pd2 shigella fl	Q52987 escherichia	Q8nyz5 brachydanio	Q8yawi listeria mo	Q92fvi listeria in	Q725g9 listeria mo	Q8tz57 methanopyru	Q57715 methanococc	Q8ydl5 brucella me	Q937ul brucella su	Q8acc0 leifsonia x	Q8lqt3 oryza sativ	Q8vuk5 paracoccus	Q27920 bradyzia hy	Q5b2n2 ashbya gos	Q26227 rhynchosia	Q977p2 uncultured	Q817l2 arabidopsis	Q6bwu8 debaryomyce	Q8mpg5 trypanosoma	Q8mpg7 trypanosoma	Q61xx3 methanococc	Q8qta3 trypanosoma	Q7rrv9 plasmodium	Q8bmr0 m mus muscu	Q9n425 caenorhabdi	Q6ft30 candida gla	Q8es70 oceanobacil	Q7qxx4 giardia lam	Q6l4x6 oryza sativ	Q7r9g1 plasmodium	Q8rac5 thermoanaer	Q64s11 bacteroides	Q64vm9 bacteroides	Q8kgz8 rhizobium l	Q8cb43 mus musculu	Q9y6a6 homo sapien	Q7rrc8 plasmodium	Q01345 oncorhynch	Q7qux6 giardia lam	Q95w15 trypanosoma	Q9new7 caenorhabdi	Q8new7 homo sapien
-------------------	-------------------	-------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	-------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	---------------------	--------------------	--------------------	--------------------	-------------------	------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	-------------------	--------------------	-------------------	-------------------	-------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	-------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	-------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	-------------------	-------------------	--------------------	--------------------	--------------------	--------------------

105 6 42.9 779 2 Q80417 Q80417 pseudopleur 178
106 6 42.9 785 2 Q8RXF1 Q8rxfl arabidopsis 179
107 6 42.9 794 1 Z148_HUMAN Q8rxr1 homo sapien 180
108 6 42.9 794 1 Z148_MOUSE Q61624 mus musculus 181
109 6 42.9 794 1 Z148_RAT Q82806 rattus norv 182
110 6 42.9 794 2 Q8TDH4 Q8tdh4 homo sapien 183
111 6 42.9 794 2 Q7UP50 Q7up50 rhodopirell 184
112 6 42.9 803 2 Q7RKX6 Q7rkx6 plasmodium 185
113 6 42.9 862 1 ADHE_CLOAB P33744 clostridium 186
114 6 42.9 865 2 Q8XHF4 Q8xhf4 clostridium 187
115 6 42.9 867 2 Q8IKI7 Q8iki7 plasmodium 188
116 6 42.9 869 2 Q8C744 Q8c744 arabidopsis 189
117 6 42.9 876 2 Q895B4 Q895b4 clostridium 190
118 6 42.9 888 2 Q09435 Q09435 giardia lam 191
119 6 42.9 889 2 Q9PFH9 Q9pfh9 arabidopsis 192
120 6 42.9 935 2 Q8CA26 Q8ca26 arabidopsis 193
121 6 42.9 960 2 Q8BXD5 Q8bxds debaryomyce 194
122 6 42.9 1026 2 Q8SS79 Q8ss79 arabidopsis 195
123 6 42.9 1033 1 CR2_HUMAN P20023 homo sapien 196
124 6 42.9 1066 1 KL61_DROME P46863 drosophila 197
125 6 42.9 1131 2 Q23741 Q23741 brassica ol 198
126 6 42.9 1147 2 Q8X0V3 Q8x0v3 neurospora 199
127 6 42.9 1154 2 Q7XPW1 Q7xpwl oryza sativ 200
128 6 42.9 1296 2 Q6UJG6 Q6ujg6 sorghum bic 201
129 6 42.9 1731 2 Q8WY30 Q8wy30 homo sapien 202
130 6 42.9 1776 2 Q9MA20 Q9ma20 arabidopsis 203
131 6 42.9 1844 2 Q7S601 Q7s6q1 neurospora 204
132 6 42.9 1980 2 Q7RF56 Q7rf56 plasmodium 205
133 6 42.9 3207 2 Q8IHQ0 Q8ihq0 plasmodium 206
134 6 42.9 3366 2 Q8QCE1 Q8qce1 brachydanio 207
135 6 42.9 4513 1 DY1B_CHLRE Q8mbf8 chlamydomon 208
136 6 42.9 4543 1 LRP1_CHICK P98157 gallus gall 209
137 6 42.9 4544 1 LRP1_HUMAN Q07954 homo sapien 210
138 6 42.9 4545 2 Q91ZX7 Q91zx7 mus musculus 211
139 6 42.9 4545 2 Q820Y4 Q820y4 mus musculus 212
140 6 42.9 4545 2 Q61291 Q61291 mus musculus 213
141 6 42.9 4599 1 LR1B_HUMAN Q9nzzr2 homo sapien 214
142 6 42.9 4599 1 LR1B_MOUSE Q9jil8 mus musculus 215
143 6 42.9 6994 2 Q17343 Q17343 caenorhabdi 216
144 6 42.9 6994 2 Q17490 Q17490 caenorhabdi 217
145 5 35.7 16 2 Q7M1D3 Q7m1d3 unidentified 218
146 5 35.7 28 1 COXB_SOLTU P80499 solanum tub 219
147 5 35.7 39 2 Q7RKY0 Q7rky0 plasmodium 220
148 5 35.7 40 2 Q6GAQ3 Q6gaq3 staphylococ 221
149 5 35.7 40 2 Q6GGL0 Q6gg10 staphylococ 222
150 5 35.7 43 2 Q7M055 Q7m055 mus sp. gen 223
151 5 35.7 50 2 Q19112 Q19112 caenorhabdi 224
152 5 35.7 51 2 Q8YHB3 Q8ynb3 ambystoma t 225
153 5 35.7 55 2 Q6S465 Q6s465 burkholderi 226
154 5 35.7 61 2 Q8S4V1 Q8s4v1 arabidopsis 227
155 5 35.7 64 2 Q8IBX4 Q8ibx4 plasmodium 228
156 5 35.7 64 2 Q8JFG5 Q8jfg5 brachydanio 229
157 5 35.7 68 2 Q85WS9 Q85ws9 pinus korai 230
158 5 35.7 70 2 Q8KEZ8 Q8kez8 tetraodon n 231
159 5 35.7 72 2 Q9S5J72 Q9s5j72 arabidopsis 232
160 5 35.7 73 2 Q6VXZ6 Q6vxz6 echinococcu 233
161 5 35.7 73 2 Q74EW1 Q74ew1 geobacter s 234
162 5 35.7 74 1 YM34_MARPO P38476 marchantia 235
163 5 35.7 74 2 Q83H11 Q83h11 bacillus ce 236
164 5 35.7 74 2 Q73FF6 Q73ff6 bacillus ce 237
165 5 35.7 74 2 Q81VY8 Q81vy8 bacillus an 238
166 5 35.7 74 2 Q8HPW5 Q8hpw5 bacillus th 239
167 5 35.7 74 2 Q83940 Q83940 olive laten 240
168 5 35.7 75 2 Q6VXZ5 Q6vxz5 echinococcu 241
169 5 35.7 76 2 Q8PSU2 Q8psu2 methanosarc 242
170 5 35.7 76 2 Q8H810 Q8h810 oryza sativ 243
171 5 35.7 77 2 Q8CJU0 Q8cj0 streptomyce 244
172 5 35.7 79 2 Q8FAZ7 Q8faz7 escherichia 245
173 5 35.7 80 2 Q61LW8 Q61lw8 methanococc 246
174 5 35.7 84 2 Q6K6X5 Q6k6x5 oryza sativ 247
175 5 35.7 84 2 Q9RXT2 Q9rxt2 deinococcus 248
176 5 35.7 84 2 Q919H0 Q919h0 culex nigri 249
177 5 35.7 86 2 Q8LDR2 Q8ldr2 arabidopsis 250

Q909Y4 human immu 35.7 88 2 Q909Y4
Q8RXU8 methospora 35.7 89 2 Q8RXU8
Q8tm63 methanosarc 35.7 92 2 Q8TM63
Q8gwv2 arabidopsis 35.7 92 2 Q8GWV2
Q8g9v7 escherichia 35.7 92 2 Q8G9V7
Q8elw6 streptococc 35.7 93 2 Q8ELW6
Q8g9v6 escherichia 35.7 94 2 Q8G9V6
Q6dt49 arabidopsis 35.7 96 2 Q6DT49
Q27127 methanobact 35.7 98 1 RL3E_METTH
Q8A016 bacteroides 35.7 98 2 Q8A016
Q14287 schizosacch 35.7 99 2 Q14287
Q8cp2 methanosarc 35.7 100 2 Q8CTP2
Q8bn15 mus musculu 35.7 100 2 Q8BN15
Q9CVP1 mus musculu 35.7 100 2 Q9CVP1
Q66099 carnation r 35.7 100 2 Q66099
Q6s3h0 brassica ju 35.7 101 2 Q6S3H0
Q6s3l1 brassica ju 35.7 101 2 Q6S3L1
Q8qds microplitis 35.7 102 2 Q8QDS
Q8zb6 debaryomyce 35.7 103 2 Q6BZB6
Q9hm66 thermoplas 35.7 104 1 VATF_THEAC
Q6evd9 avena barba 35.7 107 2 Q6EVD9
Q92c09 listeria in 35.7 107 2 Q92C09
Q6sxn0 ctenopharyn 35.7 107 2 Q6SXN0
Q8641 methanococc 35.7 108 1 YC44_METJA
Q8rt9 escherichia 35.7 108 2 Q8RTC9
Q7yux8 trypanosoma 35.7 109 2 Q7YUX8
Q7xk05 oryza sativ 35.7 109 2 Q7XK05
Q7fy22 arabidopsis 35.7 110 2 Q7FY22
Q7mi06 vibrio vuln 35.7 110 2 Q7MI06
Q8dbw3 vibrio vuln 35.7 110 2 Q8DBW3
Q80gn5 human herpe 35.7 110 2 Q80GN5
Q8icn9 bacillus ce 35.7 111 2 Q8ICN9
Q9fdy5 arabidopsis 35.7 115 2 Q9FDY5
Q7rmd5 plasmodium 35.7 116 2 Q7RMD5
Q7vle1 haemophilus 35.7 116 2 Q7VLE1
Q7rb5 plasmodium 35.7 117 2 Q7RBS5
Q6jig7 bacterioph 35.7 117 2 Q6JIG7
Q665g9 yersinia ps 35.7 117 2 Q665Q9
Q80kv1 hepatitis c 35.7 117 2 Q80KV1
Q6uvp6 pseudococl 35.7 119 2 Q6UVP6
Q50632 bacillus ha 35.7 121 1 RS13_BACHD
Q2w42 rhizobium m 35.7 122 2 Q92W42
Q6lsg5 photobacter 35.7 122 2 Q6LSG5
Q7s2f8 neurospora 35.7 123 2 Q7S2F8
Q9xx40 caenorhabdi 35.7 123 2 Q9XX40
Q63an2 bacillus ce 35.7 126 2 Q63AN2
Q737b6 bacillus ce 35.7 126 2 Q737B6
Q81pu1 bacillus an 35.7 126 2 Q81PU1
Q8hil9 bacillus th 35.7 126 2 Q6H1I9
Q8zxy7 pyrobaculum 35.7 127 2 Q8ZXY7
Q6ij1t drosophila 35.7 127 2 Q6IJT1
Q953c4 cucitogast 35.7 127 2 Q953C4
Q74bc7 geobacter s 35.7 127 2 Q74BC7
Q91l80 white spot 35.7 127 2 Q91L80
Q7ctm4 white spot 35.7 127 2 Q7CTM4
P7310 escherichia 35.7 128 1 NIFU_ECOLI
Q6n819 rhodopseudo 35.7 130 2 Q6N819
Q6evd8 avena longi 35.7 130 2 Q6EVD8
Q7ngv4 gloeobacter 35.7 131 2 Q7NGV4
Q66md1 hepatitis c 35.7 131 2 Q66MD1
Q88946 tomato yell 35.7 131 2 Q88946
Q8pw94 methanosarc 35.7 133 2 Q8PW94
Q7x9d0 pyrus pyrif 35.7 133 2 Q7X9D0
Q84xx2 brassica ra 35.7 135 2 Q84XX2
Q62pq0 bacillus li 35.7 135 2 Q62PQ0
Q8w601 bacterioph 35.7 136 2 Q8W601
Q84rq4 chlamydomon 35.7 136 2 Q84RQ4
Q8svz4 arabidopsis 35.7 137 2 Q9SVZ4
Q99iy9 uncultured 35.7 137 2 Q99IY9
Q9czf7 mus musculu 35.7 138 2 Q9CZF7
Q15486 homo sapien 35.7 140 1 SMP3_HUMAN
Q15487 homo sapien 35.7 140 1 SMP4_HUMAN
Q15488 homo sapien 35.7 140 1 SMP5_HUMAN

251	5	35.7	140	1	SMPL_HUMAN	Q9nqg0	homo sapien	324	5	35.7	177	2	Q7PLC9	Q7plc9	drosophila
252	5	35.7	141	2	Q6FQW3	Q6fqw3	candida gla	325	5	35.7	178	2	Q7UT14	Q7uti14	rhodospirella
253	5	35.7	142	2	Q8H127	Q8h127	arabidopsis	326	5	35.7	179	2	Q8SX75	Q8sx75	drosophila
254	5	35.7	143	2	Q9PV16	Q9pv16	dicentrarch	327	5	35.7	179	2	Q7Q705	Q7q705	anopheles g
255	5	35.7	143	1	PSE1_ARATH	Q9831	arabidopsis	328	5	35.7	180	2	Q84HR5	Q84hr5	rhizobium g
256	5	35.7	143	2	Q96ZM6	Q96zm6	sulfolobus	329	5	35.7	180	2	Q84HR6	Q84hr6	rhizobium g
257	5	35.7	143	2	Q8LC58	Q8lc58	arabidopsis	330	5	35.7	180	2	Q84HR8	Q84hr8	rhizobium g
258	5	35.7	143	2	Q8LG63	Q8lg63	arabidopsis	331	5	35.7	180	2	Q9X9T2	Q9x9t2	synechococ
259	5	35.7	144	2	Q7RK64	Q7rk64	plasmodium	332	5	35.7	181	2	Q9X9T2	Q9x9t2	synechococ
260	5	35.7	144	2	Q9S4X0	Q9s4x0	escherichia	333	5	35.7	182	2	Q9X9T2	Q9x9t2	synechococ
261	5	35.7	145	1	Q81346	Q81346	hepatitis c	334	5	35.7	182	2	Q6XLZ1	Q6xlz1	feldmannia
262	5	35.7	145	1	PSE2_ARATH	Q95714	arabidopsis	335	5	35.7	183	2	Q6BNF9	Q6bnf9	debaromyce
263	5	35.7	145	2	Q9V8Y6	Q9v8y6	drosophila	336	5	35.7	184	2	Q8KP48	Q8kp48	peptostrept
264	5	35.7	145	2	Q8RD77	Q8rd77	human papil	337	5	35.7	185	2	Q82898	Q82898	escherichia
265	5	35.7	146	2	Q899W9	Q899w9	clostridium	338	5	35.7	185	2	Q16556	Q16556	caenorhabdi
266	5	35.7	149	2	O59021	O59021	pyrococcus	339	5	35.7	185	2	Q8V3H5	Q8v3h5	swinepox vi
267	5	35.7	151	2	Q9NV63	Q9nv63	homo sapien	340	5	35.7	187	2	Q64CV4	Q64cv4	uncultured
268	5	35.7	151	2	Q6SED9	Q6sed9	lactobacill	341	5	35.7	187	2	Q84Y12	Q84y12	capsella ru
269	5	35.7	151	2	Q8EJ21	Q8ej21	shewanella	342	5	35.7	188	2	Q9M448	Q9m448	cicer ariet
270	5	35.7	151	2	Q85PP8	Q85pp8	lactobacill	343	5	35.7	188	2	Q9J3A4	Q9j3a4	hepatitis c
271	5	35.7	152	2	Q8IEN4	Q8ien4	plasmodium	344	5	35.7	188	2	Q9J3A5	Q9j3a5	hepatitis c
272	5	35.7	152	2	Q8HCR4	Q8hcr4	oryza sativ	345	5	35.7	188	2	Q9J3A6	Q9j3a6	hepatitis c
273	5	35.7	152	2	Q6DA87	Q6da87	erwinia car	346	5	35.7	188	2	Q9J3A7	Q9j3a7	hepatitis c
274	5	35.7	154	2	Q7RA51	Q7ra51	plasmodium	347	5	35.7	188	2	Q9J3A8	Q9j3a8	hepatitis c
275	5	35.7	154	2	Q7RCG8	Q7rcg8	plasmodium	348	5	35.7	188	2	Q9J3B1	Q9j3b1	hepatitis c
276	5	35.7	154	2	Q8W628	Q8w628	cyanophaga	349	5	35.7	188	2	Q9J3B2	Q9j3b2	hepatitis c
277	5	35.7	154	2	Q92CE7	Q92ce7	listeria mo	350	5	35.7	188	2	Q9J3B3	Q9j3b3	hepatitis c
278	5	35.7	154	2	Q720G5	Q720g5	listeria mo	351	5	35.7	188	2	Q9J3B4	Q9j3b4	hepatitis c
279	5	35.7	154	2	Q72T44	Q72t44	leptospira	352	5	35.7	189	2	Q9J3B5	Q9j3b5	hepatitis c
280	5	35.7	154	2	Q7AP06	Q7ap06	listeria in	353	5	35.7	189	2	Q9J3B6	Q9j3b6	hepatitis c
281	5	35.7	154	2	Q8F2B0	Q8f2b0	leptospira	354	5	35.7	189	2	Q9J3B7	Q9j3b7	hepatitis c
282	5	35.7	154	2	Q7T0K7	Q7t0k7	ambystoma m	355	5	35.7	190	2	Q8JPH1	Q8jph1	hepatitis c
283	5	35.7	155	2	Q9HDZ6	Q9hdz6	schistosacch	356	5	35.7	190	2	Q9Q3W1	Q9q3w1	hepatitis c
284	5	35.7	155	2	Q6EVE2	Q6eve2	avena insul	357	5	35.7	190	2	Q9Q3W2	Q9q3w2	hepatitis c
285	5	35.7	155	2	Q6EVE3	Q6eve3	avena longi	358	5	35.7	190	2	Q9Q3W3	Q9q3w3	hepatitis c
286	5	35.7	156	2	Q9VU00	Q9vu00	sulfolobus	359	5	35.7	190	2	Q9Q3W4	Q9q3w4	hepatitis c
287	5	35.7	156	2	Q8S4V2	Q8s4v2	arabidopsis	360	5	35.7	191	2	Q7ZZP4	Q7zzp4	agkistrodon
288	5	35.7	156	2	Q8S8C9	Q8s8c9	arabidopsis	361	5	35.7	191	2	Q8N1Y3	Q8n1y3	homo sapien
289	5	35.7	160	1	THY1_CHICK	Q88C9	arabidopsis	362	5	35.7	191	2	Q6R9G2	Q6r9g2	zea mays (m
290	5	35.7	160	1	TPC2_CAEBL	Q07212	gallus gall	363	5	35.7	191	2	Q8JPH2	Q8jph2	hepatitis c
291	5	35.7	160	1	Q6ZW30	Q6zw30	homo sapien	364	5	35.7	191	2	Q8JPH3	Q8jph3	hepatitis c
292	5	35.7	160	2	Q7PN38	Q7pn38	anopheles g	365	5	35.7	191	2	Q8JPH4	Q8jph4	hepatitis c
293	5	35.7	160	2	Q97TE5	Q97te5	clostridium	366	5	35.7	191	2	Q8JPH5	Q8jph5	hepatitis c
294	5	35.7	160	2	Q7T252	Q7t252	gallus gall	367	5	35.7	191	2	Q8JPH6	Q8jph6	hepatitis c
295	5	35.7	162	2	Q6MRRO	Q6mrro	bdellovibri	368	5	35.7	191	2	Q8JPH7	Q8jph7	hepatitis c
296	5	35.7	162	2	Q89PC2	Q89pc2	bradyrhizob	369	5	35.7	191	2	Q8JPH8	Q8jph8	hepatitis c
297	5	35.7	163	1	EMP3_HUMAN	P54852	homo sapien	370	5	35.7	191	2	Q8JPI0	Q8jpi0	hepatitis c
298	5	35.7	163	1	EMP3_MOUSE	O35912	mus musculus	371	5	35.7	191	2	Q8JPI1	Q8jpi1	hepatitis c
299	5	35.7	163	1	EMP3_RAT	Q9qy5	rattus norv	372	5	35.7	191	2	Q8JPI3	Q8jpi3	hepatitis c
300	5	35.7	163	2	Q61BD3	Q61bd3	homo sapien	373	5	35.7	191	2	Q8JPI4	Q8jpi4	hepatitis c
301	5	35.7	164	2	Q97BF3	Q97bf3	thermoplasm	374	5	35.7	191	2	Q8JPI5	Q8jpi5	hepatitis c
302	5	35.7	164	2	Q8N204	Q8n204	homo sapien	375	5	35.7	191	2	Q8JPI7	Q8jpi7	hepatitis c
303	5	35.7	165	2	Q975U1	Q975u1	sulfolobus	376	5	35.7	191	2	Q8JPI8	Q8jpi8	hepatitis c
304	5	35.7	165	2	Q893X4	Q893x4	clostridium	377	5	35.7	191	2	Q8JPI0	Q8jpi0	hepatitis c
305	5	35.7	166	2	Q9SCK5	Q9sck5	arabidopsis	378	5	35.7	191	2	Q8JPI2	Q8jpi2	hepatitis c
306	5	35.7	167	2	Q8ENN5	Q8enn5	oceanobacil	379	5	35.7	191	2	Q8JPI4	Q8jpi4	hepatitis c
307	5	35.7	167	2	Q6URK9	Q6urk9	bothrops ja	380	5	35.7	191	2	Q8BBM1	Q8bbm1	hepatitis c
308	5	35.7	168	2	Q6ZLB3	Q6zlb3	oryza sativ	381	5	35.7	191	2	Q8BBM3	Q8bbm3	hepatitis c
309	5	35.7	168	2	Q6CTD9	Q6ctd9	lactobacill	382	5	35.7	191	2	Q8BBM5	Q8bbm5	hepatitis c
310	5	35.7	170	2	Q639P8	Q639f8	bacillus ce	383	5	35.7	191	2	Q8BBM7	Q8bbm7	hepatitis c
311	5	35.7	170	2	Q8INL1	Q8inl1	bacillus an	384	5	35.7	191	2	Q8BBM8	Q8bbm8	hepatitis c
312	5	35.7	170	2	Q6HGR7	Q6hgr7	bacillus th	385	5	35.7	191	2	Q8BBM9	Q8bbm9	hepatitis c
313	5	35.7	171	2	Q847C9	Q847c9	nodularia s	386	5	35.7	191	2	Q8BBN0	Q8bbn0	hepatitis c
314	5	35.7	171	2	Q9CVY4	Q9cvy4	mus musculus	387	5	35.7	191	2	Q8BBN1	Q8bbn1	hepatitis c
315	5	35.7	172	2	Q8LKC4	Q8lkc4	malus pruni	388	5	35.7	191	2	Q8BBN3	Q8bbn3	hepatitis c
316	5	35.7	172	2	Q7VGM0	Q7vgm0	helicobacte	389	5	35.7	191	2	Q8BBN4	Q8bbn4	hepatitis c
317	5	35.7	173	2	Q76P34	Q76p34	dictyosteli	390	5	35.7	191	2	Q8BBN6	Q8bbn6	hepatitis c
318	5	35.7	173	2	Q86EE3	Q86el3	schistosoma	391	5	35.7	191	2	Q8BBN7	Q8bbn7	hepatitis c
319	5	35.7	173	2	Q735G3	Q735g3	bacillus ce	392	5	35.7	191	2	Q8BBN8	Q8bbn8	hepatitis c
320	5	35.7	173	2	Q81BL3	Q81bl3	bacillus ce	393	5	35.7	191	2	Q8BBN9	Q8bbn9	hepatitis c
321	5	35.7	174	2	Q9AI91	Q9ai91	helicobacte	394	5	35.7	192	2	Q7S2P5	Q7s2p5	neurospora
322	5	35.7	174	2	Q8NRQ9	Q8nrq9	corynebacte	395	5	35.7	192	2	Q81496	Q81496	hepatitis c
323	5	35.7	175	2	Q9F191	Q9f191	arabidopsis	396	5	35.7	192	2	Q81499	Q81499	hepatitis c

397	5	35.7	192	2	Q81502	Q81502 hepatitis c	470
398	5	35.7	192	2	Q81505	Q81505 hepatitis c	471
399	5	35.7	192	2	Q81511	Q81511 hepatitis c	472
400	5	35.7	192	2	Q81514	Q81514 hepatitis c	473
401	5	35.7	192	2	Q81517	Q81517 hepatitis c	474
402	5	35.7	192	2	Q81520	Q81520 hepatitis c	475
403	5	35.7	192	2	Q81523	Q81523 hepatitis c	476
404	5	35.7	192	2	Q81526	Q81526 hepatitis c	477
405	5	35.7	192	2	Q81529	Q81529 hepatitis c	478
406	5	35.7	192	2	Q81535	Q81535 hepatitis c	479
407	5	35.7	192	2	Q81539	Q81539 hepatitis c	480
408	5	35.7	192	2	Q81543	Q81543 hepatitis c	481
409	5	35.7	192	2	Q81547	Q81547 hepatitis c	482
410	5	35.7	192	2	Q81551	Q81551 hepatitis c	483
411	5	35.7	192	2	Q81555	Q81555 hepatitis c	484
412	5	35.7	192	2	Q81559	Q81559 hepatitis c	485
413	5	35.7	192	2	Q81563	Q81563 hepatitis c	486
414	5	35.7	192	2	Q81567	Q81567 hepatitis c	487
415	5	35.7	192	2	Q81571	Q81571 hepatitis c	488
416	5	35.7	192	2	Q81575	Q81575 hepatitis c	489
417	5	35.7	192	2	Q81579	Q81579 hepatitis c	490
418	5	35.7	192	2	Q81583	Q81583 hepatitis c	491
419	5	35.7	192	2	Q81587	Q81587 hepatitis c	492
420	5	35.7	192	2	Q81591	Q81591 hepatitis c	493
421	5	35.7	192	2	Q81595	Q81595 hepatitis c	494
422	5	35.7	192	2	Q81599	Q81599 hepatitis c	495
423	5	35.7	192	2	Q81603	Q81603 hepatitis c	496
424	5	35.7	192	2	Q81607	Q81607 hepatitis c	497
425	5	35.7	192	2	Q81611	Q81611 hepatitis c	498
426	5	35.7	192	2	Q81615	Q81615 hepatitis c	499
427	5	35.7	192	2	Q81619	Q81619 hepatitis c	500
428	5	35.7	192	2	Q81623	Q81623 hepatitis c	501
429	5	35.7	192	2	Q81627	Q81627 hepatitis c	502
430	5	35.7	192	2	Q81631	Q81631 hepatitis c	503
431	5	35.7	192	2	Q81635	Q81635 hepatitis c	504
432	5	35.7	192	2	Q81639	Q81639 hepatitis c	505
433	5	35.7	192	2	Q81643	Q81643 hepatitis c	506
434	5	35.7	192	2	Q81647	Q81647 hepatitis c	507
435	5	35.7	192	2	Q81651	Q81651 hepatitis c	508
436	5	35.7	192	2	Q81655	Q81655 hepatitis c	509
437	5	35.7	192	2	Q81659	Q81659 hepatitis c	510
438	5	35.7	192	2	Q81663	Q81663 hepatitis c	511
439	5	35.7	192	2	Q81667	Q81667 hepatitis c	512
440	5	35.7	192	2	Q81671	Q81671 hepatitis c	513
441	5	35.7	192	2	Q81675	Q81675 hepatitis c	514
442	5	35.7	192	2	Q81679	Q81679 hepatitis c	515
443	5	35.7	192	2	Q81683	Q81683 hepatitis c	516
444	5	35.7	192	2	Q81687	Q81687 hepatitis c	517
445	5	35.7	192	2	Q81691	Q81691 hepatitis c	518
446	5	35.7	192	2	Q81695	Q81695 hepatitis c	519
447	5	35.7	192	2	Q81699	Q81699 hepatitis c	520
448	5	35.7	192	2	Q81703	Q81703 hepatitis c	521
449	5	35.7	192	2	Q81707	Q81707 hepatitis c	522
450	5	35.7	192	2	Q81711	Q81711 hepatitis c	523
451	5	35.7	192	2	Q81715	Q81715 hepatitis c	524
452	5	35.7	192	2	Q81719	Q81719 hepatitis c	525
453	5	35.7	192	2	Q81723	Q81723 hepatitis c	526
454	5	35.7	192	2	Q81727	Q81727 hepatitis c	527
455	5	35.7	192	2	Q81731	Q81731 hepatitis c	528
456	5	35.7	192	2	Q81735	Q81735 hepatitis c	529
457	5	35.7	192	2	Q81739	Q81739 hepatitis c	530
458	5	35.7	192	2	Q81743	Q81743 hepatitis c	531
459	5	35.7	192	2	Q81747	Q81747 hepatitis c	532
460	5	35.7	192	2	Q81751	Q81751 hepatitis c	533
461	5	35.7	192	2	Q81755	Q81755 hepatitis c	534
462	5	35.7	192	2	Q81759	Q81759 hepatitis c	535
463	5	35.7	192	2	Q81763	Q81763 hepatitis c	536
464	5	35.7	192	2	Q81767	Q81767 hepatitis c	537
465	5	35.7	192	2	Q81771	Q81771 hepatitis c	538
466	5	35.7	192	2	Q81775	Q81775 hepatitis c	539
467	5	35.7	192	2	Q81779	Q81779 hepatitis c	540
468	5	35.7	192	2	Q81783	Q81783 hepatitis c	541
469	5	35.7	192	2	Q81787	Q81787 hepatitis c	542
470	5	35.7	192	2	Q81791	Q81791 hepatitis c	543
471	5	35.7	192	2	Q81795	Q81795 hepatitis c	544
472	5	35.7	192	2	Q81799	Q81799 hepatitis c	545
473	5	35.7	192	2	Q81803	Q81803 hepatitis c	546
474	5	35.7	192	2	Q81807	Q81807 hepatitis c	547
475	5	35.7	192	2	Q81811	Q81811 hepatitis c	548
476	5	35.7	192	2	Q81815	Q81815 hepatitis c	549
477	5	35.7	192	2	Q81819	Q81819 hepatitis c	550
478	5	35.7	192	2	Q81823	Q81823 hepatitis c	551
479	5	35.7	192	2	Q81827	Q81827 hepatitis c	552
480	5	35.7	192	2	Q81831	Q81831 hepatitis c	553
481	5	35.7	192	2	Q81835	Q81835 hepatitis c	554
482	5	35.7	192	2	Q81839	Q81839 hepatitis c	555
483	5	35.7	192	2	Q81843	Q81843 hepatitis c	556
484	5	35.7	192	2	Q81847	Q81847 hepatitis c	557
485	5	35.7	192	2	Q81851	Q81851 hepatitis c	558
486	5	35.7	192	2	Q81855	Q81855 hepatitis c	559
487	5	35.7	192	2	Q81859	Q81859 hepatitis c	560
488	5	35.7	192	2	Q81863	Q81863 hepatitis c	561
489	5	35.7	192	2	Q81867	Q81867 hepatitis c	562
490	5	35.7	192	2	Q81871	Q81871 hepatitis c	563
491	5	35.7	192	2	Q81875	Q81875 hepatitis c	564
492	5	35.7	192	2	Q81879	Q81879 hepatitis c	565
493	5	35.7	192	2	Q81883	Q81883 hepatitis c	566
494	5	35.7	192	2	Q81887	Q81887 hepatitis c	567
495	5	35.7	192	2	Q81891	Q81891 hepatitis c	568
496	5	35.7	192	2	Q81895	Q81895 hepatitis c	569
497	5	35.7	192	2	Q81899	Q81899 hepatitis c	570
498	5	35.7	192	2	Q81903	Q81903 hepatitis c	571
499	5	35.7	192	2	Q81907	Q81907 hepatitis c	572
500	5	35.7	192	2	Q81911	Q81911 hepatitis c	573
501	5	35.7	192	2	Q81915	Q81915 hepatitis c	574
502	5	35.7	192	2	Q81919	Q81919 hepatitis c	575
503	5	35.7	192	2	Q81923	Q81923 hepatitis c	576
504	5	35.7	192	2	Q81927	Q81927 hepatitis c	577
505	5	35.7	192	2	Q81931	Q81931 hepatitis c	578
506	5	35.7	192	2	Q81935	Q81935 hepatitis c	579
507	5	35.7	192	2	Q81939	Q81939 hepatitis c	580
508	5	35.7	192	2	Q81943	Q81943 hepatitis c	581
509	5	35.7	192	2	Q81947	Q81947 hepatitis c	582
510	5	35.7	192	2	Q81951	Q81951 hepatitis c	583
511	5	35.7	192	2	Q81955	Q81955 hepatitis c	584
512	5	35.7	192	2	Q81959	Q81959 hepatitis c	585
513	5	35.7	192	2	Q81963	Q81963 hepatitis c	586
514	5	35.7	192	2	Q81967	Q81967 hepatitis c	587
515	5	35.7	192	2	Q81971	Q81971 hepatitis c	588
516	5	35.7	192	2	Q81975	Q81975 hepatitis c	589
517	5	35.7	192	2	Q81979	Q81979 hepatitis c	590
518	5	35.7	192	2	Q81983	Q81983 hepatitis c	591
519	5	35.7	192	2	Q81987	Q81987 hepatitis c	592
520	5	35.7	192	2	Q81991	Q81991 hepatitis c	593
521	5	35.7	192	2	Q81995	Q81995 hepatitis c	594
522	5	35.7	192	2	Q81999	Q81999 hepatitis c	595
523	5	35.7	192	2	Q82003	Q82003 hepatitis c	596
524	5	35.7	192	2	Q82007	Q82007 hepatitis c	597
525	5	35.7	192	2	Q82011	Q82011 hepatitis c	598
526	5	35.7	192	2	Q82015	Q82015 hepatitis c	599
527	5	35.7	192	2	Q82019	Q82019 hepatitis c	600
528	5	35.7	192	2	Q82023	Q82023 hepatitis c	601
529	5	35.7	192	2	Q82027	Q82027 hepatitis c	602
530	5	35.7	192	2	Q82031	Q82031 hepatitis c	603
531	5	35.7	192	2	Q82035	Q82035 hepatitis c	604
532	5	35.7	192	2	Q82039	Q82039 hepatitis c	605
533	5	35.7	192	2	Q82043	Q82043 hepatitis c	606
534	5	35.7	192	2	Q82047	Q82047 hepatitis c	607
535	5	35.7	192	2	Q82051	Q82051 hepatitis c	608
536	5	35.7	192	2	Q82055	Q82055 hepatitis c	609
537	5	35.7	192	2	Q82059	Q82059 hepatitis c	610
538	5	35.7	192	2	Q82063	Q82063 hepatitis c	611
539	5	35.7	192	2	Q82067	Q82067 hepatitis c	612
540	5	35.7	192	2	Q82071	Q82071 hepatitis c	613
541	5	35.7	192	2	Q82075	Q82075 hepatitis c	614
542	5	35.7	192	2	Q82079	Q82079 hepatitis c	615
543	5	35.7	192	2	Q82083	Q82083 hepatitis c	616
544	5	35.7	192	2	Q82087	Q82087 hepatitis c	617
545	5	35.7	192	2	Q82091	Q82091 hepatitis c	618
546	5	35.7	192	2	Q82095	Q82095 hepatitis c	619
547	5	35.7	192	2	Q82099	Q82099 hepatitis c	620
548	5	35.7	192	2	Q82103	Q82103 hepatitis c	621
549	5	35.7	192	2	Q82107	Q82107 hepatitis c	622
550	5	35.7	192	2	Q82111	Q82111 hepatitis c	623
551	5	35.7	192	2	Q82115	Q82115 hepatitis c	624
552	5	35.7	192	2	Q82119	Q82119 hepatitis c	625
553	5	35.7	192	2	Q82123	Q82123 hepatitis c	626
554	5	35.7	192	2	Q82127	Q82127 hepatitis c	627
555	5	35.7	192	2	Q82131	Q82131 hepatitis c	628
556	5	35.7	192	2	Q82135	Q82135 hepatitis c	629
557	5	35.7	192	2	Q82139	Q82139 hepatitis c	630
558	5	35.7	192	2	Q82143	Q82143 hepatitis c	631
559	5	35.7	192	2	Q82147	Q82147 hepatitis c	632
560	5	35.7	192	2	Q82151	Q82151 hepatitis c	633
561	5	35.7	192	2	Q82155	Q82155 hepatitis c	634

543	5	35.7	237	2	Q612U4	Q612u4 picrophilus	616
544	5	35.7	237	2	Q6NQX8	Q6nqk8 arabidopsis	617
545	5	35.7	237	2	Q93421	Q93421 agkistrodon	618
546	5	35.7	237	2	Q8UUU2	Q8uuu2 agkistrodon	619
547	5	35.7	238	1	VSP1_AGKHA	P81176 agkistrodon	620
548	5	35.7	239	1	GRPE_PROMP	Q7v3q4 prochloroco	621
549	5	35.7	239	2	Q7AR64	Q7ar64 campylobact	622
550	5	35.7	239	2	Q6T5L0	Q6t5l0 gloydius sh	623
551	5	35.7	240	2	Q51151	Q51151 borrelia bu	624
552	5	35.7	240	2	Q894J9	Q894j9 clostridium	625
553	5	35.7	241	2	Q75J75	Q75j75 dictyosteli	626
554	5	35.7	241	2	Q9K198	Q9k198 neisseria m	627
555	5	35.7	241	2	Q6APJ4	Q6apj4 desulfotale	628
556	5	35.7	242	2	Q8E0E7	Q8e0e7 streptococc	629
557	5	35.7	242	2	Q8E621	Q8e621 streptococc	630
558	5	35.7	242	2	Q68UW9	Q68uw9 ageratum ye	631
559	5	35.7	243	2	Q6L2N4	Q6l2n4 picrophilus	632
560	5	35.7	243	2	Q6ZPW6	Q6zpw6 mus musculu	633
561	5	35.7	244	1	FABG_VIBCH	Q6kqh7 vibrio chol	634
562	5	35.7	244	1	FABG_VIBHA	P55336 vibrio harv	635
563	5	35.7	244	1	MABC_RAT	P08661 rattus norv	636
564	5	35.7	244	2	Q94130	Q94190 caenorhabdi	637
565	5	35.7	244	2	Q87N22	Q87n22 vibrio para	638
566	5	35.7	245	2	Q6AV58	Q6av58 oryza sativ	639
567	5	35.7	246	1	PCNA_THEAC	Q8hjQ0 thermoplas	640
568	5	35.7	246	1	PCNA_THEVO	Q979s2 thermoplas	641
569	5	35.7	246	2	Q370G3	Q970g3 sulfobolus	642
570	5	35.7	246	2	Q8RV42	Q8rv42 arabidopsis	643
571	5	35.7	246	2	Q8EPH3	Q8eph3 oceanobacil	644
572	5	35.7	247	2	P95849	P95849 sulfobolus	645
573	5	35.7	248	1	VGL2_EBV	P03218 epstein-bar	646
574	5	35.7	248	2	Q9BS20	Q9bs20 homo sapien	647
575	5	35.7	248	2	Q67RY1	Q67ry1 symbiobacte	648
576	5	35.7	248	2	Q9EUG8	Q9eug8 salmonella	649
577	5	35.7	248	2	Q7M7J8	Q7m7j8 vibrio vuln	650
578	5	35.7	248	2	Q8D8G8	Q8d8g8 vibrio vuln	651
579	5	35.7	249	2	Q777B4	Q777b4 human herpe	652
580	5	35.7	249	2	Q6VED7	Q6ved7 emilliania h	653
581	5	35.7	249	2	Q8RJ22	Q8rjb2 bacillus ce	654
582	5	35.7	249	2	Q8RS28	Q8rs28 bacillus ce	655
583	5	35.7	250	2	Q9GK32	Q9gke2 sus scrofa	656
584	5	35.7	251	2	Q7PP50	Q7pp50 anopheles g	657
585	5	35.7	252	1	TFIS_MYCGA	Q7naq4 mycoplasma	658
586	5	35.7	252	2	Q68726	Q68726 yersinia pe	659
587	5	35.7	252	2	Q05582	Q05582 mycobacteri	660
588	5	35.7	252	2	Q93G84	Q93g84 salmonella	661
589	5	35.7	252	2	Q72V02	Q72vq2 leptospira	662
590	5	35.7	252	2	Q7U0V7	Q7u0v7 mycobacteri	663
591	5	35.7	252	2	Q7UK23	Q7uk23 rhodopirell	664
592	5	35.7	252	2	Q7UK24	Q7uk24 rhodopirell	665
593	5	35.7	252	2	Q8F9A9	Q8f9a9 leptospira	666
594	5	35.7	253	2	Q9A521	Q9a5z1 caulobacter	667
595	5	35.7	253	2	Q9SN12	Q9sn12 arabidopsis	668
596	5	35.7	253	2	Q88F23	Q88f23 pseudomonas	669
597	5	35.7	253	2	Q8UZE2	Q8uze2 cercopithe	670
598	5	35.7	254	2	Q8XL23	Q8xl23 clostridium	671
599	5	35.7	254	2	Q6MU28	Q6mu28 mycoplasma	672
600	5	35.7	254	2	Q88D33	Q88dg3 pseudomonas	673
601	5	35.7	255	1	VSPA_BOTAT	P04971 bothrops at	674
602	5	35.7	255	2	Q8TSW3	Q8tsw3 methanosarc	675
603	5	35.7	255	2	Q9BZ16	Q9bzi6 homo sapien	676
604	5	35.7	255	2	Q6YQ34	Q6yq34 onion yello	677
605	5	35.7	256	2	Q8IB17	Q8ib17 plasmodium	678
606	5	35.7	257	1	VSP1_TRIMU	Q91507 trimeresuru	679
607	5	35.7	257	1	VSP2_BOTJA	Q13069 bothrops ja	680
608	5	35.7	257	1	VSP2_TRIMU	Q91508 trimeresuru	681
609	5	35.7	257	1	VSP3_AGRAC	Q918x0 agkistrodon	682
610	5	35.7	257	1	VSP3_TRIFL	Q13058 trimeresuru	683
611	5	35.7	257	1	VSP3_TRIMU	Q91509 trimeresuru	684
612	5	35.7	257	1	VSPA_TRIMU	Q91510 trimeresuru	685
613	5	35.7	257	1	VSP5_TRIMU	Q91511 trimeresuru	686
614	5	35.7	257	1	VSP7_TRIMU	Q9cg84 trimeresuru	687
615	5	35.7	257	2	Q9SNV4	Q9env4 antirrhinum	688
Q6dsz5	2	35.7	257	2	Q6DSZ5	Q6dsz5 helicobacte	
Q8jh62	2	35.7	257	2	Q8JH62	Q8jh62 vipera lebe	
Q8qg86	2	35.7	257	2	Q8Qg86	Q8qg86 bothrops in	
Q71qH8	2	35.7	257	2	Q71QH8	Q71qH8 trimeresuru	
Q71qI3	2	35.7	257	2	Q71QI3	Q71qI3 trimeresuru	
Q8pt13	2	35.7	257	2	Q8PT13	Q8pt13 agkistrodon	
Q9jgJ9	2	35.7	257	2	Q9JGU9	Q9jgJ9 agkistrodon	
P38930	1	35.7	258	1	KC2C_YEAST	P38930 saccharomyc	
Q13059	1	35.7	258	1	VSP1_TRIGA	Q13059 trimeresuru	
Q13056	1	35.7	258	1	VSP1_TRIST	Q13056 trimeresuru	
Q15151	1	35.7	258	1	VSP2_AGRAC	Q15151 agkistrodon	
Q47797	1	35.7	258	1	VSP2_AGRH	Q47797 agkistrodon	
Q9df67	1	35.7	258	1	VSP2_TRIGUE	Q9df67 trimeresuru	
Q9ptu8	1	35.7	258	1	VSP3_BOTJA	Q9ptu8 bothrops ja	
Q716Q5	2	35.7	258	2	Q716Q5	Q716q5 mycobacteri	
Q8p4E8	2	35.7	258	2	Q8PAE8	Q8p4E8 xanthomonas	
Q8pg10	2	35.7	258	2	Q8PG10	Q8pg10 xanthomonas	
Q8ghk2	2	35.7	258	2	Q8GHK2	Q8ghk2 crotalus at	
Q98tt5	2	35.7	258	2	Q98TT5	Q98tt5 agkistrodon	
Q71qH6	2	35.7	258	2	Q71QH6	Q71qH6 trimeresuru	
Q71qH7	2	35.7	258	2	Q71QH7	Q71qH7 trimeresuru	
Q71qI1	2	35.7	258	2	Q71QI1	Q71qI1 trimeresuru	
Q71qI2	2	35.7	258	2	Q71QI2	Q71qI2 trimeresuru	
Q7szei	2	35.7	258	2	Q7SZE1	Q7szei gloydius sa	
Q8ay78	2	35.7	258	2	Q8AY78	Q8ay78 trimeresuru	
Q8ay80	2	35.7	258	2	Q8AY80	Q8ay80 trimeresuru	
Q91961	2	35.7	258	2	Q91961	Q91961 agkistrodon	
Q9w781	2	35.7	258	2	Q9W781	Q9w781 agkistrodon	
Q8pvX0	2	35.7	259	2	Q8PVX0	Q8pvX0 methanosarc	
Q04819	2	35.7	259	2	Q04819	Q04819 salmonella	
Q89wX4	2	35.7	259	2	Q89WX4	Q89wX4 bradyrhizob	
Q8uuK2	2	35.7	259	2	Q8UUK2	Q8uuK2 crotalus ad	
VSP1_AGRAC	1	35.7	260	1	VSP1_AGRAC	Q918x2 agkistrodon	
VSP2_AGRHP	1	35.7	260	1	VSP2_AGRHP	P05620 trimeresuru	
VSP2_VIPLE	1	35.7	260	1	VSP2_VIPLE	Q9yg16 agkistrodon	
VSP6_TRIMU	1	35.7	260	1	VSP6_TRIMU	Q9pt40 vipera lebe	
Q662N6	2	35.7	260	2	Q662N6	Q662n6 borrelia ga	
Q8YTAL	2	35.7	260	2	Q8YTAL	Q8ytal anabaena sp	
Q73800	2	35.7	260	2	Q73800	Q73800 agkistrodon	
Q93502	2	35.7	260	2	Q93502	Q93502 agkistrodon	
Q8uvX1	2	35.7	260	2	Q8UVX1	Q8uvX1 agkistrodon	
Q6t6S7	2	35.7	260	2	Q6T6S7	Q6t6S7 bitis gabon	
Q71qH9	2	35.7	260	2	Q71QH9	Q71qH9 trimeresuru	
Q71qI4	2	35.7	260	2	Q71QI4	Q71qI4 trimeresuru	
Q71qJ2	2	35.7	260	2	Q71QJ2	Q71qJ2 trimeresuru	
Q71qJ4	2	35.7	260	2	Q71QJ4	Q71qJ4 trimeresuru	
Q7c229	2	35.7	260	2	Q7T229	Q7c229 bothrops ja	
Q8ay81	2	35.7	260	2	Q8AY81	Q8ay81 trimeresuru	
Q91053	1	35.7	262	1	VSP1_AGRKA	Q91053 agkistrodon	
Q61131	2	35.7	262	2	Q61131	Q61131 plasmodium	
Q7RNH6	2	35.7	262	2	Q7RNH6	Q7rnH6 plasmodium	
Q819Y2	2	35.7	262	2	Q819Y2	Q819y2 arabidopsis	
Q33wt2	2	35.7	262	2	Q33WT2	Q33wt2 sorghum bic	
Q94115	2	35.7	262	2	Q94115	Q94115 sorghum bic	
Q94E14	2	35.7	262	2	Q94E14	Q94e14 sorghum aru	
Q8QHK3	2	35.7	262	2	Q8QHK3	Q8qhk3 crotalus at	
Q8qbd9	2	35.7	263	2	Q98BD9	Q8qbd9 rhizobium l	
Q611h2	2	35.7	263	2	Q611H2	Q611h2 photobacter	
Q7Q513	2	35.7	263	2	Q7Q513	Q7q513 anopheles g	
Q8z386	2	35.7	264	2	Q8Z386	Q8z386 oryza sativ	
Q6Z386	2	35.7	264	2	Q6Z386	Q6z386 oryza sativ	
Q88110	2	35.7	264	2	Q88110	Q88110 pseudomonas	
Q9RIE1	2	35.7	265	2	Q9RIE1	Q9riel yersinia pe	
Q98SR5	2	35.7	265	2	Q98SR5	Q98sr5 anas platyr	
Q25538	1	35.7	266	1	1433_NEOCA	Q25538 neospora ca	
P18338	1	35.7	266	1	MOV8_TMGNV	P18338 tobacco mil	
Q60955	2	35.7	266	2	Q60955	Q60955 toxoplasma	
Q8G053	2	35.7	266	2	Q8G053	Q8g053 brucella su	
P50200	1	35.7	267	1	HDHA_CLOSO	P50200 clostridium	
Q7G4h6	2	35.7	267	2	Q7Q4H6	Q7g4h6 anopheles g	
Q89tw7	2	35.7	268	2	Q89TW7	Q89tw7 bradyrhizob	
Q8pwn6	2	35.7	269	2	Q8PWN6	Q8pwn6 methanosarc	
Q15781	2	35.7	269	2	Q15781	Q15781 babesia bov	

689	5	35.7	269	2	Q8KK72	Q8kk72 proteus vul	762	5	35.7	294	2	Q9R8S4	Q9r8s4 rhizobium s
690	5	35.7	269	2	Q7UBG4	Q7ubg4 shigella fl	763	5	35.7	294	2	Q9R8T0	Q9r8t0 rhizobium s
691	5	35.7	269	2	Q87M90	Q87m90 vibrio para	764	5	35.7	294	2	Q8FDB0	Q8fdb0 escherichia
692	5	35.7	269	2	Q87R24	Q87r24 vibrio para	765	5	35.7	295	2	Q6LX48	Q6lx48 methanococc
693	5	35.7	269	2	Q8VZ73	Q8vz73 canarypox v	766	5	35.7	295	2	Q9P4T9	Q9p4t9 agaricus bi
694	5	35.7	270	1	DAPF_RICCN	Q92141 rickettsia	767	5	35.7	295	2	Q9R8S9	Q9r8s9 rhizobium s
695	5	35.7	270	2	Q6UA71	Q6ua71 flavobacter	768	5	35.7	295	2	Q6NFK5	Q6nfk5 corynebacte
696	5	35.7	270	2	Q7PBT8	Q7pbt8 rickettsia	769	5	35.7	296	2	Q6FRK5	Q6frk5 candida gla
697	5	35.7	270	2	Q8YXL4	Q8yxl4 anabaena sp	770	5	35.7	296	2	Q77092	Q77092 plasmodium
698	5	35.7	270	2	Q8F9S8	Q8f9s8 acinetobact	771	5	35.7	296	2	Q7RI03	Q7ri03 plasmodium
699	5	35.7	271	2	Q83JH8	Q83jh8 shigella fl	772	5	35.7	296	2	Q9VGJ9	Q9vgj9 drosophila
700	5	35.7	272	1	T2AI_RUEGB	Q83jh8 shigella fl	773	5	35.7	296	2	Q9R8S9	Q9r8s9 rhizobium s
701	5	35.7	272	1	Q93WT1	Q93wt1 sorghum ge	774	5	35.7	296	2	Q9Z3I8	Q9z3i8 rhizobium s
702	5	35.7	272	2	Q8CEY2	Q8cey2 mus musculu	775	5	35.7	296	2	Q9Z3J0	Q9z3j0 rhizobium s
703	5	35.7	273	2	Q8KC15	Q8kc15 chlorobium	776	5	35.7	296	2	Q9Z3J3	Q9z3j3 rhizobium s
704	5	35.7	273	2	Q72U20	Q72u20 leptospira	777	5	35.7	296	2	Q8YHR2	Q8yhr2 brucella me
705	5	35.7	273	2	Q81W84	Q81w84 bacillus an	778	5	35.7	297	2	Q94M25	Q94m25 haemophilus
706	5	35.7	274	2	Q6CS09	Q6cs09 kluyveromyc	779	5	35.7	297	2	Q8S4V5	Q8s4v5 arabidopsis
707	5	35.7	274	2	Q6SAR1	Q6sar1 yerzinia pe	780	5	35.7	297	2	Q9R8S6	Q9r8s6 rhizobium s
708	5	35.7	275	2	Q44584	Q44584 caenorhabdi	781	5	35.7	297	2	Q9Z3J2	Q9z3j2 rhizobium s
709	5	35.7	275	2	Q8MNJ5	Q8mnj5 dictyosteli	782	5	35.7	297	2	Q6F9E6	Q6f9e6 acinetobact
710	5	35.7	276	2	Q87WJ4	Q87wj4 sulfobus	783	5	35.7	297	2	Q83BY6	Q83by6 coxiella bu
711	5	35.7	276	2	Q8CHD9	Q8chd9 yarrowia li	784	5	35.7	297	2	Q8R2D3	Q8r2d3 mus musculu
712	5	35.7	276	2	Q9RFT6	Q9rft6 mesorhizobi	785	5	35.7	298	1	VPO_BPHP1	Vp1719 bacterioph
713	5	35.7	276	2	Q9RFT7	Q9rft7 mesorhizobi	786	5	35.7	298	2	Q8UK76	Q8uk76 agrobacteri
714	5	35.7	276	2	Q9RFT8	Q9rft8 mesorhizobi	787	5	35.7	299	2	Q82EP3	Q82ep3 streptomyce
715	5	35.7	276	2	Q8PA04	Q8paq4 xanthomonas	788	5	35.7	300	2	Q8R7E5	Q8r7e5 thermocoe
716	5	35.7	276	2	Q8PMG1	Q8pmg1 xanthomonas	789	5	35.7	300	2	Q6K1B4	Q6k1b4 mycoplasma
717	5	35.7	276	2	Q87DC9	Q87dc9 xyella fas	790	5	35.7	300	2	Q883B5	Q883b5 pseudomonas
718	5	35.7	276	2	Q93Y99	Q93y99 clostridium	791	5	35.7	300	2	Q89ME0	Q89me0 bradyrhizob
719	5	35.7	276	2	Q8EUB1	Q8eub1 mycoplasma	792	5	35.7	301	1	PAL_POLAN	Q9u6w0 polistes an
720	5	35.7	276	2	Q9HXC9	Q9hxc9 pseudomonas	793	5	35.7	302	2	Q6FW12	Q6fw12 candida gla
721	5	35.7	276	2	Q9PD34	Q9pd34 xyella fas	794	5	35.7	302	2	Q7UFJ5	Q7ufj5 rhodopirell
722	5	35.7	278	2	Q7RV73	Q7rv73 neurospora	795	5	35.7	303	2	Q8LPM8	Q8lpm8 arabidopsis
723	5	35.7	278	2	Q6F8B1	Q6f8b1 acinetobact	796	5	35.7	303	2	Q30377	Q30377 aeromonas s
724	5	35.7	280	2	Q6PAB4	Q6pab4 xenopus lae	797	5	35.7	304	2	Q6BXX8	Q6bxx8 debaryomyce
725	5	35.7	281	2	Q8BTB0	Q8btb0 mus musculu	798	5	35.7	304	2	Q7P4N4	Q7p4n4 fusobacteri
726	5	35.7	282	2	Q8CAG7	Q8cag7 mus musculu	799	5	35.7	305	2	Q812K2	Q812k2 plasmodium
727	5	35.7	283	2	Q9F7T2	Q9f7t2 corynebacte	800	5	35.7	305	2	Q84QG4	Q84qg4 arabidopsis
728	5	35.7	283	2	Q9DM81	Q9dm81 rat cytomeg	801	5	35.7	305	2	Q9C719	Q9c719 arabidopsis
729	5	35.7	284	1	PUR7_CHRVO	Q9d1p8 chromobacte	802	5	35.7	305	2	Q764A2	Q764a2 helicobacte
730	5	35.7	284	2	Q9R8S7	Q9r8s7 rhizobium s	803	5	35.7	306	2	Q86HZ8	Q86hz8 dictyosteli
731	5	35.7	284	2	Q9EWP8	Q9ewp8 streptomyce	804	5	35.7	307	1	TF2B_METKA	Q8tx21 methanopyru
732	5	35.7	285	2	Q8QFQ2	Q8qfq2 xenopus lae	805	5	35.7	307	2	Q6LIG4	Q6lig4 photobacter
733	5	35.7	286	2	Q8S4V6	Q8s4v6 arabidopsis	806	5	35.7	308	2	Q8R2C7	Q8r2c7 mus musculu
734	5	35.7	287	1	PUR7_NEIMA	Q91v73 neisseria m	807	5	35.7	308	2	Q91TS5	Q91ts5 tupaiid her
735	5	35.7	287	1	PUR7_NEIME	Q9k063 neisseria m	808	5	35.7	309	2	Q8S484	Q8s484 zea mays (m
736	5	35.7	287	2	Q72E00	Q72eu0 desulfovibr	809	5	35.7	309	2	Q68S26	Q68s26 hepatitis c
737	5	35.7	287	2	Q881W5	Q881w5 pseudomonas	810	5	35.7	310	2	Q9SHR6	Q9shr6 arabidopsis
738	5	35.7	288	2	Q25668	Q25668 helicobacte	811	5	35.7	310	2	Q7UNSG	Q7uns6 rhodopirell
739	5	35.7	288	2	Q97S28	Q97s28 streptococc	812	5	35.7	312	1	MCAL_HUMAN	Q12904 homo sapien
740	5	35.7	288	2	Q9ZM23	Q9zm23 helicobacte	813	5	35.7	312	2	Q6G1P0	Q6g1p0 bartonella
741	5	35.7	289	1	EX53_AQUAE	Q87550 aquifex aeo	814	5	35.7	313	2	Q65ZK4	Q65zk4 caenorhabdi
742	5	35.7	289	1	THTR_CHICK	P25324 gallus gall	815	5	35.7	313	2	Q9ZH27	Q9zh27 thioacallu
743	5	35.7	289	2	Q97WF2	Q97wf2 sulfolobus	816	5	35.7	313	2	Q97ND7	Q97nd7 streptococc
744	5	35.7	289	2	Q6GN00	Q6gn00 xenopus lae	817	5	35.7	313	2	Q8DN48	Q8dn48 streptococc
745	5	35.7	290	2	Q8PSW4	Q8psw4 methanosaar	818	5	35.7	314	2	Q6WAU1	Q6wau1 mentha pipe
746	5	35.7	290	2	Q8YTU4	Q8ytu4 anabaena sp	819	5	35.7	315	2	Q8TMV8	Q8tmv8 methanosaar
747	5	35.7	290	2	Q8CRP9	Q8crr9 staphylococ	820	5	35.7	315	2	Q7R9Y8	Q7r9y8 plasmodium
748	5	35.7	290	2	Q8UIK2	Q8uik2 agrobacteri	821	5	35.7	315	2	Q75GR3	Q75gr3 oryza sativ
749	5	35.7	291	2	Q9HKW7	Q9hk7 thermoplasm	822	5	35.7	316	1	LORI_HUMAN	P23490 homo sapien
750	5	35.7	291	2	Q72LRS	Q72lrs leptospira	823	5	35.7	316	2	Q6PHY3	Q6phy3 homo sapien
751	5	35.7	291	2	Q89L69	Q89l69 bradyrhizob	824	5	35.7	316	2	Q6Q249	Q6q249 polistes do
752	5	35.7	291	2	Q8EY71	Q8ey71 leptospira	825	5	35.7	316	2	Q6Q250	Q6q250 polistes do
753	5	35.7	292	2	Q8KIQ2	Q8kiq2 escherichia	826	5	35.7	316	2	Q6Q251	Q6q251 polistes do
754	5	35.7	292	2	Q85FX0	Q85fx0 bacillus li	827	5	35.7	316	2	Q86FA4	Q86fa4 drosophila
755	5	35.7	292	2	Q8XAC6	Q8xac6 escherichia	828	5	35.7	316	2	Q89ER1	Q89er1 bradyrhizob
756	5	35.7	293	1	PUR7_BORBR	Q7wmi1 bordetella	829	5	35.7	317	2	Q6KZQ1	Q6kzq1 picrophilus
757	5	35.7	293	1	PUR7_BORPA	Q7wb15 bordetella	830	5	35.7	317	2	Q41681	Q41681 vigna radia
758	5	35.7	293	1	PUR7_BORPE	Q7vy42 bordetella	831	5	35.7	317	2	Q7FY62	Q7fy62 phascolus a
759	5	35.7	293	2	Q9R8T1	Q9r8t1 rhizobium s	832	5	35.7	317	2	Q89V25	Q89v25 bradyrhizob
760	5	35.7	294	1	ATHB_MOUSE	P50992 mus musculu	833	5	35.7	317	2	Q9KM71	Q9km71 vibrio chol
761	5	35.7	294	1	GGFP_BOVIN	P56966 b geranylyge	834	5	35.7	317	2	Q8UBZ1	Q8ubz1 agrobacteri

835	5	35.7	318	2	Q8THP8	Q8thp8 methanosarc	908	5	35.7	337	2	Q6GIL9	Q6gil9 staphylococ
836	5	35.7	318	2	Q9HRU5	Q9hrus halobacteri	909	5	35.7	337	2	Q6HLI8	Q6hli8 bacillus th
837	5	35.7	318	2	Q7R5B5	Q7r5b5 giardia lam	910	5	35.7	338	2	Q8TUJ8	Q8tuj8 methanosarc
838	5	35.7	318	2	Q82ND5	Q82nd5 streptomyce	911	5	35.7	338	2	Q6O354	Q6o354 homo sapien
839	5	35.7	319	2	Q82QC8	Q82qc8 salmonella	912	5	35.7	339	2	Q92VE5	Q92ve5 rhizobium m
840	5	35.7	319	2	Q6N0V4	Q6n0v4 rhodopseudo	913	5	35.7	339	2	Q6GLG8	Q6glg8 xenopus tro
841	5	35.7	319	2	Q88GL5	Q88gl5 pseudomonas	914	5	35.7	340	2	Q7QPD1	Q7qpd1 anopheles g
842	5	35.7	319	2	Q8BNK2	Q8bnk2 oceanobacil	915	5	35.7	340	2	Q33352	Q33352 chorthippus
843	5	35.7	320	2	Q7QWQ8	Q7qwq8 giardia lam	916	5	35.7	340	2	Q33355	Q33355 chorthippus
844	5	35.7	320	2	Q9CAA2	Q9caa2 arabidopsis	917	5	35.7	340	2	Q8ZK50	Q8zk50 salmonella
845	5	35.7	320	2	Q66JE7	Q66je7 xenopus tro	918	5	35.7	340	2	Q6FFV7	Q6ffv7 acinetobact
846	5	35.7	321	2	Q7D3J2	Q7d3j2 agrobacteri	919	5	35.7	341	1	PSA_XENLA	PSa_xenla xenopus lae
847	5	35.7	322	2	Q97V31	Q97v31 sulfolobus	920	5	35.7	341	2	Q725R3	Q725r3 desulfovibr
848	5	35.7	322	2	Q6H890	Q6h890 oryza sativ	921	5	35.7	342	1	RALB_TODPA	RAlb_todpa todarodes p
849	5	35.7	322	2	Q8H1M6	Q8h1m6 arabidopsis	922	5	35.7	342	2	Q6IGS7	Q6igs7 drosophila
850	5	35.7	322	2	Q9LEZ7	Q9lez7 arabidopsis	923	5	35.7	342	2	Q898X0	Q898x0 clostridium
851	5	35.7	322	2	Q92Q36	Q92q36 arabidopsis	924	5	35.7	344	1	VPQ_BPP2	VPq_bpp2 bacterioph
852	5	35.7	322	2	Q6LPV9	Q6lpv9 photobacter	925	5	35.7	344	2	Q28906	Q28906 archaeoglob
853	5	35.7	322	2	Q6DIB3	Q6dib3 mus musculu	926	5	35.7	344	2	Q7Y4E8	Q7y4e8 bacterioph
854	5	35.7	322	2	Q6R256	Q6r256 carassius a	927	5	35.7	344	2	Q858W8	Q858w8 bacterioph
855	5	35.7	323	2	Q8KDU7	Q8kdj7 chlorobium	928	5	35.7	344	2	Q9X5D5	Q9x5d5 zymomonas m
856	5	35.7	323	2	Q99H22	Q99h22 helicoverpa	929	5	35.7	344	2	Q8UCR7	Q8ucr7 agrobacteri
857	5	35.7	323	2	Q77K94	Q77k94 helicoverpa	930	5	35.7	345	2	Q9VQM9	Q9vqm9 drosophila
858	5	35.7	323	2	Q77LY8	Q77ly8 helicoverpa	931	5	35.7	345	2	Q87J59	Q87j59 vibrio para
859	5	35.7	324	2	Q6IAC9	Q6iac9 homo sapien	932	5	35.7	346	2	Q6M0N8	Q6m0n8 methanococ
860	5	35.7	324	2	Q85X47	Q85x47 drosophila	933	5	35.7	346	2	Q50068	Q50068 arabidopsis
861	5	35.7	324	2	Q95OM3	Q95om3 staphylococ	934	5	35.7	346	2	Q8C4C2	Q8c4c2 mus musculu
862	5	35.7	324	2	Q9QX98	Q9qx98 mus musculu	935	5	35.7	347	2	Q703W7	Q703w7 thermoprote
863	5	35.7	324	2	Q9QYF5	Q9qyf5 mus musculu	936	5	35.7	347	2	Q8T651	Q8t651 giardia lam
864	5	35.7	325	2	Q6Z057	Q6z057 oryza sativ	937	5	35.7	347	2	Q891X4	Q891x4 clostridium
865	5	35.7	326	2	Q970C6	Q970c6 sulfolobus	938	5	35.7	349	2	Q8NS43	Q8ns43 corynebacte
866	5	35.7	327	2	Q8PSH1	Q8psh1 methanosarc	939	5	35.7	350	1	YB04_AQUAB	YB04_aquab aquifex aeo
867	5	35.7	327	2	Q9V4C4	Q9v4c4 drosophila	940	5	35.7	351	2	Q8UYW9	Q8uyw9 sri lankan
868	5	35.7	327	2	Q9VAL1	Q9val1 drosophila	941	5	35.7	351	2	Q6PMS0	Q6pms0 tomato yell
869	5	35.7	327	2	Q94CX3	Q94cx3 oryza sativ	942	5	35.7	351	2	Q709N7	Q709n7 indian case
870	5	35.7	328	1	GALE_CORDI	GAle_cordi corynebacte	943	5	35.7	351	2	Q7T6E9	Q7t6e9 sri lankan
871	5	35.7	328	2	Q86X73	Q86x73 homo sapien	944	5	35.7	352	2	Q8THN6	Q8thn6 methanosarc
872	5	35.7	328	2	Q8IIN3	Q8iin3 trypanosoma	945	5	35.7	352	2	Q8RG15	Q8rg15 fusobacteri
873	5	35.7	328	2	Q8FPG5	Q8fpg5 corynebacte	946	5	35.7	352	2	Q8XL25	Q8xl25 clostridium
874	5	35.7	329	2	Q27459	Q27459 methanobact	947	5	35.7	353	2	Q7PR97	Q7pr97 anopheles g
875	5	35.7	329	2	Q8S4V7	Q8s4v7 arabidopsis	948	5	35.7	353	2	Q7QED4	Q7qed4 anopheles g
876	5	35.7	329	2	Q9L7P3	Q9l7p3 rhodococcus	949	5	35.7	353	2	Q9FR28	Q9fr28 petroselinu
877	5	35.7	330	2	Q8TMU0	Q8tmu0 methanosarc	950	5	35.7	353	2	Q6L673	Q6l673 alysia cal
878	5	35.7	330	2	Q9VQNO	Q9vqno drosophila	951	5	35.7	354	2	Q6RCU6	Q6rcu6 pepper yell
879	5	35.7	331	1	TR38_MOUSE	TR38_mouse mus musculu	952	5	35.7	354	2	Q9IN42	Q9in42 south afric
880	5	35.7	331	2	P73723	P73723 synecocyst	953	5	35.7	356	2	Q96B14	Q96b14 homo sapien
881	5	35.7	331	2	Q67ES4	Q67es4 rattus norv	954	5	35.7	356	2	Q655L6	Q655l6 oryza sativ
882	5	35.7	332	2	Q43977	Q43977 babesia bov	955	5	35.7	356	2	Q668H0	Q668h0 yersinia ps
883	5	35.7	333	2	Q8TKV5	Q8tkv5 escherichia	956	5	35.7	356	2	Q8ZCE3	Q8zce3 yersinia pe
884	5	35.7	333	2	Q8YYA6	Q8yya6 anabaena sp	957	5	35.7	357	1	CYSA_BACCL	CYsa_baccl bacillus ce
885	5	35.7	334	2	Q6M0J6	Q6m0j6 methanococc	958	5	35.7	357	2	Q9DJP9	Q9djp9 citrus tris
886	5	35.7	334	2	Q8HWA3	Q8hwa3 mus musculu	959	5	35.7	357	2	Q6GP68	Q6gp68 xenopus lae
887	5	35.7	334	2	Q9D205	Q9d205 mus musculu	960	5	35.7	358	2	Q6GP68	Q6gp68 xenopus lae
888	5	35.7	335	1	ZDH1_STAAM	ZDH1_staam staphylococ	961	5	35.7	359	1	VAL1_TYLCU	VAL1_tylicu tomato yell
889	5	35.7	335	1	ZDH1_STAAM	ZDH1_staam staphylococ	962	5	35.7	359	1	VAL1_TYLCU	VAL1_tylicu tomato yell
890	5	35.7	335	2	Q9F5Q8	Q9f5q8 vibrio chol	963	5	35.7	359	2	Q8JNF1	Q8jnf1 tomato leaf
891	5	35.7	335	2	Q91HQ5	Q91hq5 hepatitis c	964	5	35.7	359	2	Q8JNF7	Q8jnf7 tomato yell
892	5	35.7	336	2	Q7S6P4	Q7s6p4 neurospora	965	5	35.7	359	2	Q8JNG3	Q8jng3 tomato leaf
893	5	35.7	336	2	Q8ZTS2	Q8zts2 rhizobium m	966	5	35.7	359	2	Q8JVE8	Q8jve8 tomato curl
894	5	35.7	337	2	Q8PX57	Q8px57 methanosarc	967	5	35.7	359	2	Q8UYX3	Q8uyx3 south afric
895	5	35.7	337	2	Q77324	Q77324 plasmodium	968	5	35.7	359	2	Q8V380	Q8v380 east africa
896	5	35.7	337	2	Q6Q252	Q6q252 polistes do	969	5	35.7	359	2	Q91M86	Q91m86 ageratum ye
897	5	35.7	337	2	Q63E13	Q63e13 bacillus ce	970	5	35.7	359	2	Q91M88	Q91m88 tobacco lea
898	5	35.7	337	2	Q61W70	Q61w70 photobacter	971	5	35.7	359	2	Q66UV7	Q66uv7 tomato yell
899	5	35.7	337	2	Q73BB1	Q73bb1 bacillus ce	972	5	35.7	359	2	Q67620	Q67620 tomato yell
900	5	35.7	337	2	Q7A1F6	Q7a1f6 staphylococ	973	5	35.7	359	2	Q6RCV2	Q6rcv2 tomato yell
901	5	35.7	337	2	Q7A2U8	Q7a2u8 staphylococ	974	5	35.7	359	2	Q764D4	Q764d4 tomato yell
902	5	35.7	337	2	Q7A6Q3	Q7a6q3 staphylococ	975	5	35.7	359	2	Q764E0	Q764e0 tomato yell
903	5	35.7	337	2	Q81G49	Q81g49 bacillus ce	976	5	35.7	359	2	Q764E6	Q764e6 tomato yell
904	5	35.7	337	2	Q81TA8	Q81ta8 bacillus an	977	5	35.7	359	2	Q764F2	Q764f2 tomato yell
905	5	35.7	337	2	Q8CPY6	Q8cpy6 staphylococ	978	5	35.7	359	2	Q764F8	Q764f8 tomato yell
906	5	35.7	337	2	Q8Z5C6	Q8z5c6 staphylococ	979	5	35.7	359	2	Q76C58	Q76c58 tomato yell
907	5	35.7	337	2	Q6GB59	Q6gb59 staphylococ	980	5	35.7	359	2	Q77W92	Q77w92 tomato yell

981 5 35.7 359 2 Q7TAT2 Q7tat2 south afric
 982 5 35.7 359 2 Q88942 Q88942 tomato yell
 983 5 35.7 359 2 Q88942 Q88942 tomato yell
 984 5 35.7 359 2 Q8B2Y2 Q8b2y2 tomato yell
 985 5 35.7 359 2 Q8B6S5 Q8b6s5 tomato yell
 986 5 35.7 359 2 Q8B8M8 Q8b8m8 east africa
 987 5 35.7 359 2 Q9YL27 Q9yl27 tomato yell
 988 5 35.7 359 2 Q9YUX7 Q9yux7 tomato yell
 989 5 35.7 359 2 Q9YZV2 Q9yzv2 tomato yell
 990 5 35.7 359 2 Q9YZV4 Q9yzv4 tomato yell
 991 5 35.7 360 1 QXSP_HEMSP P43156 hemerocalli
 992 5 35.7 360 2 Q84YH8 Q84yh8 nicotiana t
 993 5 35.7 360 2 Q9LRI2 Q9lri2 nicotiana t
 994 5 35.7 360 2 Q65317 Q65317 ageratum ye
 995 5 35.7 360 2 Q70P37 Q70p37 ageratum ye
 996 5 35.7 360 2 Q75Q13 Q75q13 tomato leaf
 997 5 35.7 360 2 Q80S70 Q80s70 tomato leaf
 998 5 35.7 360 2 Q9DX10 Q9dx10 ageratum ye
 999 5 35.7 360 2 Q9QCX3 Q9qcx3 tomato leaf
 1000 5 35.7 361 2 Q8QVH0 Q8qvh0 ageratum en

ALIGNMENTS

RESULT 1
 CYC1_HUMAN
 ID CYC1_HUMAN STANDARD; PRT; 377 AA.
 AC Q14094;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Cyclin I.
 GN Name=CCNI;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Forebrain cortex;
 RX MEDLINE=96086776; PubMed=7493655; DOI=10.1006/excr.1995.1406;
 RA Nakamura T., Sanokawa R., Sasaki Y.F., Ayusawa D., Oishi M., Mori N.;
 RT "Cyclin I: a new cyclin encoded by a gene isolated from human brain.";
 RL Exp. Cell Res. 221:534-542(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Chen J.H., Luo W.Q., Zhou Y., Zhou H.J., Huang X.W., Yuan J.G.,
 RA Qiang B.Q.;
 RT "Isolating a new cDNA coding for human cyclin protein.";
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A., AND VARIANT ILE-207.
 RA Kieder M.J., Livingston R.J., Daniels M.R., Montoya M.A., Chung M.-W.,
 RA Miyamoto K.E., Nguyen D.A., Poel C.L., Robertson P.D.,
 RA Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;
 RT "NIHES-SNP, environmental genome project, NIHES ES15478, Department
 of Genome Sciences, Seattle, WA (URL: <http://legp.gs.washington.edu>).";
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney, and Muscle;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshitsuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP SEQUENCE OF 1-178 FROM N.A.
 RC TISSUE=testis;
 RX MEDLINE=98381026; PubMed=9705831; DOI=10.1006/bbrc.1998.9052;
 RA Zhu X., Naz R.K.;
 RT "Expression of a novel isoform of cyclin I in human testis.";
 RL Biochem. Biophys. Res. Commun. 249:56-60(1998).
 CC -!- TISSUE SPECIFICITY: Highest levels in adult heart, brain and
 skeletal muscle. Lower levels in adult placenta, lung, kidney and
 pancreas. Also high levels in fetal brain and lower levels in
 fetal lung, liver and kidney. Also abundant in testis and thyroid.
 CC -!- DEVELOPMENTAL STAGE: Expression is independent of the cell cycle
 in lung fibroblasts.
 CC -!- SIMILARITY: Belongs to the cyclin family.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (see <http://www.isb-sib.ch/announce/>)
 or send an email to license@isb-sib.ch.
 CC
 CC EMBL; D50310; BAA08849.1; -;
 CC EMBL; AY207372; AA013492.1; -;
 CC EMBL; BC000420; AAH00420.1; -;
 CC EMBL; BC004975; AAH04975.1; -;
 CC EMBL; AF135162; AAF43786.1; -;
 CC PIR; JE0264; JE0264.
 CC Genew; HGNC:1595; CCNI.
 CC H-InvDB; HIX0004313; -;
 CC GO; GO:0007283; P:spermatogenesis; NAS.
 CC InterPro; IPR006670; Cyclin.
 CC InterPro; IPR011028; Cyclin like.
 CC InterPro; IPR006671; Cyclin_N.
 CC Pfam; PF00134; Cyclin_N; 1.
 CC SMART; SM00385; CYCLIN; 1.
 CC PROSITE; PS00292; CYCLINS; FALSE_NEG.
 KW Cyclin; Polymorphism.
 FT VARIANT 207 207 V -> I (in dbSNP:4252903).
 FT CONFLICT 9 9 N -> D (in Ref. 5).
 FT CONFLICT 58 58 Q -> R (in Ref. 5).
 FT CONFLICT 75 75 R -> G (in Ref. 5).
 SQ SEQUENCE 377 AA; 42557 MW; 2DE84EFA/4698F6C CRC64;
 Query Match 100.0%; Score 14; DB 1; Length 377;
 Best Local Similarity 100.0%; Pred. No. 5.4e-07;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 EDNVSENVGVCVT 14
 Db 343 EDNVSENVGVCVT 356
 RESULT 2
 Q6FHH0 PRELIMINARY; PRT; 377 AA.
 ID Q6FHH0
 AC Q6FHH0; (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE CCNI protein (Fragment).

```

GN Name=CCNI;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Halleck A., Ebert L., Moundinya M., Schick M., Eisenstein S.,
RA Neubert P., Kstrang K., Schatten R., Shen B., Henze S., Mar W.,
RA Korn B., Zuo D., Hu Y., Labaer J.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the cyclin family.
DR EMBL; CR541783; CAG46382.1; -.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR011028; Cyclin_like.
DR Pfam; PF00134; Cyclin_N.
DR SMART; SM00385; CYCLIN_N.1.
DR Cyclin.
KW NON_TER. 377 377
SQ SEQUENCE 377 AA; 42486 MW; D950A5CCF0D0F514 CRC64;

Query Match 100.0%; Score 14; DB 2; Length 377;
Best Local Similarity 100.0%; Pred. No. 5.4e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EDNVSENVSVCGT 14
Db 343 EDNVSENVSVCGT 356
|||||
|||||

RESULT 3
CYCI_MOUSE
ID CYCI_MOUSE STANDARD; PRT; 377 AA.
AC Q922V9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cyclin I.
GN Name=Ccni;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99172101; PubMed=10072591;
RA Jensen M.R., Audolfsson T., Keck C.L., Zimonjic D.B.,
RA Thorgeirsson S.S.;
RT "Assignment of the cyclin I gene (Ccni) to mouse chromosome 5E3.3-F1.
RL Cytogenet. Cell Genet. 83:242-243(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20509992; PubMed=11054536; DOI=10.1016/S0378-1119(00)00361-9;
RA Jensen M.R., Audolfsson T., Factor V.M., Thorgeirsson S.S.;
RT "In vivo expression and genomic organization of the mouse cyclin I
RL gene (Ccni).";
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RL prepare full-length cDNA libraries for rapid discovery of new genes.";
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanaki M.,

```

```

DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR011028; Cyclin_like.
DR Pfam; PF00134; Cyclin_N.
DR SMART; SM00385; CYCLIN_N.1.
DR PROSITE; PS00292; CYCLINS; FALSE_NEG.
KW Cyclin.
SQ SEQUENCE 377 AA; 42261 MW; 4151141C6D9AB677 CRC64;

Query Match 64.3%; Score 9; DB 1; Length 377;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ENVGSVCGT 14
Db 348 ENVGSVCGT 356
|||||
|||||

RESULT 4
Q8C7E2
ID Q8C7E2 PRELIMINARY; PRT; 377 AA.
AC Q8C7E2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus adult pancreas islet cells cDNA, RIKEN full-length
DE enriched library, clone: C820001G04 product: cyclin I, full insert
DE sequence.
GN Name=Ccni;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Pancreas;
RA The FANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of
RL 60,770 full-length cDNAs.";
RN [4]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RL prepare full-length cDNA libraries for rapid discovery of new genes.";
RN [5]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanaki M.,

```

```

RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki K., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akai H., Tanaka T., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the cyclin family.
DR EMBL; AK050465; BAC34271.1; -.
DR MGD; MGI:1341077; Ccni.
DR GO; GO:0000074; P:regulation of cell cycle; TAS.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR011028; Cyclin like.
DR InterPro; IPR006671; Cyclin_N.
DR Pfam; PF00134; Cyclin_N; 1.
DR SMART; SM00385; CYCLIN; 1.
KW Cyclin.
SQ SEQUENCE 377 AA; 42206 MW; A1B803EBE135B0E8 CRC64;

Query Match 64.3%; Score 9; DB 2; Length 377;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ENVGSVCGT 14
DB 348 ENVGSVCGT 356

RESULT 5
Q99LF2 PRELIMINARY; PRT; 377 AA.
AC Q99LF2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cyclin I.
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Mammary tumor;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

```

```

RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Mammary tumor;
RA Strausberg R.;
EL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the cyclin family.
DR EMBL; BC003290; AA03290.1; -.
DR MGD; MGI:1341077; Ccni.
DR GO; GO:0000074; P:regulation of cell cycle; TAS.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR011028; Cyclin like.
DR InterPro; IPR006671; Cyclin_N.
DR Pfam; PF00134; Cyclin_N; 1.
DR SMART; SM00385; CYCLIN; 1.
KW Cyclin.
SQ SEQUENCE 377 AA; 42227 MW; FDA2D896A5366A9F CRC64;

Query Match 64.3%; Score 9; DB 2; Length 377;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ENVGSVCGT 14
DB 348 ENVGSVCGT 356

RESULT 6
Q6BXL7 PRELIMINARY; PRT; 600 AA.
ID Q6BXL7;
AC Q6BXL7;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Debaryomyces hansenii chromosome B of strain CBS767 of Debaryomyces
DE hansenii.
GN ORFNames=DEHA0801958g;
OS Debaryomyces hansenii CBS767.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Debaryomyces.
OX NCBI_TaxID=284592;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CBS767;
RG Genolevures;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neugeglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Boisrame A., Boyer J., Cattolico L., Confanioli F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.M., Nikolaki M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
RA Swenne D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron R., Scarpetti C., Gaillardin C., Weissenbach J.,
RA Wincker P., Souciet J.L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44(2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CBS767;
RA Genoscope;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR382134; CAG85038.1; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR InterPro; IPR001357; BRCT.

```

DR InterPro; IPR010613; Pescadillo.N.
DR Pfam; PF00533; BRCT; 1.
DR Pfam; PF06732; Pescadillo.N; 1.
DR SMART; SMO0292; BRCT; 1.
DR PROSITE; PS01072; BRCT; 1.
SQ SEQUENCE 600 AA; 68399 MW; 028055D2B9277B42 CRC64;
Query Match 57.1%; Score 8; DB 2; Length 600;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EDNVSENV 8
Db 316 EDNVSENV 323
RESULT 7
ID Q8SVJ3 PRELIMINARY; PRT; 310 AA.
AC Q8SVJ3;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE R56714p.
GN ORFNames=CG14855;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celisner S.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
DR EMBL; AY071512; AAL49134.1; -;
DR FlyBase; FBgn0038260; CG14855.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005215; P:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR007114; MFS.
DR InterPro; IPR005828; Sub transporter.
DR Pfam; PF00083; Sugar_tr_1.
DR PROSITE; PS00850; MFS; 1.
KW Transmembrane.
SQ SEQUENCE 310 AA; 35861 MW; 0A6475F0154AF711 CRC64;
Query Match 50.0%; Score 7; DB 2; Length 310;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 8 VGSVCGT 14
Db 131 VGSVCGT 137
RESULT 8
ID Q8GP73 PRELIMINARY; PRT; 423 AA.
AC Q8GP73;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Eps10G.
GN Name=eps10G;
OS Streptococcus thermophilus.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;

OC Streptococcus.
OX NCBI_TaxID=1308;
RN [1]
RP SEQUENCE FROM N.A.
RA Rallu F., Ehrlich D.S., Renault P.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF454500; AAN63767.1; -;
SQ SEQUENCE 423 AA; 49055 MW; BBC9BF6895D6DACC CRC64;
Query Match 50.0%; Score 7; DB 2; Length 423;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 VSENVGS 10
Db 366 VSENVGS 372
RESULT 9
ID Q9AH92 PRELIMINARY; PRT; 423 AA.
AC Q9AH92;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE WciU.
GN Name=wciU;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21116929; PubMed=11179285;
RX DOI=10.1128/IAI.69.3.1244-1255.2001;
RA Jiang S.M., Wang L., Reeves P.R.;
RT "Molecular characterization of Streptococcus pneumoniae type 4, 6B, 8,
RT and 18c capsular polysaccharide gene clusters.";
RL Infect. Immun. 69:1244-1255(2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Jiang S.-M., Wang L., Reeves P.R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF316642; AAK20713.1; -;
DR GO; GO:0009058; P:biosynthesis; IEA.
SQ SEQUENCE 423 AA; 532A56D8661ED1C4 CRC64;
Query Match 50.0%; Score 7; DB 2; Length 423;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 VSENVGS 10
Db 366 VSENVGS 372
RESULT 10
ID YP33 YEAST STANDARD; PRT; 446 AA.
AC P19541;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Putative transcriptional regulatory protein YPL133C.
GN OrderedLocusNames=YPL133C; ORFNames=LPI12C;
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RX MEDLINE=97313271; PubMed=9169875;

RA Bussey H., Storms R.K., Ahmed A., Albermann K., Allen E., Ansonge W.,
RA Araujo R., Aparicio A., Barrell B.G., Badcock K., Benes V.,
RA Botstein D., Bowman S., Bruckner M., Carpenter J., Cherry J.M.,
RA Chung E., Churcher C.M., Coster F., Davis K., Davis R.W.,
RA Dietrich F.S., Delius H., Dipaolo T., Dubois E., Duesterhoeft A.,
RA Duncan M., Floeth M., Fortin N., Friese J.D., Fritz C., Goffeau A.,
RA Hall J., Hebling U., Heumann K., Hilbert H., Hillier L.W.,
RA Hunkle-Smith S., Hyman R., Johnston M., Kalman S., Kleine K.,
RA Komp C., Kurdi O., Lashkari D., Lew H., Lin A., Lin D., Louis E.J.,
RA Marathe R., Messing F., Mewes H.-W., Mirtipati S., Moestl D.,
RA Mueller-Auer S., Namath A., Nentwich U., Oefner P., Pearson D.,
RA Petel F.X., Pohl T.M., Purnelle D., Schafer M., Scharfe M.,
RA Scherens B., Schramm S., Schroeder M., Sdicu A.M., Tettelin H.,
RA Urrestarazu L.A., Ushinsky S., Vierdeels F., Vissers S., Voss H.,
RA Walsh S.V., Wambutt R., Wang Y., Wedler E., Wedler H., Winnett E.,
RA Zhong W.W., Zollner A., Vo D.H., Hani J.,
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome XVI.",
RL Nature 387:103-105 (1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288c;
RA Marischky G., Rolfs A., Richardson A., Kane M., Baqui M., Taycher E.,
RA Hu Y., Vamberg E., Weger J., Kramer J., Moreira D., Kelley F.,
RA Zuo D., Raphael J., Hogle C., Jepson D., Williamson J., Camargo A.,
RA Gonzaga L., Vasconcelos A.T., Simpson A., Kolodner R., Harlow E.,
RA Labaer J.;
RT "Creation of the YFLEX clone resource: cloning of Saccharomyces
RT cerevisiae ORFs in the Gateway recombinational cloning system.",
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 1-95 FROM N.A.
RX MEDLINE=90360986; PubMed=2167832;
RA Tzagoloff A., Capitano N., Nobrega M.P., Gatti D.;
RT "Cytochrome oxidase assembly in yeast requires the product of COX11, a
RT homolog of the P. denitrificans protein encoded by ORF3.",
RL EMBL J. 9:2759-2764 (1990).
RN [4]
RP PRESENCE OF A ZN(2)-CYS(6) FUNGAL-TYPE BINUCLEAR CLUSTER.
RX MEDLINE=93284106; PubMed=1304897;
RA Bork P., Ouzounis C., Sander C., Scharf M., Schneider R.,
RA Sonhammer E.;
RT "Comprehensive sequence analysis of the 182 predicted open reading
RT frames of yeast chromosome III.",
RL Protein Sci. 1:1677-1690 (1992).
CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -!- SIMILARITY: Contains 1 Zn(2)-Cys(6) fungal-type binuclear cluster
CC domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U43703; AAB68226.1; -.
DR EMBL; AY693168; AAT93187.1; -.
DR EMBL; X55731; CAA39262.1; -.
DR PIR; S69051; S69051.
DR HSSP; P12351; 1PVC.
DR INACT; P19541; -.
DR GeneOnline; I44115; -.
DR SGD; S00006054; RDS2.
DR GO; GO:0005737; C:cytoplasm; IDA.
DR GO; GO:0005634; C:nucleus; IDA.
DR GO; GO:0003700; F:transcription factor activity; IMP.
DR GO; GO:0009410; P:response to xenobiotic stimulus; IMP.
DR InterPro; IPR001138; Fungi_Tscrp_N.
DR InterPro; IPR000014; PAS.
DR Pfam; PF00172; Zn_clus; 1.
DR SMART; SM00066; GAL4; 1.
DR SMART; SM00091; PAS; 1.

DR PROSITE; PS00463; ZN2_Cy6_FUNGAL_1; 1.
DR PROSITE; PS50048; ZN2_Cy6_FUNGAL_2; 1.
KW DNA-binding; Hypothetical protein; Metal-binding; Nuclear protein;
KW Transcription regulation; Zinc.
FT DNA BIND 15 45 Zn(2)-Cys(6), fungal-type.
SQ SEQUENCE 446 AA; 50081 MW; C78D3632DDCC3EAO CRC64;
Query Match 50.0%; Score 7; DB 1; Length 446;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 VSENVGS 10
Db 125 VSENVGS 131
|||||
RESULT 11
Q6FJY2 PRELIMINARY; PRT; 462 AA.
ID AC Q6FJY2
AC Q6FJY2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Similar to sp|P19541|Saccharomyces cerevisiae YPL133c.
GN ORFNames=CAGL0M02651g;
OS Candida glabrata CBS138.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OK NCBI_TaxID=284593;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CBS138;
RG Genolevures;
RA Daion B., Sherman D., Fischer G., Durrans P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthonard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Boissame A., Boyer J., Cattolico L., Confanioli F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Karrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenn S., Potier S., Richard G.F., Straub M.L., Suleau A.,
RA Swennene D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zenion-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA Wincker P., Souciet J.L.;
RT "Genome evolution in yeasts.",
RL Nature 430:35-44 (2004).
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -!- SIMILARITY: Contains 1 Zn(2)-Cys(6) fungal-type binuclear cluster
CC domain.
DR EMBL; CR380959; CAG62438.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001138; Fungi_Tscrp_N.
DR Pfam; PF00172; Zn_clus; 1.
DR SMART; SM00066; GAL4; 1.
DR PROSITE; PS00463; ZN2_Cy6_FUNGAL_1; 1.
DR PROSITE; PS50048; ZN2_Cy6_FUNGAL_2; 1.
KW DNA-binding; Metal-binding; Nuclear protein; Transcription;
KW Transcription regulation; Zinc.
SQ SEQUENCE 462 AA; 52279 MW; 9195A1BCE41626B0 CRC64;
Query Match 50.0%; Score 7; DB 2; Length 462;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 VSENVGS 10
Db 115 VSENVGS 121
|||||

DR WormBase; WBGene00003476; mtm-3.
 DR WormPep; T2411.1b; CE28087.
 DR GO; GO:0004721; P:phosphoprotein phosphatase activity; IEA.
 DR GO; GO:0006270; P:zinc ion binding; IEA.
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
 DR InterPro; IPR011011; FYVE PHD Znf.
 DR InterPro; IPR010569; Myotub-related.
 DR InterPro; IPR000387; TYR phosphatase.
 DR InterPro; IPR000306; Znf_FYVE.
 DR Pfam; PF01363; FYVE; 1.
 DR Pfam; PF08602; Myotub-related; 1.
 DR SMART; SM00064; FYVE; 1.
 DR PROSITE; PS00383; TYR PHOSPHATASE_1; 1.
 DR PROSITE; PS01178; ZF_FYVE; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 1006 AA; 113613 MW; BEFC03296E74DB1A CRC64;
 Query Match 50.0%; Score 7; DB 2; Length 1006;
 Best Local Similarity 100.0%; Pred.No. 40;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 DNVSENV 8
 Db |||||
 917 DNVSENV 923
 RESULT 14
 Q9J746 PRELIMINARY; PRT; 1069 AA.
 AC Q9J746;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Exodeoxyribonuclease V (EC 3.1.11.5).
 GN Name=recC; OrderedLocNames=NMAL974;
 OS Neisseria meningitidis (serogroup A).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 OC Neisseriaceae; Neisseria.
 OX NCBI_TaxID=65699;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Z2491 / Serogroup A / Serotype 4b;
 RX MEDLINE=20222556; PubMed=10761919; DOI=10.1038/35006655;
 RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.M.,
 RA Klee S.R., Morelli G., Baeham D., Brown D., Chillingworth T.,
 RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
 RA Jagels K., Leather S., Moule S., Mungall K.L., Quail M.A.,
 RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
 RA Whitehead S., Spratt B.G., Barrell B.G.;
 RT "Complete DNA sequence of a serogroup A strain of Neisseria
 meningitidis Z2491".
 RL Nature 404:502-506(2000).
 DR EMBL; AL162757; CAB85194.1; --.
 DR PIR; D81826; D81826.
 DR GO; GO:0009338; C:exodeoxyribonuclease V complex; IEA.
 DR GO; GO:000854; F:exodeoxyribonuclease V activity; IEA.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR InterPro; IPR011034; FMT_C_like.
 DR InterPro; IPR006697; RecC.
 DR Pfam; PF04257; Exonuc_V_gamma; 1.
 DR TIGRFAMs; TIGR01450; recC; 1.
 KW Complete proteome; Hydrolase.
 SQ SEQUENCE 1069 AA; 120606 MW; 57C8E76A62FD705C CRC64;
 Query Match 50.0%; Score 7; DB 2; Length 1069;
 Best Local Similarity 100.0%; Pred.No. 42;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 SENVSUV 11
 Db |||||
 317 SENVSUV 323

RESULT 15
 Q9HS95 PRELIMINARY; PRT; 1190 AA.
 AC Q9HS95;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Chromosome segregation.
 GN Name=smcI; OrderedLocNames=VNG0342G;
 OS Halobacterium sp. (strain NRC-1 / ATCC 700922 / JCM 11081).
 OC Archaea; Euryarchaeota; Halobacteriales;
 OC Halobacteriaceae; Halobacterium.
 OX NCBI_TaxID=64091;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRC-1 / ATCC 700922 / JCM 11081;
 RX MEDLINE=20504483; PubMed=11016950; DOI=10.1073/pnas.190337797;
 RA Ng W.V., Kennedy S.P., Mahairas G.G., Bergquist B., Pan M.,
 RA Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
 RA Swartzell S., Weir D., Hall J., Dahl T.A., Welter R., Goo Y.A.,
 RA Leithauser B., Kellier K., Cruz R., Danson M.J., Hough D.W.,
 RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
 RA Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.D., Jung K.-H.,
 RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
 RA Ehardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
 RT "Genome sequence of Halobacterium species NRC-1".
 RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
 DR EMBL; AE004993; AAG18913.1; --.
 DR PIR; E84193; E84193.
 DR HSP; Q9X0R4; I869.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0042826; F:ATPase activity; IEA.
 DR GO; GO:0005525; F:GTP binding; IEA.
 DR GO; GO:0007059; P:chromosome segregation; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR003439; ABC transporter.
 DR InterPro; IPR005289; GTP-binding.
 DR InterPro; IPR003405; SMC_C.
 DR InterPro; IPR010935; SMC_hinge.
 DR InterPro; IPR003395; SMC_N.
 DR InterPro; IPR000533; Tropomyosin.
 DR Pfam; PF02483; SMC_C; 1.
 DR Pfam; PF06470; SMC_hinge; 1.
 DR Pfam; PF02463; SMC_N; 1.
 DR Pfam; PF00261; Tropomyosin; 1.
 DR ProDom; PD000006; ABC transporter; 1.
 DR TIGRFAMs; TIGR00650; MG442; 1.
 KW Complete proteome.
 SQ SEQUENCE 1190 AA; 131678 MW; 6994631722219EA4 CRC64;
 Query Match 50.0%; Score 7; DB 2; Length 1190;
 Best Local Similarity 100.0%; Pred.No. 46;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 SENVSUV 11
 Db |||||
 106 SENVSUV 112
 Search completed: February 11, 2005, 03:18:44
 Job time : 28.7238 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 11, 2005, 07:56:46 ; Search time 285.55 Seconds
(without alignments)
2375.673 Million cell updates/sec

Title: US-09-736-250-5
Perfect score: 14
Sequence: 1 EDNVSENVGSVCGT 14

Scoring table:
OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Word size: 1

Total number of hits satisfying chosen parameters: 9400932

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
-O=/cgn2 1/USPTO.spool/US09736250/runat 07022005 154942 20650/app query.fasta_1.718
-DB=GenEmbl -QWTF=fastap -SUFFIX=oligo.rge -MINMATCH=0.1 -LOOPCL=0 -LOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi -LIST=1000
-DOCALIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09736250.@CGN 1 1 3890 @runat 07022005 154942 20650 -NCPU=6 -ICPU=3
-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAEXT=60 -FGAPOP=6
-FGAEXT=7 -YGAPOP=60 -YGAEXT=60 -DELOP=6 -DELEXT=7

Database :

GenEmbl:*
1: gb.ba:*
2: gb.htg:*
3: gb.in:*
4: gb.om:*
5: gb.ov:*
6: gb.pat:*
7: gb.ph:*
8: gb.pl:*
9: gb.pr:*
10: gb.ro:*
11: gb.sts:*
12: gb.sy:*
13: gb.un:*
14: gb.vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Length	DB ID	SUMMARIES	
				Description	
1	14	100.0	136	6	A74835 Sequence 52
2	14	100.0	136	6	A77814 Sequence 52
3	14	100.0	288	6	CQ712652 Sequence
4	14	100.0	350	6	CQ675890 Sequence

AX397198	Sequence	444	6	AX397198	Sequence
AX198885	Sequence	447	6	AX198885	Sequence
AX209412	Sequence	447	6	AX209412	Sequence
BV180201	sgm10841	601	11	BV180201	sgm10841
BD079737	Cancer-as	804	6	BD079737	Cancer-as
CR541783	Homo sapi	1131	9	CR541783	Homo sapi
AR145734	Sequence	1133	6	AR145734	Sequence
AK087353	Sequence	1260	6	AK087353	Sequence
CQ812312	Sequence	1260	6	CQ812312	Sequence
AR281918	Sequence	1260	6	AR281918	Sequence
AR380354	Sequence	1260	6	AR380354	Sequence
D50310	Human mRNA	1260	9	HUMCVI	
AF135162	Homo sapi	1384	9	AF135162	Homo sapi
BD194541	Human nuc	1493	6	BD194541	Human nuc
AX015395	Sequence	1493	6	AX015395	Sequence
BC000420	Homo sapi	1817	9	BC000420	Homo sapi
CQ468129	Sequence	1889	6	CQ468129	Sequence
BC004975	Homo sapi	1889	6	BC004975	Homo sapi
CQ414223	Sequence	2146	6	CQ414223	Sequence
CQ414515	Sequence	2755	6	CQ414515	Sequence
AY207372	Homo sapi	29867	9	AY207372	Homo sapi
AC111196	Homo sapi	35191	9	AC111196	Homo sapi
AP002874	Homo sapi	178916	2	AP002874	Homo sapi
AC079051	Homo sapi	179443	2	AC079051	Homo sapi
AX914031	Sequence	304	6	AX914031	Sequence
BD049564	Sequence	304	6	BD049564	Sequence
CQ696855	Sequence	308	6	CQ696855	Sequence
AC099472	Rattus no	241543	2	AC099472	Rattus no
AC111318	Rattus no	260517	2	AC111318	Rattus no
AC113213	Rattus no	270068	2	AC113213	Rattus no
CQ660642	Sequence	200	6	CQ660642	Sequence
AF005886	Mus muscu	1535	10	AF005886	Mus muscu
BC003290	Mus muscu	2348	10	BC003290	Mus muscu
AF228740	Mus muscu	11793	10	AF228740	Mus muscu
AC003001	Homo sapi	101981	9	AC003001	Homo sapi
Z95971	Human DNA s	104002	9	HS398N15	
AC117658	Mus muscu	179333	2	AC117658	Mus muscu
AC134827	Mus muscu	193811	10	AC134827	Mus muscu
AC101881	Mus muscu	200850	2	AC101881	Mus muscu
AC124646	Mus muscu	202228	2	AC124646	Mus muscu
AC110019	Homo sapi	67380	2	AC110019	Homo sapi
Continuation (2 of		110000	8	CR382134_01	
CR323884	Zebrafish	137509	5	EX323884	
AC067871	Homo sapi	181118	9	AC067871	Homo sapi
AC073253	Homo sapi	187045	2	AC073253	Homo sapi
AC122199	Mus muscu	202975	10	AC122199	Mus muscu
AC124931	Rattus no	22594	2	AC124931	Rattus no
AC106995	Rattus no	22823	2	AC106995	Rattus no
CR354610	Danio rer	22860	2	CR354610	Danio rer
AC096022	Rattus no	239423	2	AC096022	Rattus no
AC097676	Rattus no	270387	2	AC097676	Rattus no
A74630	Sequence 31	135	6	A74630	Sequence 31
A77609	Sequence 31	135	6	A77609	Sequence 31
A74629	Sequence 31	183	6	A74629	Sequence 31
A77608	Sequence 31	183	6	A77608	Sequence 31
Z57845	H.sapiens C	245	9	HS1A7F	
AX660625	Sequence	845	6	AX660625	Sequence
AY064628	Arabidops	924	8	AY064628	Arabidops
IAJ507598	Isoetes a	980	8	IAJ507598	Isoetes a
AB119060	Arabidops	1105	8	AB119060	Arabidops
AJ507593	Isoetes 1	1149	8	IAJ507593	Isoetes 1
AR448407	Sequence	1226	6	AR448407	Sequence
AY042817	Arabidops	1273	8	AY042817	Arabidops
AY085109	Arabidops	1287	8	AY085109	Arabidops
AX684960	Sequence	1338	6	AX684960	Sequence
AY693168	Saccharom	1341	8	AY693168	Saccharom
AF522193	Drosophil	1434	3	AF522193	Drosophil
AY603424	Rattus no	1550	10	AY603424	Rattus no
CQ608643	Sequence	1671	6	CQ608643	Sequence
AY071512	Drosophil	1987	3	AY071512	Drosophil
AF505865	Drosophil	2004	3	AF505865	Drosophil
BC078340	Danio rer	2030	5	BC078340	Danio rer
AK105285	Oryza sat	2137	8	AK105285	Oryza sat

78	7	50.0	2182	8	AK109896	AK109896 Oryza sat	c 151	7	50.0	157665	9	AC104695	AC104695 Homo sapi
79	7	50.0	3235	5	AF111857	AF111857 Gallus ga	152	7	50.0	157843	2	BN950217	BN950217 Danio rer
80	7	50.0	3868	6	CQ608642	CQ608642 Sequence	153	7	50.0	158214	2	CNS0507C0	AL352981 Human chr
81	7	50.0	3912	3	AF031519	AF031519 Caenorhab	154	7	50.0	158447	2	AC087435	AC087435 Homo sapi
82	7	50.0	4685	5	BC076538	BC076538 Danio rer	155	7	50.0	159284	2	AC084369	AC084369 Homo sapi
83	7	50.0	10286	1	AE004993	AE004993 Halobacte	c 156	7	50.0	161087	9	AC146261	AC146261 Pan trogl
84	7	50.0	13525	8	AF523678	AF523678 Streptoco	c 157	7	50.0	161297	9	BS000531	BS000531 Pan trogl
85	7	50.0	21648	1	AF316642	AF316642 Streptoco	c 158	7	50.0	161433	2	AC022047	AC022047 Homo sapi
86	7	50.0	24935	8	AC092423	AC092423 Homo sapi	c 159	7	50.0	162481	2	CR788290	CR788290 Homo sapi
87	7	50.0	28170	1	AF454500	AF454500 Streptoco	c 160	7	50.0	162681	2	CR788290	CR788290 Homo sapi
88	7	50.0	28170	6	AX283721	AX283721 Sequence	c 161	7	50.0	162892	5	EX005067	EX005067 Zebrafish
89	7	50.0	30655	3	CET24A11	CET24A11 Sequence	c 162	7	50.0	163179	9	AC022541	AC022541 Homo sapi
90	7	50.0	32960	3	CEK02E11	CEK02E11 Sequence	c 163	7	50.0	163635	2	CR392027	CR392027 Danio rer
91	7	50.0	33993	9	AL162581	AL162581 Human DNA	c 164	7	50.0	165638	3	AC148636	AC148636 Callithr
92	7	50.0	35484	8	SCU43703	SCU43703 Saccharomy	c 165	7	50.0	167195	3	AC007808	AC007808 Drosophi
93	7	50.0	40441	2	AC145714	AC145714 Homo sapi	c 166	7	50.0	167284	9	AC112719	AC112719 Homo sapi
94	7	50.0	41153	10	AL808114	AL808114 Mouse DNA	c 167	7	50.0	167852	9	AC072061	AC072061 Homo sapi
95	7	50.0	46289	9	AC084793	AC084793 Homo sapi	c 168	7	50.0	168851	9	AC079336	AC079336 Homo sapi
96	7	50.0	50988	9	AC104776	AC104776 Homo sapi	c 169	7	50.0	169152	9	AC151000	AC151000 Homo sapi
97	7	50.0	63114	5	CR377227	CR377227 Zebrafish	c 170	7	50.0	169819	9	AC078991	AC078991 Homo sapi
98	7	50.0	66796	2	AC017435	AC017435 Drosophi	c 171	7	50.0	170807	9	AC124307	AC124307 Homo sapi
99	7	50.0	76711	2	AC091341	AC091341 Continu	c 172	7	50.0	170966	5	EX000991	EX000991 Zebrafish
100	7	50.0	78596	2	AC023030	AC023030 Homo sapi	c 173	7	50.0	171224	2	AC091600	AC091600 Homo sapi
101	7	50.0	80074	9	AC008389	AC008389 Homo sapi	c 174	7	50.0	172148	9	AC092764	AC092764 Pan trogl
102	7	50.0	85599	8	AB023045	AB023045 Arabidops	c 175	7	50.0	172761	9	AC092764	AC092764 Pan trogl
103	7	50.0	92563	6	AX695695	AX695695 Sequence	c 176	7	50.0	174652	2	AC024630	AC024630 Homo sapi
104	7	50.0	97982	8	AC140722	AC140722 Medicago	c 177	7	50.0	174920	3	AC010701	AC010701 Drosophi
105	7	50.0	100290	9	AC061992	AC061992 Homo sapi	c 178	7	50.0	175036	9	AC068069	AC068069 Homo sapi
106	7	50.0	103287	2	AC084034	AC084034 Homo sapi	c 179	7	50.0	175036	9	AC068069	AC068069 Homo sapi
107	7	50.0	107977	9	AC002119	AC002119 Homo sapi	c 180	7	50.0	175468	2	AC147862	AC147862 Papio anu
108	7	50.0	110000	2	AC120430	AC120430 Continu	c 181	7	50.0	175965	10	AC121921	AC121921 Mus muscu
109	7	50.0	110000	2	AC151905	AC151905 Continu	c 182	7	50.0	177242	2	AC113393	AC113393 Homo sapi
110	7	50.0	110000	8	CR380959	CR380959 Continu	c 183	7	50.0	177242	2	AC147237	AC147237 Mus muscu
111	7	50.0	110000	8	CR380959	CR380959 Continu	c 184	7	50.0	177423	2	CR356242	CR356242 Danio rer
112	7	50.0	110000	8	CR382134	CR382134 Continu	c 185	7	50.0	178095	2	CR753874	CR753874 Danio rer
113	7	50.0	110000	8	CR382135	CR382135 Continu	c 186	7	50.0	178344	2	AC149182	AC149182 Papio anu
114	7	50.0	114104	9	AC128712	AC128712 Homo sapi	c 187	7	50.0	179876	10	AC102157	AC102157 Mus muscu
115	7	50.0	115884	2	AC017581	AC017581 Drosophi	c 188	7	50.0	180187	2	AC117965	AC117965 Rattus no
116	7	50.0	116803	2	AC097718	AC097718 Homo sapi	c 189	7	50.0	180488	10	AC141632	AC141632 Mus muscu
117	7	50.0	121946	9	AC114771	AC114771 Homo sapi	c 190	7	50.0	180573	10	AL831753	AL831753 Mouse DNA
118	7	50.0	123037	9	AC109443	AC109443 Homo sapi	c 191	7	50.0	181027	2	CR354600	CR354600 Danio rer
119	7	50.0	126730	2	CR548621	CR548621 Danio rer	c 192	7	50.0	181319	2	AC110497	AC110497 Mus muscu
120	7	50.0	126889	10	AC141867	AC141867 Mus muscu	c 193	7	50.0	181328	9	AC104945	AC104945 Homo sapi
121	7	50.0	127017	10	AC140445	AC140445 Mus muscu	c 194	7	50.0	181842	10	AC137127	AC137127 Mus muscu
122	7	50.0	130870	10	AL731775	AL731775 Mouse DNA	c 195	7	50.0	182203	2	AC109374	AC109374 Rattus no
123	7	50.0	133052	9	AL136325	AL136325 Human DNA	c 196	7	50.0	182203	2	AC128779	AC128779 Rattus no
124	7	50.0	137925	2	EX927291	EX927291 Danio rer	c 197	7	50.0	183936	2	AL49620	AL49620 Papio anu
125	7	50.0	138851	10	AL645938	AL645938 Mouse DNA	c 198	7	50.0	185138	10	AL845172	AL845172 Mouse DNA
126	7	50.0	138864	10	AC155832	AC155832 Mus muscu	c 199	7	50.0	187278	2	EX571888	EX571888 Danio rer
127	7	50.0	139594	2	AC025085	AC025085 Homo sapi	c 200	7	50.0	187341	10	AC117184	AC117184 Mus muscu
128	7	50.0	142576	9	AC010609	AC010609 Homo sapi	c 201	7	50.0	187415	2	AC110802	AC110802 Homo sapi
129	7	50.0	142807	9	H333B19	AL035693 Human DNA	c 202	7	50.0	187490	2	AC048378	AC048378 Homo sapi
130	7	50.0	143220	9	AL389887	AL389887 Human DNA	c 203	7	50.0	187792	2	CR407545	CR407545 Danio rer
131	7	50.0	143334	9	AC005293	AC005293 Homo sapi	c 204	7	50.0	188476	10	AC122238	AC122238 Mus muscu
132	7	50.0	144260	9	AC006598	AC006598 Homo sapi	c 205	7	50.0	189263	10	AC134595	AC134595 Mus muscu
133	7	50.0	145226	9	AF004284	AF004284 Homo sapi	c 206	7	50.0	189771	2	AC112921	AC112921 Homo sapi
134	7	50.0	145603	2	AC148823	AC148823 Pan trogl	c 207	7	50.0	190558	2	AC119478	AC119478 Rattus no
135	7	50.0	145721	2	OSUN00145	AL662933 Oryza sat	c 208	7	50.0	190860	10	AC144776	AC144776 Mus muscu
136	7	50.0	147521	5	EX649434	EX649434 Zebrafish	c 209	7	50.0	192944	2	AC146902	AC146902 Callicebu
137	7	50.0	147775	5	EX649434	EX649434 Zebrafish	c 210	7	50.0	193015	2	AC150074	AC150074 Gallus ga
138	7	50.0	148485	5	AL590147	AL590147 Zebrafish	c 211	7	50.0	194304	9	AC016708	AC016708 Homo sapi
139	7	50.0	148592	2	AC125190	AC125190 Mus muscu	c 212	7	50.0	194464	2	AC146119	AC146119 Pan trogl
140	7	50.0	149277	2	AL627207	AL627207 Homo sapi	c 213	7	50.0	194827	2	EX294106	EX294106 Danio rer
141	7	50.0	149617	2	AC068052	AC068052 Homo sapi	c 214	7	50.0	195673	10	AC102310	AC102310 Mus muscu
142	7	50.0	150634	2	AC113371	AC113371 Homo sapi	c 215	7	50.0	195673	2	AC147722	AC147722 Mouse DNA
143	7	50.0	150794	9	AC025211	AC025211 Homo sapi	c 216	7	50.0	197912	10	AL672070	AL672070 Mouse DNA
144	7	50.0	151406	10	AC122196	AC122196 Mus muscu	c 217	7	50.0	197912	2	AL672070	AL672070 Mouse DNA
145	7	50.0	152787	2	EX323075	EX323075 Danio rer	c 218	7	50.0	198404	10	AC114621	AC114621 Mus muscu
146	7	50.0	153087	2	AC020546	AC020546 Homo sapi	c 219	7	50.0	198576	10	AC068908	AC068908 Mus muscu
147	7	50.0	155299	9	AC009479	AC009479 Homo sapi	c 220	7	50.0	198604	10	AC128828	AC128828 Mus muscu
148	7	50.0	155725	9	AL161723	AL161723 Human DNA	c 221	7	50.0	198759	2	AC020772	AC020772 Homo sapi
149	7	50.0	155775	2	AC011943	AC011943 Homo sapi	c 222	7	50.0	198838	2	AC093647	AC093647 Homo sapi
150	7	50.0	155819	9	AL358372	AL358372 Human DNA	c 223	7	50.0	198893	2	AC133116	AC133116 Rattus no

c 224	7	50.0	199946	2	AC135863	AC135863 Mus muscu	297	7	50.0	257396	2	AC130569	AC130569 Rattus no
c 225	7	50.0	200187	5	BX510327	BX510327 Zebrafish	298	7	50.0	257398	2	AC131885	AC131885 Rattus no
c 226	7	50.0	200679	10	AC112662	AC112662 Mus muscu	c 299	7	50.0	258873	2	AC096935	AC096935 Rattus no
c 227	7	50.0	200688	2	AC112757	AC112757 Rattus no	300	7	50.0	260168	2	AC094547	AC094547 Rattus no
c 228	7	50.0	200688	10	AL671963	AL671963 Mouse DNA	c 301	7	50.0	260625	2	AC096018	AC096018 Rattus no
c 229	7	50.0	200841	10	AC108830	AC108830 Mus muscu	c 302	7	50.0	260925	2	AC110478	AC110478 Rattus no
c 230	7	50.0	201239	2	AC135866	AC135866 Rattus no	c 303	7	50.0	261089	2	AC094807	AC094807 Rattus no
c 231	7	50.0	202236	10	AC124513	AC124513 Mus muscu	c 304	7	50.0	264473	2	AC132979	AC132979 Rattus no
c 232	7	50.0	203221	10	AC102689	AC102689 Mus muscu	c 305	7	50.0	264754	2	AC128542	AC128542 Rattus no
c 233	7	50.0	203480	2	AC146136	AC146136 Pan trogl	c 306	7	50.0	269670	2	AC121698	AC121698 Rattus no
c 234	7	50.0	203802	2	AC133417	AC133417 Rattus no	c 307	7	50.0	272055	2	AC118859	AC118859 Rattus no
c 235	7	50.0	204191	10	AC099615	AC099615 Mus muscu	c 308	7	50.0	272605	2	AC095738	AC095738 Rattus no
c 236	7	50.0	204478	10	AC127306	AC127306 Mus muscu	c 309	7	50.0	272621	2	AC095191	AC095191 Rattus no
c 237	7	50.0	205702	2	AC145116	AC145116 Mus muscu	c 310	7	50.0	284471	2	AC095933	AC095933 Rattus no
c 238	7	50.0	206331	2	CR388075	CR388075 Danio rer	c 311	7	50.0	299180	1	AP005080	AP005080 Vibrio pa
c 239	7	50.0	207126	2	AC140461	AC140461 Mus muscu	c 312	7	50.0	310137	2	AC111625	AC111625 Rattus no
c 240	7	50.0	207206	9	AC090260	AC090260 Homo sapi	c 313	7	50.0	314906	3	AE003594	AE003594 Drosophil
c 241	7	50.0	207295	2	AC101998	AC101998 Mus muscu	c 314	7	50.0	324430	2	AC118529	AC118529 Rattus no
c 242	7	50.0	207563	2	AC116577	AC116577 Mus muscu	c 315	7	50.0	326301	1	NMA622491	AL162757 Neisseria
c 243	7	50.0	210018	2	AC015557	AC015557 Homo sapi	c 316	7	50.0	347286	2	AC102740	AC102740 Mus muscu
c 244	7	50.0	210018	2	AC015557	AC015557 Homo sapi	c 317	7	50.0	348174	3	CR382399	CR382399 Plasmodiu
c 245	7	50.0	210854	2	AC123995	AC123995 Mus muscu	c 318	6	42.9	19	6	AR294906	AR294906 Sequence
c 246	7	50.0	212284	2	AC131732	AC131732 Mus muscu	c 319	6	42.9	60	6	CQ546488	CQ546488 Sequence
c 247	7	50.0	212421	2	AC109591	AC109591 Homo sapi	c 320	6	42.9	100	6	AX989903	AX989903 Sequence
c 248	7	50.0	213178	10	AC148021	AC148021 Mus muscu	c 321	6	42.9	108	6	CQ081052	CQ081052 Sequence
c 249	7	50.0	214049	2	AC130983	AC130983 Rattus no	c 322	6	42.9	108	6	CQ115545	CQ115545 Sequence
c 250	7	50.0	216449	2	AC115772	AC115772 Mus muscu	c 323	6	42.9	108	6	CQ154345	CQ154345 Sequence
c 251	7	50.0	216851	2	AC146740	AC146740 Callithri	c 324	6	42.9	108	6	CQ186913	CQ186913 Sequence
c 252	7	50.0	217769	2	AC102447	AC102447 Mus muscu	c 325	6	42.9	108	6	CQ237598	CQ237598 Sequence
c 253	7	50.0	217777	2	AC113891	AC113891 Rattus no	c 326	6	42.9	108	6	CQ275218	CQ275218 Sequence
c 254	7	50.0	218157	2	AC134263	AC134263 Rattus no	c 327	6	42.9	108	6	CQ312196	CQ312196 Sequence
c 255	7	50.0	219683	2	AC103126	AC103126 Rattus no	c 328	6	42.9	108	6	CQ349602	CQ349602 Sequence
c 256	7	50.0	220788	2	AC130904	AC130904 Rattus no	c 329	6	42.9	159	6	AX719130	AX719130 Sequence
c 257	7	50.0	222251	2	AC110936	AC110936 Rattus no	c 330	6	42.9	159	6	AX766254	AX766254 Sequence
c 258	7	50.0	222292	2	AC118839	AC118839 Rattus no	c 331	6	42.9	169	10	RAJ10024	RAJ10024 Rattus no
c 259	7	50.0	222330	2	AC096255	AC096255 Rattus no	c 332	6	42.9	171	6	CQ448299	CQ448299 Sequence
c 260	7	50.0	222965	2	AC115879	AC115879 Mus muscu	c 333	6	42.9	174	6	CQ695388	CQ695388 Sequence
c 261	7	50.0	223061	2	AC098658	AC098658 Rattus no	c 334	6	42.9	175	11	AU050020	AU050020 Rattus no
c 262	7	50.0	224400	2	AC111100	AC111100 Mus muscu	c 335	6	42.9	194	1	AB080996	AB080996 Salmonell
c 263	7	50.0	224561	2	AC103154	AC103154 Rattus no	c 336	6	42.9	201	6	AR387165	AR387165 Sequence
c 264	7	50.0	225066	2	AC112674	AC112674 Mus muscu	c 337	6	42.9	201	11	BV169998	BV169998 sqnm28245
c 265	7	50.0	226351	2	AC106508	AC106508 Rattus no	c 338	6	42.9	201	11	BV183159	BV183159 sqnm13661
c 266	7	50.0	226650	2	AC120485	AC120485 Rattus no	c 339	6	42.9	255	8	AY298897	AY298897 Trichoder
c 267	7	50.0	228051	2	AC097434	AC097434 Rattus no	c 340	6	42.9	256	6	AX911508	AX911508 Sequence
c 268	7	50.0	230236	10	AC093366	AC093366 Mus muscu	c 341	6	42.9	256	6	BD047041	BD047041 Sequence
c 269	7	50.0	230448	2	AC128463	AC128463 Rattus no	c 342	6	42.9	256	9	HSREP133	HSREP133 Homo sapi
c 270	7	50.0	230993	2	AC150072	AC150072 Gallus ga	c 343	6	42.9	257	9	AY530102	AY530102 Gorilla g
c 271	7	50.0	231234	2	AC134014	AC134014 Rattus no	c 344	6	42.9	258	9	AY530103	AY530103 Gorilla g
c 272	7	50.0	233097	10	AL772239	AL772239 Mouse DNA	c 345	6	42.9	260	11	BV183203	BV183203 sqnm13702
c 273	7	50.0	233141	2	AC128327	AC128327 Rattus no	c 346	6	42.9	263	6	CQ671671	CQ671671 Sequence
c 274	7	50.0	233345	2	AC150066	AC150066 Gallus ga	c 347	6	42.9	273	9	GORMTDLOOP	L76749 Gorilla gor
c 275	7	50.0	234526	2	AC120414	AC120414 Mus muscu	c 348	6	42.9	277	9	GORMTDLOOR	L76751 Gorilla gor
c 276	7	50.0	234526	2	AC111227	AC111227 Rattus no	c 349	6	42.9	279	6	CQ667273	CQ667273 Sequence
c 277	7	50.0	237260	2	AC095010	AC095010 Rattus no	c 350	6	42.9	283	9	GORMTDLOOQ	L76750 Gorilla gor
c 278	7	50.0	238896	2	AC137226	AC137226 Rattus no	c 351	6	42.9	287	9	GORMTDLOOS	L76752 Gorilla gor
c 279	7	50.0	240350	2	AC124154	AC124154 Rattus no	c 352	6	42.9	289	6	CQ670575	CQ670575 Sequence
c 280	7	50.0	240992	2	AC131467	AC131467 Rattus no	c 353	6	42.9	293	6	AR272809	AR272809 Sequence
c 281	7	50.0	242413	2	AC106264	AC106264 Rattus no	c 354	6	42.9	293	6	AR276390	AR276390 Sequence
c 282	7	50.0	242510	2	AC128507	AC128507 Rattus no	c 355	6	42.9	293	6	AR406665	AR406665 Sequence
c 283	7	50.0	242974	2	AC103570	AC103570 Rattus no	c 356	6	42.9	293	6	AR440515	AR440515 Sequence
c 284	7	50.0	243252	2	AC120850	AC120850 Mus muscu	c 357	6	42.9	293	6	AR472673	AR472673 Sequence
c 285	7	50.0	243545	2	AC135739	AC135739 Rattus no	c 358	6	42.9	293	6	AR543326	AR543326 Sequence
c 286	7	50.0	246083	2	AC106313	AC106313 Rattus no	c 359	6	42.9	293	6	AX062911	AX062911 Sequence
c 287	7	50.0	246369	2	AC125707	AC125707 Rattus no	c 360	6	42.9	293	6	AX367828	AX367828 Sequence
c 288	7	50.0	246805	2	AC098750	AC098750 Rattus no	c 361	6	42.9	305	11	G49065	G49065 SHGC-82968
c 289	7	50.0	247469	2	AC096287	AC096287 Rattus no	c 362	6	42.9	308	6	CQ437347	CQ437347 Sequence
c 290	7	50.0	249791	5	BX537133	BX537133 Zebrafish	c 363	6	42.9	308	10	MMU81277	MMU81277 Mus musculu
c 291	7	50.0	250277	2	AC122757	AC122757 Mus muscu	c 364	6	42.9	309	6	CQ697708	CQ697708 Sequence
c 292	7	50.0	251914	2	AC111366	AC111366 Rattus no	c 365	6	42.9	313	11	G22286	G22286 human STS W
c 293	7	50.0	252843	2	AC096261	AC096261 Rattus no	c 366	6	42.9	316	11	G36015	G36015 STS h14a147
c 294	7	50.0	254400	2	AC096497	AC096497 Rattus no	c 367	6	42.9	346	6	CQ656116	CQ656116 Sequence
c 295	7	50.0	254961	3	AE003706	AE003706 Drosophil	c 368	6	42.9	346	6	CQ690011	CQ690011 Sequence
c 296	7	50.0	257258	2	AC105322	AC105322 Mus muscu	c 369	6	42.9	347	4	ECA272106	ECA272106 Equus cab

C 370	6	42.9	347	6	CQ691350 Sequence	CQ691350 Sequence	443	550	7	STSP02	X01583 Bacterioph
C 371	6	42.9	349	11	Z51386 H. sapiens	Z51386 H. sapiens	444	552	1	UBA309652	AJ309652 Unculture
C 372	6	42.9	357	6	AX414007 Sequence	AX414007 Sequence	C 445	556	6	BD151108	BD151108 Primer fo
C 373	6	42.9	357	6	AX415799 Sequence	AX415799 Sequence	C 446	556	6	AX871046	AX871046 Sequence
C 374	6	42.9	358	5	AF373872 Sequence	AF373872 Xenopus l	447	557	3	AME509690	AJ509690 Apis mell
C 375	6	42.9	358	6	BD059685 Sequence	BD059685 Secreted	448	557	6	AX341833 Sequence	AX341833 Sequence
C 376	6	42.9	360	1	AY015541 Unculture	AY015541 Unculture	C 449	559	11	G78268	G78268 S209P6075FF
C 377	6	42.9	361	11	BV088295 Sequence	BV088295 RPAMMSEQO	C 450	560	6	CQ782375	CQ782375 Sequence
C 378	6	42.9	361	11	BV097338 Sequence	BV097338 RPAMMSEQO	C 451	560	6	BD127084	BD127084 Primer fo
C 379	6	42.9	362	10	MUSURF44	ME26034 Mouse surfe	C 452	563	6	AX237376	AX237376 Sequence
C 380	6	42.9	368	6	AX451492 Sequence	AX451492 Sequence	C 453	563	6	AX237504	AX237504 Sequence
C 381	6	42.9	374	9	AF089820 Gorilla g	AF089820 Gorilla g	C 454	563	6	AX237673	AX237673 Sequence
C 382	6	42.9	380	11	G36260	G36260 STS h14a232	C 455	565	5	AY216588	AY216588 Danio rer
C 383	6	42.9	398	6	CQ675091	CQ675091 Sequence	C 456	575	14	AF529736	AF529736 Hepatitis
C 384	6	42.9	400	11	G16689	G16689 SHGC-15279	C 457	578	11	BV157551	BV157551 RPAMMSEQO
C 385	6	42.9	401	6	CQ218447	CQ218447 Sequence	C 458	581	9	HS430600	HS430600 Homo sapi
C 386	6	42.9	401	6	CQ257059	CQ257059 Sequence	C 459	585	6	CQ594120	CQ594120 Sequence
C 387	6	42.9	401	11	BV193531	BV193531 sqm17816	C 460	593	11	G96850	G96850 S208P6100FF
C 388	6	42.9	402	8	AY558316	AY558316 Saccharom	C 461	594	6	AX437779	AX437779 Sequence
C 389	6	42.9	408	11	BV179335	BV179335 sqm10491	C 462	594	6	AX437779	AX437779 Sequence
C 390	6	42.9	414	8	BT004730	BT004730 Arabidops	C 463	597	9	HS8PT057	HS8PT057
C 391	6	42.9	425	4	AF140590	AF140590 Lepionych	C 464	598	9	HS4326609	HS4326609 Homo sapi
C 392	6	42.9	429	6	CQ468289	CQ468289 Sequence	C 465	598	11	G75913	G75913 S208P6693RB
C 393	6	42.9	432	1	UBA428143	UBA428143 unculture	C 466	601	11	BV021655	BV021655 S212P6237
C 394	6	42.9	436	6	CQ671069	CQ671069 Sequence	C 467	601	11	BV179336	BV179336 sqm10491
C 395	6	42.9	445	6	CQ711533	CQ711533 Sequence	C 468	603	8	AK118607	AK118607 Arabidops
C 396	6	42.9	446	6	AX332954	AX332954 Sequence	C 469	603	11	BV070510	BV070510 S212P6238
C 397	6	42.9	446	6	AX334706	AX334706 Sequence	C 470	606	11	G97070	G97070 S208P6379FC
C 398	6	42.9	446	6	AX335909	AX335909 Sequence	C 471	607	11	BV020047	BV020047 S212P6864
C 400	6	42.9	448	11	G37471	G37471 SHGC-57684	C 472	610	5	AF402828	AF402828 Ictulurus
C 401	6	42.9	448	11	BV145671	BV145671 PZA02544	C 473	615	9	AF032900	AF032900 Homo sapi
C 402	6	42.9	450	6	CQ477457	CQ477457 Sequence	C 474	619	11	G88550	G88550 S208P6113FC
C 403	6	42.9	465	6	CQ736493	CQ736493 Sequence	C 475	622	9	AF374413	AF374413 Homo sapi
C 404	6	42.9	471	6	CQ671835	CQ671835 Sequence	C 476	627	1	AY029581	AY029581 Ascomonas
C 405	6	42.9	475	6	AX072032	AX072032 Sequence	C 477	628	5	BC042226	BC042226 Xenopus l
C 406	6	42.9	477	6	CQ070005	CQ070005 Sequence	C 478	629	8	AB108388	AB108388 Phleum pr
C 407	6	42.9	477	6	CQ097608	CQ097608 Sequence	C 479	630	6	AX370934	AX370934 Sequence
C 408	6	42.9	477	6	CQ136449	CQ136449 Sequence	C 480	635	10	AF053770	AF053770 Mus muscu
C 409	6	42.9	477	6	CQ174429	CQ174429 Sequence	C 481	639	6	AR387211	AR387211 Sequence
C 410	6	42.9	477	6	CQ219755	CQ219755 Sequence	C 482	644	11	BV074312	BV074312 S212P6014
C 411	6	42.9	477	6	CQ258218	CQ258218 Sequence	C 483	646	11	BV017612	BV017612 S212P6008
C 412	6	42.9	477	6	CQ295562	CQ295562 Sequence	C 484	649	11	PM3A3B	PM3A3B
C 413	6	42.9	477	6	CQ332151	CQ332151 Sequence	C 485	650	11	BV056242	BV056242 S212P6039
C 414	6	42.9	478	6	CQ498660	CQ498660 Sequence	C 486	651	5	CR389463	CR389463 Gallus ga
C 415	6	42.9	478	6	CQ507634	CQ507634 Sequence	C 487	651	11	BV018666	BV018666 S212P6046
C 416	6	42.9	480	6	BD209567	BD209567 Compositi	C 488	654	10	AF080850	AF080850 Mus muscu
C 417	6	42.9	480	6	BD209658	BD209658 Compositi	C 489	655	11	BV018096	BV018096 S208P6653
C 418	6	42.9	480	6	AR341373	AR341373 Sequence	C 490	656	11	BV033488	BV033488 S212P6039
C 419	6	42.9	480	6	AR341464	AR341464 Sequence	C 491	660	10	AF551099	AF551099 Mus muscu
C 420	6	42.9	482	11	G63503	G63503 SHGC-141216	C 492	661	10	AF551146	AF551146 Mus muscu
C 421	6	42.9	491	9	HS430598	HS430598 Homo sapi	C 493	662	10	AF551025	AF551025 Mus muscu
C 422	6	42.9	496	11	G56059	G56059 SHGC-101321	C 494	664	10	AF551186	AF551186 Mus muscu
C 423	6	42.9	498	6	BD210362	BD210362 Human gen	C 495	664	11	AF551125	AF551125 Mus muscu
C 424	6	42.9	499	11	G870477	G870477 S209P6403FA	C 496	664	11	G94347	G94347 S208P6022RF
C 425	6	42.9	504	6	CQ720891	CQ720891 Sequence	C 497	667	11	BV042472	BV042472 S212P6052
C 426	6	42.9	506	8	ATH532204	ATH532204 Arabidops	C 498	675	5	SHPCRP	SHPCRP
C 427	6	42.9	519	5	MTLSNADH6	Y10311 L. svetica m	C 499	677	11	BV022780	BV022780 S212P6548
C 428	6	42.9	520	6	CQ071852	CQ071852 Sequence	C 500	678	11	UBA309618	UBA309618 Unculture
C 429	6	42.9	520	6	CQ141401	CQ141401 Sequence	C 501	687	11	BV045333	BV045333 S212P6041
C 430	6	42.9	520	6	CQ177039	CQ177039 Sequence	C 502	692	6	CQ425606	CQ425606 Sequence
C 431	6	42.9	520	6	CQ224688	CQ224688 Sequence	C 503	693	1	UBA309604	UBA309604 Unculture
C 432	6	42.9	520	6	CQ262703	CQ262703 Sequence	C 504	694	11	BV017936	BV017936 S212P6029
C 433	6	42.9	520	6	CQ299763	CQ299763 Sequence	C 505	702	1	UBA309603	UBA309603 Unculture
C 434	6	42.9	520	6	CQ336930	CQ336930 Sequence	C 506	706	9	HUMEBUR03	HUMEBUR03
C 435	6	42.9	521	6	CQ781334	CQ781334 Sequence	C 507	708	6	AF377545	AF377545 Sequence
C 436	6	42.9	521	6	BD126043	BD126043 Primer fo	C 508	710	3	AF385460	AF385460 Paracalan
C 437	6	42.9	532	10	AF551020	AF551020 Mus muscu	C 509	710	6	BD021649	BD021649 Novel gen
C 438	6	42.9	532	10	AF551031	AF551031 Mus muscu	C 511	710	6	BD101587	BD101587 Novel gen
C 439	6	42.9	533	6	AX244776	AX244776 Sequence	C 512	714	8	AF028523	AF028523 Gallus ga
C 440	6	42.9	536	6	AX390656	AX390656 Sequence	C 513	717	8	AF028523	AF028523 Bombax bu
C 441	6	42.9	541	11	G81105	G81105 S210P6204FC	C 514	720	8	BT000530	BT000530 Arabidops
C 442	6	42.9					C 515				

516	6	42.9	723	9	HS3335912	6	42.9	920	6	AX8339519	AX8339519 Sequence
517	6	42.9	725	1	UBA3309623	6	42.9	932	6	BD191268	BD191268 186 human
518	6	42.9	732	11	BV019291	6	42.9	936	6	AX924778	AX924778 Sequence
519	6	42.9	732	11	BV166869	6	42.9	935	6	AX416096	AX416096 Sequence
520	6	42.9	735	9	HS3326419	6	42.9	944	6	BD268172	BD268172 Proteins
521	6	42.9	737	1	UBA309620	6	42.9	944	8	AF410335	AF410335 Arabidops
522	6	42.9	738	8	RICSINE11	6	42.9	950	5	BC072975	BC072975 Xenopus l
523	6	42.9	741	8	ABI217108	6	42.9	952	5	AY485809	AY485809 Sebastee
524	6	42.9	743	6	BD148734	6	42.9	959	1	STYCRP	MJ3773 S.typhimuri
525	6	42.9	743	6	AX868672	6	42.9	959	1	ECOADAB	J02607 E.coli alkB
526	6	42.9	760	10	RNU46149	6	42.9	962	6	I34238	I34238 Sequence 14
527	6	42.9	761	1	AY594269	6	42.9	962	11	CNS061DF	AL400153 T7 end of
528	6	42.9	763	5	CR762111	6	42.9	968	5	EX934478	EX934478 Gallus ga
529	6	42.9	771	11	CNS06P43	6	42.9	974	8	AY085457	AY085457 Arabidops
530	6	42.9	773	5	AY100639	6	42.9	975	9	BC034158	BC034158 Homo sapi
531	6	42.9	778	11	BV098574	6	42.9	979	1	KPNCAP	MG8973 Klebsiella
532	6	42.9	778	11	BV155950	6	42.9	988	8	AB051210	AB051210 Chlamydom
533	6	42.9	785	11	BV018763	6	42.9	988	8	AR283967	AR283967 Sequence
534	6	42.9	791	11	AF167531	6	42.9	1001	6	AR283968	AR283968 Sequence
535	6	42.9	791	11	AF167531	6	42.9	1001	6	AR283968	AR283968 Sequence
536	6	42.9	793	1	AY594270	6	42.9	1008	3	AY324875	AY324875 Ropphido
537	6	42.9	794	11	BV061926	6	42.9	1008	3	SJRNASER	X70969 S.japonicum
538	6	42.9	810	1	UBA309589	6	42.9	1008	3	CQ786530	CQ786530 Sequence
539	6	42.9	811	11	BV063108	6	42.9	1026	6	CQ721383	CQ721383 Sequence
540	6	42.9	812	5	EX935386	6	42.9	1038	12	AY659153	AY659153 Synthetic
541	6	42.9	820	9	AF098948	6	42.9	1047	10	AF188007	AF188007 Mus muscu
542	6	42.9	830	6	AB448175	6	42.9	1054	10	AF032714	AF032714 Mus muscu
543	6	42.9	837	9	HS0801617	6	42.9	1054	11	G05872	G05872 human SYS W
544	6	42.9	841	5	CR385362	6	42.9	1060	8	S75714	S75714 TRK2-membra
545	6	42.9	843	8	AK062643	6	42.9	1077	5	AF407126	AF407126 Motacilla
546	6	42.9	844	11	BV044376	6	42.9	1089	5	AF407129	AF407129 Carduelis
547	6	42.9	848	8	AK118647	6	42.9	1089	5	CQ574854	CQ574854 Sequence
548	6	42.9	852	1	UBA309596	6	42.9	1113	5	AF407123	AF407123 Amblyospi
549	6	42.9	859	5	EX935549	6	42.9	1113	5	AY324296	AY324296 Emblema p
550	6	42.9	862	6	AX924618	6	42.9	1122	6	BD164479	BD164479 Novel pol
551	6	42.9	863	1	UBA309592	6	42.9	1122	6	AX123262	AX123262 Sequence
552	6	42.9	865	6	BD148826	6	42.9	1127	1	ECOCRP	J01598 E.coli crp
553	6	42.9	866	6	AX868764	6	42.9	1140	6	CQ804096	CQ804096 Sequence
554	6	42.9	866	1	UBA309575	6	42.9	1140	6	AX507305	AX507305 Sequence
555	6	42.9	866	1	UBA309577	6	42.9	1140	6	AX651312	AX651312 Sequence
556	6	42.9	868	6	AX414763	6	42.9	1140	8	AY090330	AY090330 Arabidops
557	6	42.9	870	1	UBA309621	6	42.9	1163	6	AX416056	AX416056 Sequence
558	6	42.9	871	10	BC038681	6	42.9	1164	1	AB089856	AB089856 Bacillus
559	6	42.9	875	10	AF098949	6	42.9	1170	8	MPU14948	MPU14948 Macrophonin
560	6	42.9	876	9	BC003185	6	42.9	1173	1	TMPGK3	X75437 T.maritima
561	6	42.9	880	6	CQ414355	6	42.9	1174	8	SCYXR049C	Z28274 S.cerevisia
562	6	42.9	881	1	KFN278967	6	42.9	1175	8	AF178951	AF178951 Zea mays
563	6	42.9	882	1	AY064699	6	42.9	1212	5	HS096633	HS096633 Homo sapien
564	6	42.9	882	5	BC073047	6	42.9	1212	5	BC058047	BC058047 Dario rer
565	6	42.9	891	5	EX936056	6	42.9	1229	1	AY663974	AY663974 Unculture
566	6	42.9	892	6	CQ491052	6	42.9	1239	1	AY663974	AY663974 Unculture
567	6	42.9	892	6	CQ496912	6	42.9	1245	8	AK058361	AK058361 Oryza sat
568	6	42.9	895	1	UBA309651	6	42.9	1269	1	AY664182	AY664182 Unculture
569	6	42.9	895	1	UBA309605	6	42.9	1293	3	AY116878	AY116878 Heronimus
570	6	42.9	897	1	UBA309631	6	42.9	1293	3	S81932	S81932 Dlx-3-Dista
571	6	42.9	897	1	UBA309631	6	42.9	1301	1	TFE012661	TFE012661 Thiobacil
572	6	42.9	901	1	UBA309640	6	42.9	1306	1	ECOCRA	MJ3770 Salmonella
573	6	42.9	902	1	UBA309627	6	42.9	1324	1	ECOADAA	MJ0211 E.coli ada
574	6	42.9	902	1	UBA309645	6	42.9	1324	1	ECOADAA	MJ0211 E.coli ada
575	6	42.9	903	10	BC059092	6	42.9	1331	9	AK026091	AK026091 Homo sapi
576	6	42.9	904	1	UBA309650	6	42.9	1336	6	BD130224	BD130224 Human sig
577	6	42.9	907	1	UBA309606	6	42.9	1351	6	AX773727	AX773727 Sequence
578	6	42.9	907	1	UBA309619	6	42.9	1356	10	AF336041	AF336041 Rattus no
579	6	42.9	908	1	UBA309622	6	42.9	1366	5	AY208828	AY208828 Rhapiceph
580	6	42.9	908	1	UBA309612	6	42.9	1366	5	CR352521	CR352521 Gallus ga
581	6	42.9	909	1	UBA309614	6	42.9	1378	6	AX575594	AX575594 Sequence
582	6	42.9	909	1	UBA309629	6	42.9	1383	6	CQ645924	CQ645924 Sequence
583	6	42.9	909	1	UBA309632	6	42.9	1386	6	AX607876	AX607876 Sequence
584	6	42.9	909	1	UBA309647	6	42.9	1387	8	AK069993	AK069993 Oryza sat
585	6	42.9	910	1	UBA309611	6	42.9	1391	8	AY045612	AY045612 Arabidops
586	6	42.9	911	1	UBA309611	6	42.9	1410	5	EX930205	EX930205 Gallus ga
587	6	42.9	915	4	AF232218	6	42.9	1412	8	AK101684	AK101684 Oryza sat
588	6	42.9	915	3	AY071042	6	42.9	1420	8	AK107624	AK107624 Oryza sat
589	6	42.9	915	3	CR385645	6	42.9	1433	5	CR48138	CR48138 Xenopus t
590	6	42.9	919	5	CR385645	6	42.9	1455	3	PUFFC4	UI3883 Bradysea hy

C 662	6	42.9	1458	3	DME295625	735	6	42.9	1893	14	AF239269	AF239269 Avian inf
C 663	6	42.9	1467	3	AV264367	736	6	42.9	1893	14	AF239270	AF239270 Avian inf
C 664	6	42.9	1469	9	BC016149 Homo sapi	737	6	42.9	1893	14	AF239271	AF239271 Avian inf
C 665	6	42.9	1472	9	HSPAX71	738	6	42.9	1893	14	AF239272	AF239272 Avian inf
C 666	6	42.9	1473	3	TBR308033	739	6	42.9	1893	14	AF239273	AF239273 Avian inf
C 667	6	42.9	1473	3	TBR308034	740	6	42.9	1893	14	AF239274	AF239274 Avian inf
C 668	6	42.9	1473	3	TBR308036	741	6	42.9	1893	14	AF239275	AF239275 Avian inf
C 669	6	42.9	1473	3	AV526243	742	6	42.9	1893	14	AF239276	AF239276 Avian inf
C 670	6	42.9	1480	1	SPU20078	743	6	42.9	1893	14	AF239277	AF239277 Avian inf
C 671	6	42.9	1483	3	RAC8MENA	744	6	42.9	1893	14	AF239278	AF239278 Avian inf
C 672	6	42.9	1485	4	AF304106	745	6	42.9	1893	14	AF239279	AF239279 Avian inf
C 673	6	42.9	1521	5	GGYAP25	746	6	42.9	1893	14	AF239280	AF239280 Avian inf
C 674	6	42.9	1522	5	AX393569	747	6	42.9	1893	14	AF239281	AF239281 Avian inf
C 675	6	42.9	1527	1	NMU19580	748	6	42.9	1893	14	AF239282	AF239282 Avian inf
C 676	6	42.9	1527	1	AX564234	749	6	42.9	1893	14	AF239283	AF239283 Avian inf
C 677	6	42.9	1554	6	AX564234	750	6	42.9	1893	14	AF239284	AF239284 Avian inf
C 678	6	42.9	1601	8	AX087768	751	6	42.9	1893	14	AF239285	AF239285 Avian inf
C 679	6	42.9	1610	5	BC048029	752	6	42.9	1893	14	AF239286	AF239286 Avian inf
C 680	6	42.9	1635	6	CQ576231	753	6	42.9	1893	14	AF239287	AF239287 Avian inf
C 681	6	42.9	1645	11	G07197	754	6	42.9	1893	14	AF239288	AF239288 Avian inf
C 682	6	42.9	1653	3	AF115255	755	6	42.9	1893	14	AF239289	AF239289 Avian inf
C 683	6	42.9	1654	6	BD269771	756	6	42.9	1893	14	AF239290	AF239290 Avian inf
C 684	6	42.9	1658	6	BD155889	757	6	42.9	1893	14	AF239291	AF239291 Avian inf
C 685	6	42.9	1658	6	AX076003	758	6	42.9	1893	14	AF239292	AF239292 Avian inf
C 686	6	42.9	1658	9	AX001096	759	6	42.9	1893	14	AF239293	AF239293 Avian inf
C 687	6	42.9	1671	5	BC065465	760	6	42.9	1893	14	AF239294	AF239294 Avian inf
C 688	6	42.9	1696	9	HSM802552	761	6	42.9	1893	14	AF239295	AF239295 Avian inf
C 689	6	42.9	1726	6	BD155768	762	6	42.9	1893	14	AF239296	AF239296 Avian inf
C 690	6	42.9	1726	6	AX875797	763	6	42.9	1893	14	AF239297	AF239297 Avian inf
C 691	6	42.9	1726	6	AX000984	764	6	42.9	1893	14	AF239298	AF239298 Avian inf
C 692	6	42.9	1731	6	AX449702	765	6	42.9	1893	14	AF239299	AF239299 Avian inf
C 693	6	42.9	1736	5	AJ719572	766	6	42.9	1893	14	AF239300	AF239300 Avian inf
C 694	6	42.9	1740	5	BC066405	767	6	42.9	1893	14	AF239301	AF239301 Avian inf
C 695	6	42.9	1740	8	AX099167	768	6	42.9	1893	14	AF239302	AF239302 Avian inf
C 696	6	42.9	1748	1	AB126576	769	6	42.9	1893	14	AF239303	AF239303 Avian inf
C 697	6	42.9	1749	1	AB126562	770	6	42.9	1893	14	AF239304	AF239304 Avian inf
C 698	6	42.9	1749	1	AB126568	771	6	42.9	1893	14	AF239305	AF239305 Avian inf
C 699	6	42.9	1749	1	AB126569	772	6	42.9	1893	14	AF239306	AF239306 Avian inf
C 700	6	42.9	1749	1	AB126572	773	6	42.9	1893	14	AF239307	AF239307 Avian inf
C 701	6	42.9	1749	1	AB126573	774	6	42.9	1893	14	AF239308	AF239308 Avian inf
C 702	6	42.9	1749	1	AB126574	775	6	42.9	1893	14	AF239309	AF239309 Avian inf
C 703	6	42.9	1763	8	AS077765	776	6	42.9	1893	14	AF239310	AF239310 Avian inf
C 704	6	42.9	1765	6	AX506063	777	6	42.9	1893	14	AF239311	AF239311 Avian inf
C 705	6	42.9	1781	8	AB051206	778	6	42.9	1893	14	AF239312	AF239312 Avian inf
C 706	6	42.9	1787	1	AB126575	779	6	42.9	1893	14	AF239313	AF239313 Avian inf
C 707	6	42.9	1802	6	AX440493	780	6	42.9	1893	14	AF239314	AF239314 Avian inf
C 708	6	42.9	1802	8	AX072106	781	6	42.9	1893	14	AF239315	AF239315 Avian inf
C 709	6	42.9	1813	1	AB126571	782	6	42.9	1893	14	AF239316	AF239316 Avian inf
C 710	6	42.9	1814	1	AB126535	783	6	42.9	1893	14	AF239317	AF239317 Avian inf
C 711	6	42.9	1814	1	AB126536	784	6	42.9	1893	14	AF239318	AF239318 Avian inf
C 712	6	42.9	1814	1	AB126538	785	6	42.9	1893	14	AF239319	AF239319 Avian inf
C 713	6	42.9	1814	1	AB126539	786	6	42.9	1893	14	AF239320	AF239320 Avian inf
C 714	6	42.9	1814	1	AB126540	787	6	42.9	1893	14	AF239321	AF239321 Avian inf
C 715	6	42.9	1814	1	AB126577	788	6	42.9	1893	14	AF239322	AF239322 Avian inf
C 716	6	42.9	1815	1	AB126534	789	6	42.9	1893	14	AF239323	AF239323 Avian inf
C 717	6	42.9	1815	1	AB126537	790	6	42.9	1893	14	AF239324	AF239324 Avian inf
C 718	6	42.9	1815	8	AY242385	791	6	42.9	1893	14	AF239325	AF239325 Avian inf
C 719	6	42.9	1815	9	HUMFKBP25A	792	6	42.9	1893	14	AF239326	AF239326 Avian inf
C 720	6	42.9	1817	4	BOVKAD	793	6	42.9	1893	14	AF239327	AF239327 Avian inf
C 721	6	42.9	1818	8	AX128390	794	6	42.9	1893	14	AF239328	AF239328 Avian inf
C 722	6	42.9	1837	8	SCALDEH	795	6	42.9	1893	14	AF239329	AF239329 Avian inf
C 723	6	42.9	1840	6	CQ783317	796	6	42.9	1893	14	AF239330	AF239330 Avian inf
C 724	6	42.9	1840	6	BD127585	797	6	42.9	1893	14	AF239331	AF239331 Avian inf
C 725	6	42.9	1840	9	AK075217	798	6	42.9	1893	14	AF239332	AF239332 Avian inf
C 726	6	42.9	1842	6	AR269483	799	6	42.9	1893	14	AF239333	AF239333 Avian inf
C 727	6	42.9	1843	10	AF131949	800	6	42.9	1893	14	AF239334	AF239334 Avian inf
C 728	6	42.9	1845	9	BC026678	801	6	42.9	1893	14	AF239335	AF239335 Avian inf
C 729	6	42.9	1866	9	BC052246	802	6	42.9	1893	14	AF239336	AF239336 Avian inf
C 730	6	42.9	1876	9	BC003598	803	6	42.9	1893	14	AF239337	AF239337 Avian inf
C 731	6	42.9	1878	8	BT002217	804	6	42.9	1893	14	AF239338	AF239338 Avian inf
C 732	6	42.9	1890	6	AX714058	805	6	42.9	1893	14	AF239339	AF239339 Avian inf
C 733	6	42.9	1890	9	AX056121	806	6	42.9	1893	14	AF239340	AF239340 Avian inf
C 734	6	42.9	1892	14	AF239282	807	6	42.9	1893	14	AF239341	AF239341 Avian inf

808	6	42.9	2254	6	CQ721114	Sequence	881	6	42.9	2727	9	AF150734	Homo sapi
809	6	42.9	2262	6	CQ715533	Sequence	882	6	42.9	2728	6	BD156421	Primer fo
c 810	6	42.9	2271	6	CQ602048	Sequence	883	6	42.9	2728	6	AX876981	Sequence
811	6	42.9	2272	6	AX406029	Sequence	884	6	42.9	2728	8	AY001555	Homo sapi
812	6	42.9	2272	9	HSPAX7M		885	6	42.9	2740	8	AY081293	Arabidops
813	6	42.9	2285	8	AY050954		886	6	42.9	2755	9	BC030686	Homo sapi
814	6	42.9	2288	10	BC025608		887	6	42.9	2769	6	AX306106	Sequence
815	6	42.9	2289	3	AF382333	Trypanoso	888	6	42.9	2769	10	MMGRBBP	M.musculus
816	6	42.9	2297	9	BC004149	Homo sapi	889	6	42.9	2772	10	RRU30381	Rattus norv
817	6	42.9	2298	9	HSM801202		890	6	42.9	2773	14	AY502936	Tomato le
818	6	42.9	2301	10	AF316549		c 891	6	42.9	2775	5	BC076544	Danio rer
c 819	6	42.9	2305	3	AX113238		892	6	42.9	2775	10	BC047214	Mus muscu
820	6	42.9	2319	6	E021176	DNA sequenc	893	6	42.9	2806	6	CQ719943	Sequence
c 821	6	42.9	2331	3	AX113471		894	6	42.9	2806	8	AX120321	Oryza sat
c 822	6	42.9	2338	3	AF081950		895	6	42.9	2809	6	AX748342	Sequence
823	6	42.9	2345	9	AK096392	Dictyoste	896	6	42.9	2809	9	AK093861	Homo sapi
824	6	42.9	2358	6	C0804152		897	6	42.9	2809	9	BC015014	Homo sapi
c 825	6	42.9	2381	5	AJ720916		898	6	42.9	2833	9	BC029350	Homo sapi
c 826	6	42.9	2389	8	ATHC10F		899	6	42.9	2838	9	AB066623	Homo sapi
827	6	42.9	2389	8	ATHC10F		900	6	42.9	2858	9	AF039019	Homo sapi
828	6	42.9	2392	8	ATHBLA10C		901	6	42.9	2892	6	BD156467	Primer fo
829	6	42.9	2395	8	ATHITA01		902	6	42.9	2892	6	AX877068	Sequence
830	6	42.9	2412	8	D63463		903	6	42.9	2892	9	AK001593	Homo sapi
831	6	42.9	2412	8	ATHCH10E		904	6	42.9	2901	8	AY056123	Arabidops
832	6	42.9	2412	8	ATHES0G		905	6	42.9	2907	5	AY174870	Pseudople
c 833	6	42.9	2421	6	AX433126		c 906	6	42.9	2918	4	AY147192	
834	6	42.9	2426	10	MMU80078		c 907	6	42.9	2923	8	ATCADH	X77943 A.thal
c 835	6	42.9	2429	5	SMOMT003B		c 908	6	42.9	2930	8	AY122272	Zea mays
c 836	6	42.9	2429	5	SMOMT003D		909	6	42.9	2952	9	AF432210	Homo sapi
c 837	6	42.9	2429	5	SMOMT003E		910	6	42.9	2954	6	CQ593861	Sequence
c 838	6	42.9	2429	5	SMOMT003F		c 911	6	42.9	2955	6	BD160569	Primer fo
c 839	6	42.9	2429	5	SMOMT003G		c 912	6	42.9	2955	6	AX883855	Sequence
c 840	6	42.9	2429	5	SMOMT003H		c 913	6	42.9	2955	6	AK024298	Homo sapi
c 841	6	42.9	2429	5	SMOMT003I		914	6	42.9	2960	6	AX416482	Sequence
c 842	6	42.9	2429	5	SMOMT003J		915	6	42.9	2962	9	BC050260	Homo sapi
c 843	6	42.9	2429	5	SMOMT003K		c 916	6	42.9	2970	3	DDU38197	
c 844	6	42.9	2437	6	I12324		c 917	6	42.9	2983	10	BC008552	Mus muscu
c 845	6	42.9	2437	6	I70227		918	6	42.9	2994	6	AX447790	Sequence
c 846	6	42.9	2437	6	AR371464		c 919	6	42.9	3005	6	AX714290	Sequence
c 847	6	42.9	2437	9	HUMSRDA		920	6	42.9	3005	9	AK056521	Homo sapi
c 848	6	42.9	2443	1	REI556146		921	6	42.9	3007	5	AF006488	Danio rer
c 849	6	42.9	2462	8	AY048200		922	6	42.9	3007	10	BC026144	Mus muscu
c 850	6	42.9	2464	6	CQ719296		923	6	42.9	3010	10	BC006035	Mus muscu
c 851	6	42.9	2465	5	BC076414		c 924	6	42.9	3015	6	CQ598457	Sequence
852	6	42.9	2469	8	D63461		925	6	42.9	3016	6	BD175121	Androgen
853	6	42.9	2488	10	BC023291		926	6	42.9	3016	6	CQ789324	Sequence
854	6	42.9	2490	5	SMOBNHE		927	6	42.9	3016	6	AX492926	Sequence
c 855	6	42.9	2491	1	ECRCFGENE		c 928	6	42.9	3017	1	AF397144	Listeria
c 856	6	42.9	2491	5	AY485821		929	6	42.9	3023	9	AB056106	Homo sapi
c 857	6	42.9	2538	9	BC040145		930	6	42.9	3023	9	BC050296	Homo sapi
c 858	6	42.9	2562	6	AX927175		931	6	42.9	3032	9	BSA236885	Homo sapi
859	6	42.9	2570	6	BD160561		932	6	42.9	3048	1	PSEIAM	J03871 P.amylodera
860	6	42.9	2570	6	AX883843		c 933	6	42.9	3056	5	BC060902	Danio rer
861	6	42.9	2570	9	AK024291		c 934	6	42.9	3060	6	CQ595958	Sequence
862	6	42.9	2582	6	H5U23946		935	6	42.9	3077	9	BSA130894	Homo sapi
c 863	6	42.9	2582	6	AX714457		936	6	42.9	3089	9	BC002957	Homo sapi
c 864	6	42.9	2582	9	AK056791		937	6	42.9	3094	6	AF103802	Homo sapi
865	6	42.9	2593	5	AJ719513		938	6	42.9	3116	6	CQ716398	Sequence
866	6	42.9	2625	1	PSEIAMA		c 939	6	42.9	3129	8	AY080588	Arabidops
867	6	42.9	2625	6	AI0909		940	6	42.9	3135	9	AF091263	Homo sapi
868	6	42.9	2625	6	AK365014		941	6	42.9	3141	9	F325326S14	
869	6	42.9	2625	6	AX089532		942	6	42.9	3144	6	CQ574853	Sequence
c 870	6	42.9	2631	10	BC058852		c 943	6	42.9	3144	6	AB074498	Homo sapi
871	6	42.9	2646	9	AF093250	Homo sapi	c 944	6	42.9	3152	10	RAT5RHPH	J05214 Rat 5'-nucl
872	6	42.9	2653	8	AY062555		945	6	42.9	3165	5	TILGH2X	M9765 Tilapia nil
873	6	42.9	2667	6	CQ581817		946	6	42.9	3180	8	AK099512	Oryza sat
874	6	42.9	2670	10	BC070910	Rattus no	c 947	6	42.9	3188	3	AY014405	Anopheles
875	6	42.9	2683	1	ABCALDH		948	6	42.9	3189	6	AX076993	Sequence
c 876	6	42.9	2696	5	BC054680	Danio rer	949	6	42.9	3189	6	AX113966	Sequence
877	6	42.9	2704	1	AJ585346		950	6	42.9	3196	5	AJ719417	Gallus ga
878	6	42.9	2706	6	CQ594119		951	6	42.9	3208	6	BD249920	human
879	6	42.9	2715	6	AK375386		c 952	6	42.9	3210	1	AF175295	Vibrio ch
880	6	42.9	2723	9	HSM804929		c 953	6	42.9	3221	5	AJ719727	Gallus ga

```

c 954      6 42.9 3239 10 BC025581
          6 42.9 3250 5 BC068779
          6 42.9 3266 9 BC022219
          6 42.9 3268 10 BC024074
          6 42.9 3280 9 AK122945
          6 42.9 3284 9 AK095623
          6 42.9 3306 9 AB094094
          6 42.9 3320 3 GIU93353
          6 42.9 3336 6 AR365012
          6 42.9 3337 8 CRU13168
          6 42.9 3340 6 CO785752
          6 42.9 3358 8 AK025223
          6 42.9 3361 9 AK025223
          6 42.9 3420 6 AK076995
          6 42.9 3420 6 AX113968
          6 42.9 3427 6 CO728177
          6 42.9 3452 8 TA288RITS
          6 42.9 3464 6 AK144982
          6 42.9 3464 6 AX050470
          6 42.9 3464 9 HUMFOL5
          6 42.9 3474 5 AF038425
          6 42.9 3487 6 AX833295
          6 42.9 3487 9 AK094914
          6 42.9 3502 6 AR448004
          6 42.9 3516 1 AB090359
          6 42.9 3546 5 TRU345039
          6 42.9 3546 6 AR029518
          6 42.9 3546 6 AR098471
          6 42.9 3546 6 I41431
          6 42.9 3546 6 AR494980
          6 42.9 3546 6 AX441396
          6 42.9 3546 6 AX453892
          6 42.9 3623 6 CO576768
          6 42.9 3690 5 AY167041
          6 42.9 3700 8 AY536888
          6 42.9 3702 8 PPA544768
          6 42.9 3709 3 U01842
          6 42.9 3709 6 AR240582
          6 42.9 3709 6 AR240384
          6 42.9 3717 3 DMVAS1HE
          6 42.9 3723 9 HSM808835
          6 42.9 3765 10 RNLJ25
          6 42.9 3792 6 CO585768
          6 42.9 3799 6 AX743766
          6 42.9 3799 8 YSCTRK2Q
          6 42.9 3850 5 BC077134
          6 42.9 3874 10 AB093260

          BC025581 Mus muscu
          BC068779 Xenopus l
          BC022219 Homo sapi
          BC024074 Mus muscu
          AK122945 Homo sapi
          AK095623 Homo sapi
          AB094094 Homo sapi
          GIU93353 Giardia int
          AR365012 Sequence
          CRU13168 Chlamydomon
          CO785752 Sequence
          AK025223 Arabidopsi
          AK076995 Sequence
          AX113968 Sequence
          CO728177 Sequence
          Y07979 T.aequale 2
          AK144982 Sequence
          AX050470 Sequence
          J00139 Human dihyd
          AF038425 Danio rer
          AX833295 Sequence
          AK094914 Homo sapi
          AR448004 Sequence
          AB090359 Pectobact
          AJ345039 Takifugu
          AR029518 Sequence
          AR098471 Sequence
          I41431 Sequence 27
          AR494980 Sequence
          AX441396 Sequence
          AX453892 Sequence
          CO576768 Sequence
          AY167041 Pseudople
          AY536888 Arabidops
          A5544768 Physcomit
          U01842 Drosophila
          AR240582 Sequence
          AR240384 Sequence
          X82641 D.melanogas
          BX648684 Homo sapi
          X74226 R.norvegicu
          CO585768 Sequence
          AX743766 Sequence
          M65215 S.cerevisia
          BC077134 Danio rer
          AB093260 Mus muscu

ALIGNMENTS
RESULT 1
A74835 A74835 136 bp DNA linear PAT 15-OCT-1999
LOCUS Sequence 521 from Patent WO9401548.
DEFINITION A74835
ACCESSION A74835
VERSION A74835.1 GI:6064849
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 136)
AUTHORS Sibson,D.R. and Gross,J.
TITLES HUMAN NUCLEIC ACID FRAGMENTS, ISOLATED FROM BRAIN ADRENAL TISSUE,
PLACENTA OR BONE NARROW
JOURNAL Patent: WO 9401548-A 521 20-JAN-1994;
MEDICAL RES COUNCIL (GB); SIBSON DAVID ROSS (GB)
FEATURES
    source
        Location/Qualifiers
            1..136
                /organism="unidentified"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32644"
ORIGIN

c 954      6 42.9 3239 10 BC025581
          6 42.9 3250 5 BC068779
          6 42.9 3266 9 BC022219
          6 42.9 3268 10 BC024074
          6 42.9 3280 9 AK122945
          6 42.9 3284 9 AK095623
          6 42.9 3306 9 AB094094
          6 42.9 3320 3 GIU93353
          6 42.9 3336 6 AR365012
          6 42.9 3337 8 CRU13168
          6 42.9 3340 6 CO785752
          6 42.9 3358 8 AK025223
          6 42.9 3361 9 AK025223
          6 42.9 3420 6 AK076995
          6 42.9 3420 6 AX113968
          6 42.9 3427 6 CO728177
          6 42.9 3452 8 TA288RITS
          6 42.9 3464 6 AK144982
          6 42.9 3464 6 AX050470
          6 42.9 3464 9 HUMFOL5
          6 42.9 3474 5 AF038425
          6 42.9 3487 6 AX833295
          6 42.9 3487 9 AK094914
          6 42.9 3502 6 AR448004
          6 42.9 3516 1 AB090359
          6 42.9 3546 5 TRU345039
          6 42.9 3546 6 AR029518
          6 42.9 3546 6 AR098471
          6 42.9 3546 6 I41431
          6 42.9 3546 6 AR494980
          6 42.9 3546 6 AX441396
          6 42.9 3546 6 AX453892
          6 42.9 3623 6 CO576768
          6 42.9 3690 5 AY167041
          6 42.9 3700 8 AY536888
          6 42.9 3702 8 PPA544768
          6 42.9 3709 3 U01842
          6 42.9 3709 6 AR240582
          6 42.9 3709 6 AR240384
          6 42.9 3717 3 DMVAS1HE
          6 42.9 3723 9 HSM808835
          6 42.9 3765 10 RNLJ25
          6 42.9 3792 6 CO585768
          6 42.9 3799 6 AX743766
          6 42.9 3799 8 YSCTRK2Q
          6 42.9 3850 5 BC077134
          6 42.9 3874 10 AB093260

          BC025581 Mus muscu
          BC068779 Xenopus l
          BC022219 Homo sapi
          BC024074 Mus muscu
          AK122945 Homo sapi
          AK095623 Homo sapi
          AB094094 Homo sapi
          GIU93353 Giardia int
          AR365012 Sequence
          CRU13168 Chlamydomon
          CO785752 Sequence
          AK025223 Arabidopsi
          AK076995 Sequence
          AX113968 Sequence
          CO728177 Sequence
          Y07979 T.aequale 2
          AK144982 Sequence
          AX050470 Sequence
          J00139 Human dihyd
          AF038425 Danio rer
          AX833295 Sequence
          AK094914 Homo sapi
          AR448004 Sequence
          AB090359 Pectobact
          AJ345039 Takifugu
          AR029518 Sequence
          AR098471 Sequence
          I41431 Sequence 27
          AR494980 Sequence
          AX441396 Sequence
          AX453892 Sequence
          CO576768 Sequence
          AY167041 Pseudople
          AY536888 Arabidops
          A5544768 Physcomit
          U01842 Drosophila
          AR240582 Sequence
          AR240384 Sequence
          X82641 D.melanogas
          BX648684 Homo sapi
          X74226 R.norvegicu
          CO585768 Sequence
          AX743766 Sequence
          M65215 S.cerevisia
          BC077134 Danio rer
          AB093260 Mus muscu

us-09-736-250-5 (1-14) x A74835 (1-136)
Alignment Scores:
Pred. No.: 6.03e-08 Length: 136
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-09-736-250-5 (1-14) x A74835 (1-136)
Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 24 GAAGATAATGCTCAGAAAATGTGGTTCCTGTGTGGCACT 65
RESULT 2
A77814 A77814 136 bp DNA linear PAT 19-OCT-1999
LOCUS Sequence 521 from Patent EP0587279.
DEFINITION A77814
ACCESSION A77814
VERSION A77814.1 GI:6089479
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 136)
AUTHORS Sibson,D.R. and Hadfield,K.M.
TITLES HUMAN NUCLEIC ACID FRAGMENTS ISOLATED FROM BRAIN, ADRENAL TISSUE,
PLACENTA OR BONE NARROW AND THEIR USE
JOURNAL Patent: EP 0587279-A 521 16-MAR-1994;
MEDICAL RES COUNCIL (GB)
FEATURES
    source
        Location/Qualifiers
            1..136
                /organism="unidentified"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32644"
ORIGIN

Alignment Scores:
Pred. No.: 6.03e-08 Length: 136
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-09-736-250-5 (1-14) x A77814 (1-136)
Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 24 GAAGATAATGCTCAGAAAATGTGGTTCCTGTGTGGCACT 65
RESULT 3
CQ712652 CQ712652 288 bp DNA linear PAT 03-FEB-2004
LOCUS Sequence 57578 from Patent WO02070737.
DEFINITION CQ712652
ACCESSION CQ712652
VERSION CQ712652.1 GI:42273509
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Liew,C.C., Marshall,W.E. and Zhang,H.
TITLES Compositions and methods relating to osteoarthritis
JOURNAL Patent: WO 02070737-A 57578 12-SEP-2002;
MEDICAL RES COUNCIL (CA)
FEATURES
    source
        Location/Qualifiers
            1..288
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
ORIGIN
```


ORIGIN

Alignment Scores:
Pred. No.: 1.26e-07 Length: 288
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-736-250-5 (1-14) x CQ712652 (1-288)

Qy 1 GluAspAenValSerGluAenValGlySerValCysGlyThr 14
Db 63 GAAGATAATGCTCAGAAAATGTGGTTCTGTGTGGCACT 104

RESULT 4
LOCUS CQ675890 350 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 20816 from Patent WO02070737.
ACCESSION CQ675890
VERSION CQ675890.1 GI:42180044
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Liew, C.C., Marshall, W.E. and Zhang, H.
TITLE Compositions and methods relating to osteoarthritis
JOURNAL Patent: WO 02070737-A 20816 12-SEP-2002;
Chondrogene Inc. (CA)
FEATURES
source Location/Qualifiers
1..350
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Alignment Scores:
Pred. No.: 1.52e-07 Length: 350
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-736-250-5 (1-14) x CQ675890 (1-350)

Qy 1 GluAspAenValSerGluAenValGlySerValCysGlyThr 14
Db 129 GAAGATAATGCTCAGAAAATGTGGTTCTGTGTGGCACT 170

RESULT 5
LOCUS AX397198/C 444 bp DNA linear PAT 18-MAY-2002
DEFINITION Sequence 1413 from Patent WO0212328.
ACCESSION AX397198
VERSION AX397198.1 GI:21067945
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS King, G.E., Meagher, M.J., Xu, J. and Secrist, H.
TITLE Compositions and methods for the therapy and diagnosis of colon cancer
JOURNAL Patent: WO 0212328-A 1413 14-FEB-2002;
CORIXA CORPORATION (US)
FEATURES
source Location/Qualifiers
1..444
/organism="Homo sapiens"

/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Alignment Scores:
Pred. No.: 1.92e-07 Length: 444
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-736-250-5 (1-14) x AX397198 (1-444)

Qy 1 GluAspAenValSerGluAenValGlySerValCysGlyThr 14
Db 436 GAAGATAATGCTCAGAAAATGTGGTTCTGTGTGGCACT 395

RESULT 6
LOCUS AX198885 447 bp DNA linear PAT 29-AUG-2001
DEFINITION Sequence 1340 from Patent WO0151513.
ACCESSION AX198885
VERSION AX198885.1 GI:15389211
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Algate, P.A.
TITLE Ovarian tumor-associated sequences
JOURNAL Patent: WO 0151513-A 1340 19-JUL-2001;
CORIXA CORPORATION (US)
FEATURES
source Location/Qualifiers
1..447
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Alignment Scores:
Pred. No.: 1.94e-07 Length: 447
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-736-250-5 (1-14) x AX198885 (1-447)

Qy 1 GluAspAenValSerGluAenValGlySerValCysGlyThr 14
Db 93 GAAGATAATGCTCAGAAAATGTGGTTCTGTGTGGCACT 134

RESULT 7
LOCUS AX209412 447 bp DNA linear PAT 31-AUG-2001
DEFINITION Sequence 1252 from Patent WO0157207.
ACCESSION AX209412
VERSION AX209412.1 GI:15423835
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Algate, P.A. and Mannion, J.
TITLE Compositions and methods for the therapy and diagnosis of ovarian cancer
JOURNAL Patent: WO 0157207-A 1252 09-AUG-2001;
CORIXA CORPORATION (US)
FEATURES
source Location/Qualifiers

```

source
1. .447
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Alignment Scores:
Pred. No.: 1.94e-07 Length: 447
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-736-250-5 (1-14) x AX209412 (1-447)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 93 GAAGATAATGCTCAGAAAATGGGGTCTGTGTGGCACT 134

RESULT 8
BVI80201/c
LOCUS
DEFINITION
sgm108417 Human DNA (Sequenom) Homo sapiens STS genomic, sequence
tagged site.
ACCESSION
BVI80201
VERSION
BVI80201.1 GI:48017195
KEYWORDS
STS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 601)
AUTHORS
Nelson,R.M., Marnellos,G., Kammerer,S., Hoyal,C.R., Shi,M.M.,
Cantor,C.R. and Braun,A.
TITLE
Large-Scale Validation of Single Nucleotide Polymorphisms in Gene
Regions
JOURNAL
Genome Res. (2004) In press
COMMENT
Contact: Andreas Braun
Pharmaceuticals division
Sequenom, Inc.
3595 John Hopkins Court, San Diego, CA 92121, USA
Tel: 18582029018
Fax: 18582029020
Email: abraun@sequenom.com
Primer A: No primer sequence submitted
Primer B: No primer sequence submitted
STS size: 601.
Location/Qualifiers
1. .601
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone_lib="Human DNA (Sequenom)"
<1. .>601

STS
ORIGIN
Alignment Scores:
Pred. No.: 2.59e-07 Length: 601
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 11 Gaps: 0

US-09-736-250-5 (1-14) x BVI80201 (1-601)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 327 GAAGATAATGCTCAGAAAATGGGGTCTGTGTGGCACT 286

RESULT 9

source
1. .447
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Alignment Scores:
Pred. No.: 1.94e-07 Length: 447
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-736-250-5 (1-14) x BD079737 (1-804)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 301 GAAGATAATGCTCAGAAAATGGGGTCTGTGTGGCACT 260

RESULT 10
CR541783
LOCUS
DEFINITION
Homo sapiens full open reading frame cDNA clone RZPD0834E0730D for
gene CCNI, cyclin I; complete cds, without stopcodon.
ACCESSION
CR541783
VERSION
CR541783.1 GI:49456522
KEYWORDS
Full ORF shuttle clone, Gateway(TM), complete cds.
SOURCE
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1131)
AUTHORS
Halleck,A., Ebert,L., Mkoundinya,M., Schick,M., Eisenstein,S.,
Neubert,P., Kstrang,K., Schatten,R., Shen,B., Henze,S., Mar,W.,

source
1. .804
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN
Alignment Scores:
Pred. No.: 3.45e-07 Length: 804
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-736-250-5 (1-14) x BD079737 (1-804)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 301 GAAGATAATGCTCAGAAAATGGGGTCTGTGTGGCACT 260

RESULT 10
CR541783
LOCUS
DEFINITION
Homo sapiens full open reading frame cDNA clone RZPD0834E0730D for
gene CCNI, cyclin I; complete cds, without stopcodon.
ACCESSION
CR541783
VERSION
CR541783.1 GI:49456522
KEYWORDS
Full ORF shuttle clone, Gateway(TM), complete cds.
SOURCE
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1131)
AUTHORS
Halleck,A., Ebert,L., Mkoundinya,M., Schick,M., Eisenstein,S.,
Neubert,P., Kstrang,K., Schatten,R., Shen,B., Henze,S., Mar,W.,

```

Korn, B., Zuo, D., Hu, Y. and LaBaer, J.
Cloning of human full open reading frames in Gateway(TM) system
entry vector (pDONR201)
2 (bases 1 to 1131)
Halleck, A., Ebert, L., Moundinya, M., Schick, M., Eisenstein, S.,
Neubert, P., Kstrang, K., Schatten, R., Shen, B., Henze, S., Mat, W.,
Korn, B., Zuo, D., Hu, Y. and LaBaer, J.
Direct Submission
Submitted (28-JUN-2004) RZPD Deutsches Ressourcenzentrum fuer
Genomforschung GmbH, Im Neuenheimer Feld 580, D-69120 Heidelberg,
Germany
RZPD: RZPD0834E0730D, ORFNO 3592
www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=RZPD0834E0730D RZPDLIB;
Human Full ORF Clones Gateway(TM) - RZPD (kan-resist.) RZPD LIB NO.
834
www.rzpd.de/cgi-bin/products/showLib.pl.cgi?response?libNo=834
Contact: Inge Arlart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH,
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 100
Fax: +49 30 32639 111
www.rzpd.de
This clone is available from RZPD;
Contact RZPD (customer.service@rzpd.de) for further information.
Clone name at Harvard Institute of Proteomics
(www.hip.harvard.edu): FLH131015.01L
This CDS clone is part of a collection of human full ORF clones
jointly established and verified by the Harvard Institute of
Proteomics (HIP) and RZPD.
This CDS has been cloned without stopcodon.
The CDS has been inserted into pDONR201 via a BP Clonase(TM)
reaction. Additional sequence has been added in front of the start
codon: att. AAAAAA GCA GGC TCC ACC (ATG).
The last codon is followed by the 3' att site: GACCCAGCTTCTT. .att
The clone is validated by full sequence check.
Compared to the reference sequence NM 006835 (GI:17738314) we found
AA exchange(s) at position (first base of changed triplet):
223(arg->gly) 409(lys->arg)
Clone distribution: http://www.rzpd.de/products/orfclones/
Location/Qualifiers
1. .1131
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="RZPD0834E0730D"
/clone_lib="Human Full ORF Clones Gateway(TM) - RZPD"
/lab_host="DH5Alpha"
/note="vector: pDONR201, Site_1: attP1; Site_2: attP2"
1. .1131
/gene="CCNI"
1. .>1131
/gene="CCNI"
/codon_start=1
/protein_id="CAG46582.1"
/db_xref="GI:4945623"
/translation="MKFPGPLENORLSFLEKAITREAQMKVNRKMPNSQNVSPSQ
RDEVIMLAKLYQNFYPTFALASLLDGFATVKAHPKYLSCIALSCFFLAQTV
EDERIPVLKVLARDSFCGSCSSSEILRMERILDLRLWDLTATPLFLHFLHAIYS
TRPQLSLPKLSPSQHLAVTKQLLHCAQNLQFPGSGMLAMVSLWEKELIPDW
LSLFTLQLKQADSSQLIHCRLELVAHLSTLQSLPLNSVYVYRPLKHLTVTCDDGV
FRLHPSSVPGDFDKDSKPEVPVRGTAFAFHLPLAASGCKQTSTKRKBEMEVDFFY
DGIKRLYNEDNVSENVSGVCTGLSRQEGHASPFPPLQPVSM"

FEATURES

source
gene
CDS
ORIGIN
Alignment Scores:
Pred. No.: 4.82e-07 Length: 1131
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9

US-09-736-250-5 (1-14) x CR541783 (1-1131)
Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 1027 GAAGATAATCTCTCAGAAATGTGGTCTCTGTGTGGCACT 1068
RESULT 11
ARI45734
LOCUS ARI45734 1133 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 2 from patent US 6218115.
ACCESSION ARI45734
VERSION ARI45734.1 GI:15108923
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1133)
AUTHORS Nakamura, T.
TITLE Human cyclin I and genes encoding same
JOURNAL Patent: US 6218115-A 2 17-APR-2001;
FEATURES Location/Qualifiers
1. .1133
source /organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Alignment Scores:
Pred. No.: 4.83e-07 Length: 1133
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-09-736-250-5 (1-14) x ARI45734 (1-1133)
Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 1027 GAAGATAATCTCTCAGAAATGTGGTCTCTGTGTGGCACT 1068
RESULT 12
AR087353
LOCUS AR087353 1260 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 5 from patent US 5986055.
ACCESSION AR087353
VERSION AR087353.1 GI:10014116
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1260)
AUTHORS Yang M., Nandabalan, K. and Schultz, V. Peter.
TITLE CDK2 interactions
JOURNAL Patent: US 5986055-A 5 16-NOV-1999;
FEATURES Location/Qualifiers
source 1. .1260
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Alignment Scores:
Pred. No.: 5.36e-07 Length: 1260
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-09-736-250-5 (1-14) x AR087353 (1-1260)
Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14

```
Db 1027 GAAGATAATGCTCAGAAAATGGGGTTCTGTGTGGCACT 1068
|||||
RESULT 15
LOCUS AR380354 1260 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 899 from patent US 6607879.
ACCESSION AR380354
VERSION AR380354.1 GI:40087988
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1260)
AUTHORS Cocks, B.G., Stuart, S.G. and Seilhamer, J.J.
TITLE Compositions for the detection of blood cell and immunological
JOURNAL response gene expression
PATENT Patent: US 6607879-A 899 19-AUG-2003;
FEATURES
Location/Qualifiers
source 1..1260
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Alignment Scores:
Pred. No.: 5.36e-07 Length: 1260
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-09-736-250-5 (1-14) x AR380354 (1-1260)
Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
|||||
Db 1027 GAAGATAATGCTCAGAAAATGGGGTTCTGTGTGGCACT 1068
Search completed: February 11, 2005, 14:34:43
Job time : 348.55 secs

Db 1027 GAAGATAATGCTCAGAAAATGGGGTTCTGTGTGGCACT 1068
|||||
RESULT 13
LOCUS Q812312 1260 bp DNA linear PAT 24-MAY-2004
DEFINITION Sequence 64 from Patent WO2004038020.
ACCESSION Q812312
VERSION Q812312.1 GI:47601932
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Wittig, R., Poustka, A., Mollenhauer, J. and Schadendorf, D.
TITLE Target genes for the diagnosis and treatment of cancer
JOURNAL Patent: WO 2004038020-A 64 06-MAY-2004;
DEUTSCHES Krebsforschungszentrum Stiftung des oeffentlichen n Rechts
(DE)
FEATURES
Location/Qualifiers
source 1..1260
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
misc_feature 1..1260
/note="D50310"
ORIGIN
Alignment Scores:
Pred. No.: 5.36e-07 Length: 1260
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-09-736-250-5 (1-14) x Q812312 (1-1260)
Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
|||||
Db 1027 GAAGATAATGCTCAGAAAATGGGGTTCTGTGTGGCACT 1068
|||||
RESULT 14
LOCUS AR281918 1260 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 5 from patent US 6521412.
ACCESSION AR281918
VERSION AR281918.1 GI:29717848
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1260)
AUTHORS Yang, M., Nandabalan, K. and Schulz, V.P.
TITLE HsReq*1 and HsReq*2 proteins and use thereof to detect CDK2
JOURNAL Patent: US 6521412-A 5 18-FEB-2003;
FEATURES
Location/Qualifiers
source 1..1260
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Alignment Scores:
Pred. No.: 5.36e-07 Length: 1260
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-09-736-250-5 (1-14) x AR281918 (1-1260)
Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 11, 2005, 07:36:40 ; Search time 35.1969 Seconds
(without alignments)
2354.648 Million cell updates/sec

Title: US-09-736-250-5

Perfect score: 14

Sequence: 1 EDNVSENVGSVCGT 14

Scoring table:

OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Word size: 1

Total number of hits satisfying chosen parameters: 8760405

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/usPTO_spool/US09736250/runat_07022005_154941_20640/app_query.fasta_1.718
-DB=N_Geneseq_16Dec04 -QWTF=fastap -SUFFIX=oligo.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=1000 -DOCALLIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09736250 @CGN 1 1 586 @runat_07022005_154941_20640 -NCPU=6 -ICPU=3
-NO_MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : N_Geneseq_16Dec04:*

- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
- 6: geneseqn2002as:*
- 7: geneseqn2002bs:*
- 8: geneseqn2003as:*
- 9: geneseqn2003bs:*
- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004as:*
- 13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	14	100.0	136	2	AaQ76921 Human gen
c 2	14	100.0	351	8	AaD51549 Human BGA
3	14	100.0	389	10	AdK61066 Ovarian c
c 4	14	100.0	444	6	ABK45862 CDNA enco
5	14	100.0	447	4	AA525071 Human ova

6	14	100.0	447	5	AAH83716	Aah83716 Human ova
c 7	14	100.0	597	10	ADK61065	Adk61065 Ovarian c
c 8	14	100.0	804	2	AAX40003	Aax40003 Prostate
9	14	100.0	903	12	ADN01156	Adn01156 Human cel
10	14	100.0	1260	3	AAZ37836	Aaz37836 Human cyc
11	14	100.0	1260	6	ABK83672	Abk83672 Human cDN
12	14	100.0	1260	10	ADK61064	Adk61064 Ovarian c
13	14	100.0	1260	11	ADK61064	Adk61064 Ovarian cDN
14	14	100.0	1260	13	ADP13757	Adp13757 DNA encod
15	14	100.0	1328	2	AA773937	Aat773937 Breast ca
16	14	100.0	1384	8	ACC47339	Aac47339 Human pro
17	14	100.0	1493	2	AAZ41284	Aaz41284 Human nor
18	14	100.0	1651	9	AAZ57247	Aaz57247 Human CGD
19	14	100.0	1889	6	ABL87929	AbL87929 Human ova
20	14	100.0	1890	12	ADP10653	Adp10653 Reference
21	14	100.0	1890	13	ACN38124	Acn38124 Tumour-as
22	14	100.0	2146	5	ADL63082	Adl63082 Human ova
23	14	100.0	2755	5	ADL63374	Adl63374 Human ova
24	13	92.9	304	3	RAC25819	Rac25819 Human sec
25	8	57.1	791	6	ABQ37048	Abq37048 Oligonuc1
c 26	8	57.1	791	6	ABQ37049	Abq37049 Oligonuc1
27	8	57.1	796	6	ABQ34158	Abq34158 Oligonuc1
c 28	8	57.1	796	6	ABQ34159	Abq34159 Oligonuc1
29	7	50.0	135	2	AAQ76716	Aaq76716 Human gen
30	7	50.0	183	2	AAQ76715	Aaq76715 Human gen
c 31	7	50.0	293	12	ADQ19591	Adq19591 Human sof
32	7	50.0	420	8	ABX44645	Abx44645 Bovine ES
33	7	50.0	578	12	ACH79716	Ach79716 Human gen
c 34	7	50.0	840	8	ACF64409	Acf64409 Human IP1
c 35	7	50.0	845	9	ADA48912	Ada48912 Wheat gen
c 36	7	50.0	1023	12	ADO61772	Ado61772 Transcrip
c 37	7	50.0	1170	3	AAC39327	Aac39327 Arabidops
38	7	50.0	1226	6	ACA03904	AcA03904 cDNA upre
39	7	50.0	1226	12	ADL13381	Adl13381 Human ste
c 40	7	50.0	1287	3	AAC35385	Aac35385 Arabidops
41	7	50.0	1338	6	ABN79897	Abn79897 Fungal ZB
c 42	7	50.0	1428	9	AAD57460	Aad57460 Fruit fly
43	7	50.0	1671	4	ABL26107	AbL26107 Drosophil
c 44	7	50.0	1682	10	ADE25706	AdE25706 Human cDN
c 45	7	50.0	2321	8	ACA03913	AcA03913 cDNA down
c 46	7	50.0	3204	10	AB239157	Abz39157 N. gonorr
47	7	50.0	3573	13	ADF43795	Adf43795 Bacterial
48	7	50.0	3868	4	ABL26106	AbL26106 Drosophil
c 49	7	50.0	28170	6	ABA01447	AbA01447 Streptoco
c 50	7	50.0	92562	10	ADC85284	AdC85284 Human ITK
c 51	7	50.0	92563	9	ADA02804	AdA02804 Human ITK
c 52	7	50.0	92563	10	ADB72542	Adb72542 Human ITK
c 53	7	50.0	92563	12	ADM74399	Adm74399 Human car
c 54	6	42.9	19	3	AAZ72285	Aaz72285 Human bia
55	6	42.9	25	9	ACI50953	AcI50953 Human mic
56	6	42.9	25	12	ADP13757	Adp13757 Renal cel
57	6	42.9	33	2	AAV25500	Aav25500 Primer EV
c 58	6	42.9	41	6	ABK12099	Abk12099 Phytochro
c 59	6	42.9	60	6	ABN43375	Abn43375 Human spl
60	6	42.9	100	8	ACD70096	AcD70096 E. coli K
c 61	6	42.9	108	4	AAI26919	Aai26919 Probe #16
c 62	6	42.9	108	4	ABA75174	AbA75174 Human foe
c 63	6	42.9	108	4	AAI55718	Aai55718 Probe #24
c 64	6	42.9	108	4	ABA39843	AbA39843 Probe #18
c 65	6	42.9	108	4	AAK49810	Aak49810 Human bon
c 66	6	42.9	108	4	AAK23705	Aak23705 Human bra
c 67	6	42.9	108	4	ABS49447	AbS49447 Human liv
c 68	6	42.9	108	6	ABS23310	AbS23310 Human gen
c 69	6	42.9	121	12	ADO60013	Ado60013 Novel hum
70	6	42.9	159	8	ACC69095	Acc69095 Cucumber
c 71	6	42.9	171	6	ABN22791	Abn22791 Human ORF
72	6	42.9	201	11	ACH98099	Ach98099 Klebsiell
73	6	42.9	201	13	ADQ41814	Adq41814 Myocardia
74	6	42.9	213	10	ACD96463	AcD96463 Human col
75	6	42.9	235	3	AAA31903	Aaa31903 Plant mic
c 76	6	42.9	256	3	AAC23296	Aac23296 Human sec
77	6	42.9	279	8	ABX51427	AbX51427 Bovine ES
78	6	42.9	284	12	ADH00536	Adh00536 Kidney di

C 79	6	42.9	293	5	AAF68603	Aaf68603 Human lun	C 152	6	42.9	500	3	AAc93641	Aac93641 Cat flea
C 80	6	42.9	293	6	ABK38514	Abk38514 cDNA enco	153	6	42.9	505	9	ACH32958	Ach32958 Human end
C 81	6	42.9	293	8	ACR10843	Acr10843 Human lun	154	6	42.9	508	6	ABK34612	Abk34612 Human cDN
C 82	6	42.9	293	8	ABX99794	Abx99794 Lung canc	155	6	42.9	510	13	ADT42610	Adt42610 Bacterial
C 83	6	42.9	293	10	ADH46057	Adh46057 Human lun	C 156	6	42.9	520	4	AAI17719	Aai17719 Probe #76
C 84	6	42.9	293	12	ADET1809	Adet1809 Human lun	C 157	6	42.9	520	4	ABA62659	Aba62659 Human foe
C 85	6	42.9	293	13	ADJ19976	Adj19976 Human lun	C 158	6	42.9	520	4	AAI42655	Aai42655 Probe #81
C 86	6	42.9	293	13	ADJ19976	Adj19976 Human lun	C 159	6	42.9	520	4	ABA29969	Aba29969 Probe #84
C 87	6	42.9	298	10	ADD89922	Ad89922 Murine DN	C 160	6	42.9	520	4	AAK36866	Aak36866 Human bon
C 88	6	42.9	304	8	ABX43798	Abx43798 Bovine ES	C 161	6	42.9	520	4	AAK11033	Aak11033 Human bra
C 89	6	42.9	308	6	ABN17315	Abn17315 Human ORF	C 162	6	42.9	520	4	ABS36537	Abs36537 Human liv
C 90	6	42.9	328	5	AAAS87978	Aas87978 DNA enco	C 163	6	42.9	520	6	ABS10877	Abs10877 Human gen
C 91	6	42.9	337	4	AAI82014	Aai82014 Human pol	C 164	6	42.9	521	6	AAI93014	Aai93014 Human cDN
C 92	6	42.9	343	2	AAAT51191	Aat51191 Human bre	C 165	6	42.9	521	12	ADL29441	Adl29441 3' end of
C 93	6	42.9	343	4	AAH36304	Aah36304 Human col	C 166	6	42.9	526	4	AAH99409	Aah99409 Human pro
C 94	6	42.9	343	9	ADA57806	Ada57806 Human par	C 167	6	42.9	526	4	ABA08557	Aba08557 Human gro
C 95	6	42.9	348	3	AAA31744	Aaa31744 Plant mic	C 168	6	42.9	533	3	AAAS1834	Aas1834 N. mening
C 96	6	42.9	351	3	AAA31500	Aaa31500 Plant mic	C 169	6	42.9	533	4	AAAS0832	Aas0832 Human cDN
C 97	6	42.9	353	9	ACH20340	Ach20340 Human adu	C 170	6	42.9	536	6	ABN65617	Abn65617 Human can
C 98	6	42.9	354	13	ADS050742	Ads050742 Bacterial	C 171	6	42.9	538	6	ABV98619	Abv98619 Human pan
C 99	6	42.9	357	6	ABQ68185	Bq68185 Listeria	C 172	6	42.9	543	11	ADT96434	Adt96434 Colon can
C 100	6	42.9	357	6	ABQ69977	Bq69977 Listeria	C 173	6	42.9	545	4	AAK74167	Aak74167 Human imm
C 101	6	42.9	358	2	AAV87567	Aav87567 EST clone	C 174	6	42.9	549	6	ABQ37879	Abq37879 Oligonuc
C 102	6	42.9	360	9	ACH20362	Ach20362 Human adu	C 175	6	42.9	549	6	ABQ37879	Abq37879 Oligonuc
C 103	6	42.9	368	6	ABA99099	Aba99099 Human col	C 176	6	42.9	556	4	AAH09116	Aah09116 Human cDN
C 104	6	42.9	379	4	AAK74206	Aak74206 Human imm	C 177	6	42.9	557	6	ABL38491	Abi38491 Human col
C 105	6	42.9	380	4	AAK74208	Aak74208 Human imm	C 178	6	42.9	560	4	AAK94055	Aak94055 Human cDN
C 106	6	42.9	382	4	AAK74207	Aak74207 Human imm	C 179	6	42.9	560	12	ADL30482	Adl30482 3' end of
C 107	6	42.9	386	3	AAA31444	Aaa31444 Plant mic	C 180	6	42.9	561	6	ABV88029	Abv88029 Human col
C 108	6	42.9	392	4	AAH99207	Aah99207 Human pro	C 181	6	42.9	563	4	AAK54627	Aak54627 Human hae
C 109	6	42.9	393	13	ADR61795	Adr61795 Cotton cd	C 182	6	42.9	563	4	AAK54755	Aak54755 Human hae
C 110	6	42.9	399	9	ACH49522	Ach49522 Human leu	C 183	6	42.9	563	6	AAK54924	Aak54924 Human hae
C 111	6	42.9	401	4	ABA57015	Aba57015 Human foe	C 184	6	42.9	565	6	ABQ37134	Abq37134 Oligonuc
C 112	6	42.9	401	4	ABS30296	Abs30296 Human liv	C 185	6	42.9	565	6	ABQ37135	Abq37135 Oligonuc
C 113	6	42.9	406	6	ABQ55831	Bq55831 Human ova	C 186	6	42.9	566	5	AAK74235	Aak74235 DNA enco
C 114	6	42.9	414	6	ABK80229	Abk80229 Bacillus	C 187	6	42.9	583	3	AAF10972	Aaf10972 Fusarium
C 115	6	42.9	429	5	ABV00164	Abv00164 Human pro	C 188	6	42.9	585	4	ABL16425	Abi16425 Drosophil
C 116	6	42.9	434	10	ACD96670	Acd96670 Human col	C 189	6	42.9	594	6	ABK78903	Abk78903 Bacillus
C 117	6	42.9	441	9	ACH41591	Ach41591 Human foe	C 190	6	42.9	608	13	ADQ57592	Adq57592 Novel can
C 118	6	42.9	446	6	ABL68081	Abi68081 Ovary can	C 191	6	42.9	622	8	ACC44873	Acc44873 Human KG-
C 119	6	42.9	446	6	ABL65126	Abi65126 Lung canc	C 192	6	42.9	630	6	ABK53349	Abk53349 Human eos
C 120	6	42.9	446	6	ABT11074	Abt11074 Human bre	C 193	6	42.9	633	10	ACF70015	Acf70015 Photorhab
C 121	6	42.9	450	5	ABV09333	Abv09333 Human pro	C 194	6	42.9	638	6	ABQ22263	Abq22263 Oligonuc
C 122	6	42.9	455	10	ADD32322	Add32322 Human mit	C 195	6	42.9	638	6	ABQ22262	Abq22262 Oligonuc
C 123	6	42.9	458	9	ACH24078	Ach24078 Human adu	C 196	6	42.9	639	11	ACH98145	Ach98145 Klebsiell
C 124	6	42.9	465	9	ACH48012	Ach48012 Human lun	C 197	6	42.9	677	13	ADQ53349	Adq53349 Novel can
C 125	6	42.9	465	9	ACH24024	Ach24024 Human adu	C 198	6	42.9	692	4	AAI18173	Aai18173 Human bre
C 126	6	42.9	469	6	ABL93459	Abi93459 Arabidops	C 199	6	42.9	702	8	ACA36744	Aca36744 Prokaryot
C 127	6	42.9	472	4	AAAC99781	Aac99781 Skin cell	C 200	6	42.9	708	10	ADF02266	Adf02266 Bacterial
C 128	6	42.9	472	6	ABL34933	Abi34933 Murine cD	C 201	6	42.9	710	4	AAI97812	Aai97812 Human neu
C 129	6	42.9	475	5	AAF66748	Aaf66748 Novel hum	C 202	6	42.9	712	6	ABQ35812	Abq35812 Oligonuc
C 130	6	42.9	476	10	ADG90946	Adg90946 Hepatic s	C 203	6	42.9	712	6	ABQ35813	Abq35813 Oligonuc
C 131	6	42.9	477	4	AAI15872	Aai15872 Probe #58	C 204	6	42.9	743	4	AAH06742	Aah06742 Human cDN
C 132	6	42.9	477	4	ABA58174	Aba58174 Human foe	C 205	6	42.9	772	10	ADJ26344	Adj26344 Novel end
C 133	6	42.9	477	4	AAI37781	Aai37781 Probe #64	C 206	6	42.9	772	11	ADM68457	Adm68457 Mosaicic vi
C 134	6	42.9	477	4	AAK58740	Aak58740 Human imm	C 207	6	42.9	772	12	ADP26610	Adp26610 Heterodup
C 135	6	42.9	477	4	ABA27359	Aba27359 Probe #58	C 208	6	42.9	772	13	ADQ88432	Adq88432 TMV-U2/To
C 136	6	42.9	477	4	AAK31914	Aak31914 Human bon	C 209	6	42.9	772	13	ADQ88432	Adq88432 TMV-U2/To
C 137	6	42.9	477	4	AAK06254	Aak06254 Human bra	C 210	6	42.9	773	13	ADQ817186	Adq817186 Cotton cd
C 138	6	42.9	477	4	AAK31604	Aak31604 Human liv	C 211	6	42.9	810	4	AAK23014	Aak23014 DNA enco
C 139	6	42.9	477	6	ABS06676	Abs06676 Human gen	C 212	6	42.9	822	3	AAA81751	Aaa81751 N. mening
C 140	6	42.9	477	10	ADG90945	Adg90945 Hepatic s	C 213	6	42.9	830	12	ADL13129	Adl13129 Human ste
C 141	6	42.9	478	5	ABV39482	Abv39482 Human pro	C 214	6	42.9	846	6	ABN98868	Abn98868 Arabidops
C 142	6	42.9	478	5	ABV30509	Abv30509 Human pro	C 215	6	42.9	852	4	AAH73329	Aah73329 Human cer
C 143	6	42.9	480	3	AAZ61644	Aaz61644 cDNA enco	C 216	6	42.9	858	10	ADD34369	Add34369 Mouse mit
C 144	6	42.9	480	3	AAZ61735	Aaz61735 cDNA enco	C 217	6	42.9	862	2	AAV59573	Aav59573 Human sec
C 145	6	42.9	480	4	AAAC99668	Aac99668 Skin cell	C 218	6	42.9	862	6	ABV73560	Abv73560 Human cDN
C 146	6	42.9	480	4	AAAC99577	Aac99577 Skin cell	C 219	6	42.9	862	8	AAI51234	Aai51234 Human CD2
C 147	6	42.9	480	6	ABL34820	Abi34820 Murine cD	C 220	6	42.9	862	8	ABZ52002	Abz52002 Aspergill
C 148	6	42.9	480	6	ABL34729	Abi34729 Murine cD	C 221	6	42.9	862	9	ACD82703	Acd82703 cDNA sequ
C 149	6	42.9	483	6	ABS69274	Abs69274 Novel mur	C 222	6	42.9	862	10	ADJ22788	Adj22788 Human enco
C 150	6	42.9	488	13	ADQ57723	Adq57723 Novel can	C 223	6	42.9	862	12	ADH73790	Adh73790 Human sec
C 151	6	42.9	498	3	AAZ80168	Aaz80168 Human col	C 224	6	42.9	865	4	AAH06834	Aah06834 Human cDN

C 225	6	42.9	868	6	ABQ68941	Listeria	Abq68941	298	6	42.9	1239	8	ACA26709	Prokaryot
C 226	6	42.9	879	8	ACA53933	Prokaryot	ACA53933	C 299	6	42.9	1309	12	ADO62646	Transcrip
C 227	6	42.9	880	5	ADL63214	Human ova	ADL63214	C 300	6	42.9	1309	13	ADL43410	Plant tra
C 228	6	42.9	892	5	ABV22930	Human pro	ABV22930	C 301	6	42.9	1310	12	ADR03265	Maize cin
C 229	6	42.9	892	5	ABV28761	Human pro	ABV28761	C 302	6	42.9	1316	2	AAx82082	Human sig
C 230	6	42.9	894	3	AAF07793	Fusarium	AAF07793	C 303	6	42.9	1341	6	ABQ15051	Oligonucl
C 231	6	42.9	897	4	ABL19317	Drosophil	ABL19317	C 304	6	42.9	1341	6	ABQ15050	Oligonucl
C 232	6	42.9	905	4	AAK74168	Human imm	AAK74168	C 305	6	42.9	1345	4	AAK56865	Human imm
C 233	6	42.9	920	2	AAX22225	Human sec	AAX22225	C 306	6	42.9	1351	11	ADL65886	C. glutam
C 234	6	42.9	920	2	ACD40469	CDNA sequ	ACD40469	C 307	6	42.9	1371	5	AAx77912	DNA encod
C 235	6	42.9	932	2	AAV59733	Human sec	AAV59733	C 308	6	42.9	1371	5	AAx85776	DNA encod
C 236	6	42.9	932	2	ABx73724	Human cDN	ABx73724	C 309	6	42.9	1371	5	AAx74951	DNA encod
C 237	6	42.9	932	2	ACD82867	CDNA sequ	ACD82867	C 310	6	42.9	1378	6	ABZ78076	Human bre
C 238	6	42.9	932	10	ADI22952	CDNA encod	ADI22952	C 311	6	42.9	1383	6	ABN67484	Streptoco
C 239	6	42.9	932	12	ADH73954	Human sec	ADH73954	C 312	6	42.9	1395	3	AAAC48533	Arabisdops
C 240	6	42.9	935	6	ABQ70274	Listeria	ABQ70274	C 313	6	42.9	1413	4	AAx28941	CDNA encod
C 241	6	42.9	944	3	AAA58789	CDNA encod	AAA58789	C 314	6	42.9	1413	4	AAx30179	DNA encod
C 242	6	42.9	962	2	AAQ89874	Bryodin-2	AAQ89874	C 315	6	42.9	1413	4	AAx34809	CDNA encod
C 243	6	42.9	974	3	AAx35170	Arabisdops	AAx35170	C 316	6	42.9	1413	4	AAI99580	Human exp
C 244	6	42.9	974	3	AAx48947	Arabisdops	AAx48947	C 317	6	42.9	1413	4	ABA06435	Human cDN
C 245	6	42.9	976	6	ABN74460	Bovine em	ABN74460	C 318	6	42.9	1413	4	AAI62753	Human cDN
C 246	6	42.9	990	12	ADO41953	Human DNA	ADO41953	C 319	6	42.9	1413	4	ABK43513	DNA encod
C 247	6	42.9	991	8	ABZ51858	Aspergill	ABZ51858	C 320	6	42.9	1413	5	AAx29549	Human end
C 248	6	42.9	1001	3	AAH51126	Human MGS	AAH51126	C 321	6	42.9	1413	5	ADG15105	Human 7 t
C 249	6	42.9	1001	3	AAH51127	Human MGS	AAH51127	C 322	6	42.9	1413	6	ABT07776	Novel hum
C 250	6	42.9	1002	12	ADO41949	Human DNA	ADO41949	C 323	6	42.9	1413	6	ABV83772	Human pol
C 251	6	42.9	1007	13	ADL31110	Human can	ADL31110	C 324	6	42.9	1413	8	ACD01434	Human pol
C 252	6	42.9	1054	3	ABK47317	Peroxidred	ABK47317	C 325	6	42.9	1413	10	ADC45967	Human neo
C 253	6	42.9	1077	8	ACA00711	C. glutam	ACA00711	C 326	6	42.9	1413	12	ADL53900	CDNA encod
C 254	6	42.9	1083	4	AAx35118	DNA #68 e	AAx35118	C 327	6	42.9	1455	2	AAZ35937	Streptoco
C 255	6	42.9	1083	4	AAx331496	Human DNA	AAx331496	C 328	6	42.9	1455	12	ADO41947	Human DNA
C 256	6	42.9	1083	4	AAI64007	Human pol	AAI64007	C 329	6	42.9	1512	2	ADT30346	Chicken Y
C 257	6	42.9	1083	4	ABA06842	Human gen	ABA06842	C 330	6	42.9	1530	12	ADO41962	Human DNA
C 258	6	42.9	1083	6	ABQ66820	Human pol	ABQ66820	C 331	6	42.9	1554	8	ADA70781	Rice gene
C 259	6	42.9	1083	6	ABV84179	Human pol	ABV84179	C 332	6	42.9	1554	12	ADO41951	Human DNA
C 260	6	42.9	1083	10	ADC11107	Human DNA	ADC11107	C 333	6	42.9	1599	3	AAx51542	Arabisdops
C 261	6	42.9	1083	10	ADC46560	Human neo	ADC46560	C 334	6	42.9	1600	10	ADC30763	Human nov
C 262	6	42.9	1083	12	ADM24722	Human PRO	ADM24722	C 335	6	42.9	1601	3	AAx38735	Arabisdops
C 263	6	42.9	1089	4	ABL03581	Drosophil	ABL03581	C 336	6	42.9	1618	3	AAFI5836	Human pro
C 264	6	42.9	1096	6	ABQ16834	Oligonucl	ABQ16834	C 337	6	42.9	1635	4	ABL04499	Drosophil
C 265	6	42.9	1096	6	ABQ16835	Oligonucl	ABQ16835	C 338	6	42.9	1654	3	AAx59710	Human sec
C 266	6	42.9	1112	8	ABX63464	Human cDN	ABX63464	C 339	6	42.9	1658	4	AAH13897	Human cDN
C 267	6	42.9	1113	13	ADT42478	Bacterial	ADT42478	C 340	6	42.9	1726	4	AAH13776	Human cDN
C 268	6	42.9	1122	5	AAH67243	C glutami	AAH67243	C 341	6	42.9	1726	13	ADSS1537	Bacterial
C 269	6	42.9	1129	5	AAH89999	Human bon	AAH89999	C 342	6	42.9	1731	12	ADL02680	DNA encod
C 270	6	42.9	1131	10	ACF71571	Phototrab	ACF71571	C 343	6	42.9	1782	3	AAF21846	Human bre
C 271	6	42.9	1140	4	AAx28997	Genomic s	AAx28997	C 344	6	42.9	1802	6	ABA99136	HPDE-1 en
C 272	6	42.9	1140	4	AAx30240	DNA encod	AAx30240	C 345	6	42.9	1809	8	ACA24185	Prokaryot
C 273	6	42.9	1140	4	AAx35074	DNA #24 e	AAx35074	C 346	6	42.9	1840	4	AAK94556	Human ful
C 274	6	42.9	1140	4	ABA06807	Human gen	ABA06807	C 347	6	42.9	1840	12	ADL31424	Full leng
C 275	6	42.9	1140	4	AAI62821	Human gen	AAI62821	C 348	6	42.9	1842	10	ACA55448	Signallin
C 276	6	42.9	1140	4	ABK44026	Genomic D	ABK44026	C 349	6	42.9	1842	12	ADL55244	Human pol
C 277	6	42.9	1140	5	AAx29741	Human end	AAx29741	C 350	6	42.9	1845	13	ACN41006	Tumour-as
C 278	6	42.9	1140	5	ADG15170	Human 7 t	ADG15170	C 351	6	42.9	1888	13	ADSS62059	Bacterial
C 279	6	42.9	1140	6	ABT07832	Novel hum	ABT07832	C 352	6	42.9	1890	10	ADL53174	Human cod
C 280	6	42.9	1140	6	ABZ14195	Arabisdops	ABZ14195	C 353	6	42.9	1902	8	ACA24848	Prokaryot
C 281	6	42.9	1140	6	ABV84144	Human pol	ABV84144	C 354	6	42.9	1902	3	AAx54237	Arabisdops
C 282	6	42.9	1140	8	ACD01495	Human gen	ACD01495	C 355	6	42.9	1917	3	AAx54237	Arabisdops
C 283	6	42.9	1140	8	ADA67859	Arabisdops	ADA67859	C 356	6	42.9	1932	10	ADK67263	Human can
C 284	6	42.9	1140	10	ADC46516	Human neo	ADC46516	C 357	6	42.9	1932	10	ADK67261	Human can
C 285	6	42.9	1140	12	ADL55011	Novel hum	ADL55011	C 358	6	42.9	1933	11	ADL31413	Human cDN
C 286	6	42.9	1140	12	ADN72612	Thale cre	ADN72612	C 359	6	42.9	1942	6	ABK35809	CDNA sequ
C 287	6	42.9	1146	8	ACA36279	Prokaryot	ACA36279	C 360	6	42.9	1942	12	ADQ25337	Human sof
C 288	6	42.9	1163	3	ABQ70234	Listeria	ABQ70234	C 361	6	42.9	1947	4	AAK51514	Human pol
C 289	6	42.9	1175	3	AAFI3401	Aspergill	AAFI3401	C 362	6	42.9	1947	11	ABD02444	Pseudomon
C 290	6	42.9	1178	3	AAZ33355	Human sec	AAZ33355	C 363	6	42.9	1952	6	ABA93744	Human sig
C 291	6	42.9	1182	3	ABA15955	Human ner	ABA15955	C 364	6	42.9	1965	7	AAI99552	Human exp
C 292	6	42.9	1198	10	ADI22502	Rat liver	ADI22502	C 365	6	42.9	1965	13	ADs48221	Bacterial
C 293	6	42.9	1215	6	ABQ41915	Oligonucl	ABQ41915	C 366	6	42.9	1966	4	ABA09105	Human org
C 294	6	42.9	1215	6	ABQ41914	Oligonucl	ABQ41914	C 367	6	42.9	1966	4	AAK52498	Human pol
C 295	6	42.9	1230	10	ABZ41545	N. gonorr	ABZ41545	C 368	6	42.9	1996	5	AAx29614	Human end
C 296	6	42.9	1230	10	ABZ39752	N. gonorr	ABZ39752	C 369	6	42.9	2000	8	ADA71826	Rice gene
C 297	6	42.9	1236	11	ABD02483	Pseudomon	ABD02483	C 370	6	42.9	2000	12	ADJ40860	Plant cDN

C 371	6	42.9	2028	4	AAK69011	Human imm	444	6	42.9	3039	12	ADO41967	Ado41967 Human com
372	6	42.9	2063	4	AAK94190	Human cDN	C 445	6	42.9	3060	4	ABL17650	Ab117650 Drosophil
373	6	42.9	2063	12	ADL30708	Full leng	446	6	42.9	3094	6	AAI64196	AAI64196 Human H37
374	6	42.9	2082	4	AAF64220	Human sec	447	6	42.9	3094	10	AAU58580	AAU58580 Human H37
C 375	6	42.9	2087	6	AAI45897	A thalian	448	6	42.9	3094	10	AAU58579	AAU58579 Human H37
C 376	6	42.9	2087	12	ADG74901	A thalian	449	6	42.9	3135	6	ABK83510	ABK83510 Human cDN
C 377	6	42.9	2089	2	AAV06591	Arabidops	450	6	42.9	3135	13	ADP23183	ADP23183 PRO polyP
C 378	6	42.9	2113	11	ACN45171	Human mRN	451	6	42.9	3144	4	ABL01580	ABL01580 Drosophil
C 379	6	42.9	2123	4	ABL22322	Drosophil	C 452	6	42.9	3152	10	ADU58397	ADU58397 Toxicity-
C 380	6	42.9	2136	13	ADR07776	Full leng	453	6	42.9	3189	4	AAF58654	AAF58654 Human Rep
C 381	6	42.9	2156	13	ACN41468	Human dia	454	6	42.9	3191	12	ADQ87201	ADQ87201 Human tum
C 382	6	42.9	2156	13	ACN43123	Human dia	455	6	42.9	3191	13	ADQ84924	ADQ84924 Human tum
C 383	6	42.9	2174	12	ADQ64315	Novel hum	C 456	6	42.9	3192	5	AAU75056	AAU75056 DNA encod
C 384	6	42.9	2175	8	ADA70642	Rice gene	457	6	42.9	3208	3	AAU59068	AAU59068 Human sec
C 385	6	42.9	2217	8	ACA53426	Prokaryot	458	6	42.9	3208	8	ADA97929	ADA97929 Human sec
C 386	6	42.9	2217	10	ADB63558	Human cDN	459	6	42.9	3208	8	ADA43840	ADA43840 Human sec
C 387	6	42.9	2220	12	ADQ67221	Novel hum	460	6	42.9	3208	10	ADC20088	ADC20088 Human sec
C 388	6	42.9	2223	8	ACA52331	Prokaryot	461	6	42.9	3208	10	ADP10558	ADP10558 Human sec
C 389	6	42.9	2235	1	AAU90389	DNA encod	462	6	42.9	3255	12	ADM90628	ADM90628 Human DNA
C 390	6	42.9	2271	4	ABL21710	Drosophil	463	6	42.9	3255	12	ADM91046	ADM91046 Human DNA
C 391	6	42.9	2272	6	ABN60033	Novel hum	464	6	42.9	3260	10	ADP46299	ADP46299 Rat gene
C 392	6	42.9	2286	5	ABA14652	Human ner	465	6	42.9	3300	12	ADO62058	ADO62058 Transcrip
C 393	6	42.9	2319	1	AAU90816	Membrane-	466	6	42.9	3327	2	AAQ10989	AAQ10989 B lymphoc
C 394	6	42.9	2347	6	AAU33729	Human sec	467	6	42.9	3330	12	AD143398	AD143398 Plant tra
C 395	6	42.9	2358	12	ADN72668	Thale cre	468	6	42.9	3337	1	AAU91089	AAU91089 Fragment
C 396	6	42.9	2379	6	ABE64928	Grape rib	469	6	42.9	3339	10	ADU69135	ADU69135 C. neofor
C 397	6	42.9	2394	6	AAU33706	Human sec	470	6	42.9	3340	12	ADM86615	ADM86615 Mouse and
C 398	6	42.9	2421	6	ABK74250	Bacillus	471	6	42.9	3420	4	AAU58655	AAU58655 Human IB1
C 399	6	42.9	2437	2	AAU97381	Human typ	472	6	42.9	3464	5	AAU91232	AAU91232 Human cDN
C 400	6	42.9	2437	2	AAU99802	Human gen	473	6	42.9	3487	11	ADM01734	ADM01734 Human cDN
C 401	6	42.9	2437	2	AAU88368	Human typ	474	6	42.9	3502	12	ADL12930	ADL12930 Human ste
C 402	6	42.9	2437	2	AAU88360	Human typ	475	6	42.9	3623	4	ABL04857	ABL04857 Drosophil
C 403	6	42.9	2437	2	AAU88361	Human typ	476	6	42.9	3709	4	AAU78012	AAU78012 Nucleotid
C 404	6	42.9	2437	10	ACF63370	Human SRD	477	6	42.9	3709	10	ADU98861	ADU98861 Fruit fly
C 405	6	42.9	2448	6	ABQ60808	Human Rep	478	6	42.9	3709	10	ABX14663	ABX14663 Fruitfly
C 406	6	42.9	2541	6	ABQ60807	Human pro	C 479	6	42.9	3765	10	ADU53672	ADU53672 Primary r
C 407	6	42.9	2562	10	ADF38037	Synchroni	480	6	42.9	3792	4	ABL10857	ABL10857 Drosophil
C 408	6	42.9	2566	12	AD140918	Human kin	481	6	42.9	3799	4	AAI66255	AAI66255 S. cerevis
C 409	6	42.9	2570	4	AAU18569	Human cDN	482	6	42.9	3799	10	ADU02764	ADU02764 S. cerevi
C 410	6	42.9	2575	6	ABK84270	Human cDN	483	6	42.9	3824	2	AAQ11482	AAQ11482 Sequence
C 411	6	42.9	2575	6	ABK84279	Human ben	484	6	42.9	3831	3	AAU43193	AAU43193 Arabidops
C 412	6	42.9	2582	10	ADA53573	Human cod	485	6	42.9	3887	12	ADL12931	ADL12931 Human ste
C 413	6	42.9	2606	11	ACN44255	Human mRN	486	6	42.9	3923	4	AAU89586	AAU89586 Human dig
C 414	6	42.9	2606	12	AD140919	Human kin	487	6	42.9	3923	4	AAU7765	AAU7765 Human imm
C 415	6	42.9	2625	4	AAU55430	Nucleotid	488	6	42.9	3923	4	AAU07388	AAU07388 Human rep
C 416	6	42.9	2625	8	ACA28753	Prokaryot	489	6	42.9	3923	4	ABA08191	ABA08191 Human ova
C 417	6	42.9	2652	8	ACA28241	Prokaryot	490	6	42.9	3923	4	ADU85072	ADU85072 Farnesyl
C 418	6	42.9	2667	4	ABL08223	Drosophil	491	6	42.9	3934	11	AD131740	AD131740 Human cDN
C 419	6	42.9	2670	8	ACA29227	Prokaryot	492	6	42.9	3934	13	ADP56041	ADP56041 Human PRO
C 420	6	42.9	2686	5	AAU73640	DNA encod	493	6	42.9	4011	3	AAU49498	AAU49498 Arabidops
C 421	6	42.9	2700	8	ACA44711	Prokaryot	494	6	42.9	4053	12	ADU63651	ADU63651 Transcrip
C 422	6	42.9	2705	4	ABL16424	Drosophil	C 495	6	42.9	4081	2	AAU06585	AAU06585 Arabidops
C 423	6	42.9	2715	10	ADU00107	Bacterial	496	6	42.9	4094	10	ADU67537	ADU67537 Human Lyl
C 424	6	42.9	2728	4	AAU14429	Human cDN	497	6	42.9	4106	5	AAU80045	AAU80045 DNA encod
C 425	6	42.9	2769	6	AB199771	Mouse isc	498	6	42.9	4106	5	AAU89210	AAU89210 DNA encod
C 426	6	42.9	2778	8	ACC46308	Human dit	499	6	42.9	4156	13	ADQ38385	ADQ38385 Human SNP
C 427	6	42.9	2809	10	ADU637113	Human cDN	500	6	42.9	4248	11	ABD11263	ABD11263 Pseudomon
C 428	6	42.9	2821	12	ADU05153	Antipsori	501	6	42.9	4339	4	ABL20716	ABL20716 Drosophil
C 429	6	42.9	2892	4	AAU14475	Human cDN	502	6	42.9	4365	12	ADN12096	ADN12096 Murine ca
C 430	6	42.9	2909	5	ABU15957	Human ner	503	6	42.9	4484	6	ABL68510	ABL68510 Kidney ca
C 431	6	42.9	2954	4	ABL16252	Drosophil	504	6	42.9	4484	10	ADP81541	ADP81541 Leukemia
C 432	6	42.9	2955	4	AAU18577	Human cDN	505	6	42.9	4530	8	ABX63357	ABX63357 Human cDN
C 433	6	42.9	2960	6	ABQ70660	Listeria	506	6	42.9	4530	12	ADU77193	ADU77193 Human cDN
C 434	6	42.9	2980	12	ADU44009	Novel hum	507	6	42.9	4530	12	ADU161766	ADU161766 Human cDN
C 435	6	42.9	2994	12	ADL12669	Human ste	C 508	6	42.9	4628	12	ABZ11203	ABZ11203 Human pol
C 436	6	42.9	3005	10	ADA53406	Human cod	C 509	6	42.9	4628	12	ADM43721	ADM43721 Novel hum
C 437	6	42.9	3015	4	ABL19316	Drosophil	510	6	42.9	4709	8	ACC49517	ACC49517 Tumour-as
C 438	6	42.9	3016	6	ABU53853	Human and	511	6	42.9	4736	6	ABQ70950	ABQ70950 Liesteria
C 439	6	42.9	3016	6	ABU53853	DNA encod	512	6	42.9	4819	8	ABX70845	ABX70845 Novel hum
C 440	6	42.9	3016	12	ADN00254	Human and	513	6	42.9	5047	12	ADP13275	ADP13275 Renal cel
C 441	6	42.9	3023	11	ADP65803	Human mRN	514	6	42.9	5047	12	ADQ84256	ADQ84256 Human tum
C 442	6	42.9	3023	11	ADP65723	Human DXF	515	6	42.9	5047	12	ADQ85638	ADQ85638 Human tum
C 443	6	42.9	3033	12	ADQ23033	Human sof	516	6	42.9	5047	13	ADQ86737	ADQ86737 Human tum

517	6	42.9	5124	4	ABL03554	AbL03554 Drosophil	590	6	42.9	14896	6	ABK24096	Abk24096 Human alp
518	6	42.9	5159	10	ADK1004	Adk1004 Novel hum	591	6	42.9	14896	8	ABZ34885	Abz34885 Coding se
519	6	42.9	5159	13	ADR15718	Adr15718 Kinase 40	592	6	42.9	14896	8	ACA89917	AcA89917 Gene diff
520	6	42.9	5247	4	ABL04498	AbL04498 Drosophil	593	6	42.9	14896	10	ADD14619	AdD14619 Human src
C 521	6	42.9	5298	5	RA889895	RA889895 DNA encod	594	6	42.9	14896	12	ADL15635	AdL15635 Human lip
C 522	6	42.9	5298	5	RA886664	RA886664 DNA encod	595	6	42.9	14899	4	RAK52224	RAK52224 Human pol
C 523	6	42.9	5319	4	ABL05960	AbL05960 Drosophil	596	6	42.9	15449	3	AAA81526	AAa81526 N. mening
C 524	6	42.9	5406	4	ABL06257	AbL06257 Drosophil	597	6	42.9	15518	6	ABL34172	AbL34172 Human imm
C 525	6	42.9	5574	4	ABL02492	AbL02492 Drosophil	598	6	42.9	15518	6	ABL34624	AbL34624 Human met
C 526	6	42.9	5595	2	AAQ25810	AAq25810 Insest of	599	6	42.9	15518	6	ABL70607	AbL70607 Chemicall
C 527	6	42.9	5989	4	RAA46535	RAa46535 Tumour su	600	6	42.9	15518	7	ADG99885	AdG99885 Bisulphit
C 528	6	42.9	6096	12	ADO78175	AdO78175 Human thr	601	6	42.9	16545	5	AAD19232	AAd19232 Human CGL
C 529	6	42.9	6149	4	ABL04856	AbL04856 Drosophil	602	6	42.9	16545	13	ADS09790	AdS09790 Human the
C 530	6	42.9	6343	8	ABZ10194	AbZ10194 Haenatopo	603	6	42.9	16559	11	ACN91031	AcN91031 Breast ca
C 531	6	42.9	6343	13	ADS89670	AdS89670 Oligonuc	604	6	42.9	16842	4	AA846412	AAa46412 Tumour su
C 532	6	42.9	6436	6	ABL33692	AbL33692 Human imm	605	6	42.9	16842	6	ABK31419	AbK31419 Signal tr
C 533	6	42.9	6436	6	ABK31408	AbK31408 Signal tr	606	6	42.9	16842	6	ABL70384	AbL70384 Chemicall
C 534	6	42.9	6462	4	RAF90037	RAf90037 Nucleotid	607	6	42.9	16842	6	AA861336	AAe61336 Human gen
C 535	6	42.9	6515	12	ADN06015	AdN06015 Antipeori	608	6	42.9	16842	10	ADS54136	AdS54136 Pretreat
C 536	6	42.9	6779	4	ABL10856	AbL10856 Drosophil	609	6	42.9	16842	13	ADS89286	AdS89286 Oligonuc
C 537	6	42.9	6975	4	ABL09610	AbL09610 Drosophil	610	6	42.9	17200	4	AAAL37025	AAa37025 Human mus
C 538	6	42.9	7069	4	RAA46653	RAa46653 Tumour su	611	6	42.9	17200	8	ABX60013	AbX60013 cDNA enco
C 539	6	42.9	7069	6	ABL33352	AbL33352 Human imm	612	6	42.9	17200	12	ADJ30763	AdJ30763 Human mus
C 540	6	42.9	7069	6	ABK31318	AbK31318 Signal tr	613	6	42.9	18404	8	ADJ30763	AdJ30763 Human mus
C 541	6	42.9	7069	6	ABL70291	AbL70291 Chemicall	614	6	42.9	18888	4	ABL23020	AbL23020 Drosophil
C 542	6	42.9	7069	6	AA861219	AAe61219 Human gen	615	6	42.9	18966	6	ABL37007	AbL37007 Human mus
C 543	6	42.9	7069	6	ABQ66983	AbQ66983 Human ang	616	6	42.9	18966	5	ABA20628	AbA20628 Human ner
C 544	6	42.9	7183	6	ABN80167	AbN80167 Human che	617	6	42.9	18966	8	ABX59995	AbX59995 cDNA enco
C 545	6	42.9	7421	4	RAK89313	RAk89313 Human dig	618	6	42.9	18966	12	ADJ30745	AdJ30745 Human mus
C 546	6	42.9	7431	6	ABL32081	AbL32081 Human imm	619	6	42.9	19236	6	ABN80226	AbN80226 Human che
C 547	6	42.9	7431	6	ABL28371	AbL28371 Human che	620	6	42.9	20001	13	ACN37222	AcN37222 Human per
C 548	6	42.9	7522	4	ABL06256	AbL06256 Drosophil	621	6	42.9	20682	2	AAAX20569	AAx20569 Polynucle
C 549	6	42.9	7551	12	ADN11594	AdN11594 Human CD9	622	6	42.9	21224	5	ABA20544	AbA20544 Human ner
C 550	6	42.9	7783	5	RAA574636	RAa574636 DNA encod	623	6	42.9	21721	2	AAAX83427	AAx83427 Human lip
C 551	6	42.9	7792	4	ABL08222	AbL08222 Drosophil	624	6	42.9	22976	2	AAAX83426	AAx83426 Genomic r
C 552	6	42.9	7847	8	RAA50965	RAa50965 pMON50201	625	6	42.9	23107	9	ADA02762	AdA02762 Human RUN
C 553	6	42.9	7847	8	RAA50968	RAa50968 pMON50203	626	6	42.9	23107	10	ADB72500	AdB72500 Human Run
C 554	6	42.9	7847	8	RAA50962	RAa50962 pMON50200	627	6	42.9	23107	10	ADC85242	AdC85242 Human Run
C 555	6	42.9	7847	8	RAA50967	RAa50967 pMON50202	628	6	42.9	23107	12	ADM74357	AdM74357 Human car
C 556	6	42.9	7856	6	ABN80234	AbN80234 Human che	629	6	42.9	23187	3	AAA50273	AAa50273 Human lip
C 557	6	42.9	8298	6	ABN80190	AbN80190 Human che	630	6	42.9	23187	4	AAF62331	AAf62331 Human lep
C 558	6	42.9	8325	13	ADS57889	AdS57889 Bacterial	631	6	42.9	26636	4	ABL16650	AbL16650 Drosophil
C 559	6	42.9	8530	6	ABL32433	AbL32433 Human imm	632	6	42.9	27689	6	AA819494	AAa19494 Arabidops
C 560	6	42.9	8776	6	ABK40067	AbK40067 Human che	633	6	42.9	30312	10	ACF65384	AcF65384 Continuation (6 of
C 561	6	42.9	9393	6	AB878855	Ab878855 E. coli C	634	6	42.9	30625	6	ABK12808	AbK12808 Human tum
C 562	6	42.9	9393	10	ADH80422	AdH80422 Escherich	635	6	42.9	30676	6	ABK12811	AbK12811 Human tum
C 563	6	42.9	9443	4	ABL16121	AbL16121 Drosophil	636	6	42.9	31352	6	AAAL39687	AAa39687 Genomic D
C 564	6	42.9	9448	4	RAK84656	RAk84656 Human imm	637	6	42.9	31497	8	ABX72626	AbX72626 Human cDN
C 565	6	42.9	9900	12	ADN11595	AdN11595 Human CD9	638	6	42.9	31946	11	ACN45120	AcN45120 Mouse gen
C 566	6	42.9	9935	10	AA855749	AA855749 Escherich	639	6	42.9	32328	4	ABL09994	AbL09994 Drosophil
C 567	6	42.9	10308	4	ABL05365	AbL05365 Drosophil	640	6	42.9	33486	6	AB878976	Ab878976 E. coli C
C 568	6	42.9	10308	13	ADQ89631	AdQ89631 Antagonis	641	6	42.9	33486	10	ADH80543	AdH80543 Escherich
C 569	6	42.9	10343	4	ABL14246	AbL14246 Drosophil	642	6	42.9	33925	12	ADL70331	AdL70331 Crenarcha
C 570	6	42.9	11473	6	ABK40030	AbK40030 Human che	643	6	42.9	34071	4	AAF90033	AAf90033 Nucleotid
C 571	6	42.9	11473	6	ABL33355	AbL33355 Human imm	644	6	42.9	36383	4	ABL05364	AbL05364 Drosophil
C 572	6	42.9	11809	6	RAA897394	RAa897394 Murine SA	645	6	42.9	39003	4	AAF28534	AAf28534 Genomic f
C 573	6	42.9	11809	12	ADM15732	AdM15732 Murine SA	646	6	42.9	41322	9	AAAL62633	AAa62633 Human CD3
C 574	6	42.9	12122	4	ABL08612	AbL08612 Drosophil	647	6	42.9	41936	6	ABL67924	AbL67924 Ovary can
C 575	6	42.9	12192	4	RAA28195	RAa28195 Genomic s	648	6	42.9	42717	4	AAF90032	AAf90032 Nucleotid
C 576	6	42.9	12192	10	ADG41391	AdG41391 Human res	649	6	42.9	45265	3	RAA46508	RAa46508 Sequence
C 577	6	42.9	12192	11	ADG197165	AdG197165 Human res	650	6	42.9	45845	6	ABK12809	AbK12809 Human tum
C 578	6	42.9	13260	12	ADN11596	AdN11596 Human CD9	651	6	42.9	45862	8	ABX93110	AbX93110 Genomic D
C 579	6	42.9	13332	5	ABA15106	AbA15106 Human ner	652	6	42.9	49088	11	ACN43856	AcN43856 Mouse gen
C 580	6	42.9	13635	12	ADJ27129	AdJ27129 Human LRP	653	6	42.9	50460	13	ACN44936	AcN44936 Mouse gen
C 581	6	42.9	13635	12	ADJ71873	AdJ71873 Human LRP	654	6	42.9	52253	3	AAA81478	AAa81478 N. mening
C 582	6	42.9	13638	12	ADI27128	AdI27128 Mouse LRP	655	6	42.9	57038	11	ADP65343	AdP65343 Human seq
C 583	6	42.9	13836	11	ACN44295	AcN44295 Human mRN	656	6	42.9	57082	12	ADP84151	AdP84151 Human CAL
C 584	6	42.9	14530	4	RAA51849	RAa51849 Human pol	657	6	42.9	57502	12	ADQ97092	AdQ97092 Human can
C 585	6	42.9	14648	4	ABL16120	AbL16120 Drosophil	658	6	42.9	60935	13	ACN37224	AcN37224 Human per
C 586	6	42.9	14849	6	ABK24094	AbK24094 Mouse alp	659	6	42.9	65042	8	AB855711	Ab855711 DNA encod
C 587	6	42.9	14849	6	ABK12951	AbK12951 DNA encod	660	6	42.9	65042	9	ACA63029	AcA63029 Human gen
C 588	6	42.9	14887	4	ABA08597	AbA08597 Human LDL	661	6	42.9	65042	13	ADR05761	AdR05761 Human gen
C 589	6	42.9	14889	6	ABZ35245	AbZ35245 Human gen	662	6	42.9	66566	3	AAA53450	AAa53450 Human thi

C 663	6	42.9	66765	12	ADP84154	Adp84154 Human CA1	C 736	6	42.9	304326	13	ADS15253	Adsl5253 Rat senso
C 664	6	42.9	66765	13	ADR72872	Adr72872 Human ova	C 737	6	42.9	304905	11	ADP75180	Adp75180 Human End
C 665	6	42.9	76341	12	ADM97422	Adm97422 Prostate	C 738	6	42.9	321019	13	ADS36450	Ads36450 Human aut
C 666	6	42.9	80251	4	ABL16442	Ab116442 Drosoephil	C 739	6	42.9	326014	6	ABK89296	Abk89296 Human gen
C 667	6	42.9	80251	4	ABL16448	Ab116448 Drosoephil	C 740	6	42.9	326014	12	ADQ94981	Adq94981 Human kin
C 668	6	42.9	85915	13	ADL15447	Adl15447 Streptomyl	C 741	6	42.9	329019	13	ABD32707	Abd32707 Human can
C 669	6	42.9	90220	6	ABK83576	Abk83576 Human cdn	C 742	6	42.9	339234	12	ADQ59437	Adq59437 Human can
C 670	6	42.9	92794	11	ADP65471	Adp65471 Human seq	C 743	6	42.9	339234	12	ADQ59437	Adq59437 Human can
C 671	6	42.9	93631	11	ACN43984_4	Continuation (5 of	C 744	6	42.9	347001	12	ADP43517	Adp43517 Human MAD
C 672	6	42.9	99557	9	ADA03032	Ada03032 Human mCG	C 745	6	42.9	349980	3	AAF21607	Aaf21607 Neisseria
C 673	6	42.9	99557	10	ADB72770	Adb72770 Human CA	C 746	6	42.9	349980	3	AAF21544	Aaf21544 Neisseria
C 674	6	42.9	99557	10	ADC85512	Adc85512 Human gen	C 747	6	42.9	349980	5	AAH68531	Aah68531 C glutami
C 675	6	42.9	99557	12	ADM74627	Adm74627 Human car	C 748	6	42.9	349989	10	ADC86916	Adc86916 Human GPC
C 676	6	42.9	100534	13	ABD32647	Abd32647 Mouse can	C 749	5	35.7	17	2	AAH71526	Aah71526 Human KDR
C 677	6	42.9	104900	13	ABD32848	Abd32848 Human can	C 750	5	35.7	17	6	ABV85695	Abv85695 Human pp-
C 678	6	42.9	105938	13	ABD33432	Abd33432 Human can	C 751	5	35.7	17	6	ABV85693	Abv85693 Human pp-
C 679	6	42.9	106938	13	ABD33432	Abd33432 Human can	C 752	5	35.7	17	6	ABV85694	Abv85694 Human pp-
C 680	6	42.9	107330	12	ADQ97316	Adq97316 Mouse can	C 753	5	35.7	17	8	ABT36868	Abt36868 Tumour su
C 681	6	42.9	110000	2	AAV21209_12	Continuation (13 o	C 754	5	35.7	17	10	ADB40920	Adb40920 Tumour su
C 682	6	42.9	110000	3	AAA81490_01	Continuation (2 of	C 755	5	35.7	17	10	ACC54252	Acc54252 Human tum
C 683	6	42.9	110000	3	AAA81490_03	Continuation (4 of	C 756	5	35.7	19	10	ADG45288	Adg45288 Human oes
C 684	6	42.9	110000	6	ABN71527_02	Continuation (3 of	C 757	5	35.7	19	10	ADP84831	Adp84831 Human ABL
C 685	6	42.9	110000	6	ABQ67196_2	Continuation (3 of	C 758	5	35.7	19	10	ADF84512	Adf84512 Human ABL
C 686	6	42.9	110000	6	ABQ62445_00	Abq62445 Listeria	C 759	5	35.7	19	12	ADQ88337	Adq88337 Human oes
C 687	6	42.9	110000	6	ABA03041_00	AbA03041 Listeria	C 760	5	35.7	20	2	AAV52527	Aav52527 3' primer
C 688	6	42.9	110000	6	ABA03041_08	Continuation (9 of	C 761	5	35.7	20	5	AAH85344	Aah85344 cDNA prim
C 689	6	42.9	110000	6	ABA03041_11	Continuation (12 o	C 762	5	35.7	20	6	ABQ93176	Abq93176 T. tausch
C 690	6	42.9	110000	6	ABA03041_24	Continuation (25 o	C 763	5	35.7	21	4	AAH09942	Aah09942 PCR prime
C 691	6	42.9	110000	10	ADH10017_2	Continuation (3 of	C 764	5	35.7	21	12	ADN96482	Adn96482 PCR prime
C 692	6	42.9	110000	10	ACF65385_1	Continuation (2 of	C 765	5	35.7	22	2	AAQ95801	Aaq95801 Primer B
C 693	6	42.9	110000	10	ACF67367_11	Continuation (12 o	C 766	5	35.7	22	2	AAZ18601	Aaz18601 Primer fo
C 694	6	42.9	110000	10	ACF67367_30	Continuation (31 o	C 767	5	35.7	22	3	AAA80508	Aaa80508 ASTH1 pol
C 695	6	42.9	110000	10	ACF67367_47	Continuation (48 o	C 768	5	35.7	23	10	AAH06053	Aah06053 Pseudomon
C 696	6	42.9	110000	10	ACF65388_00	AcF65388 Photorhab	C 769	5	35.7	23	3	AAA96921	Aaa96921 PCR prime
C 697	6	42.9	110000	11	ADM27081_00	Adm27081 Hypether	C 770	5	35.7	24	3	AAA66376	Aaa66376 Dog genom
C 698	6	42.9	110000	11	ACN43998_00	Acn43998 Human gen	C 771	5	35.7	24	12	ADH68518	Adh68518 Rosa sp r
C 699	6	42.9	110000	12	ADQ97047_2	Continuation (3 of	C 772	5	35.7	24	12	ADQ31884	Adq31884 Human CFT
C 700	6	42.9	110000	12	ADQ97047_2	Continuation (3 of	C 773	5	35.7	25	2	AAQ30686	Aaq30686 IL-6 prim
C 701	6	42.9	110000	13	ABD32921_2	Continuation (3 of	C 774	5	35.7	25	2	AAQ47373	Aaq47373 PCR prime
C 702	6	42.9	110000	13	ABD32629_3	Continuation (4 of	C 775	5	35.7	25	2	AAQ40998	Aaq40998 IL-6 prim
C 703	6	42.9	110021	13	ABD32859_5	Abd32859 Mouse can	C 776	5	35.7	25	2	AAQ45681	Aaq45681 Interleuk
C 704	6	42.9	114411	12	ADQ21090	Adq21090 Human sof	C 777	5	35.7	25	3	AAH61178	Aah61178 PCR prime
C 705	6	42.9	115284	11	ACN44296	Acn44296 Mouse gen	C 778	5	35.7	25	6	ABV86462	Abv86462 Human pp-
C 706	6	42.9	117574	6	AAH45288	Aah45288 Human KCN	C 779	5	35.7	25	6	ABV86464	Abv86464 Human pp-
C 707	6	42.9	124884	5	AAH74201	Aah74201 Nucleotid	C 780	5	35.7	25	6	ABV86467	Abv86467 Human pp-
C 708	6	42.9	124884	10	ADAL14878	Adal14878 Human her	C 781	5	35.7	25	6	ABV86471	Abv86471 Human pp-
C 709	6	42.9	124884	11	ADL99489	Adl99489 Varicella	C 782	5	35.7	25	6	ABV86465	Abv86465 Human pp-
C 710	6	42.9	125157	5	AAH74202	Aah74202 Nucleotid	C 783	5	35.7	25	6	ABV86470	Abv86470 Human pp-
C 711	6	42.9	127238	11	ACN44372	Acn44372 Mouse gen	C 784	5	35.7	25	6	ABV86468	Abv86468 Human pp-
C 712	6	42.9	127917	13	ADR52731	Adr52731 Drug ther	C 785	5	35.7	25	6	ABV86466	Abv86466 Human pp-
C 713	6	42.9	129021	3	AAF22296	Aaf22296 BAC conta	C 786	5	35.7	25	6	ABV86463	Abv86463 Human pp-
C 714	6	42.9	133955	11	ACN45170	Acn45170 Human gen	C 787	5	35.7	25	6	ABV86469	Abv86469 Human pp-
C 715	6	42.9	160198	10	ADL13962	Adl13962 Osteoarth	C 788	5	35.7	25	6	ABV86472	Abv86472 Human pp-
C 716	6	42.9	170170	10	ADL13643	Adl13643 Osteoarth	C 789	5	35.7	25	9	ACI13277	Act13277 Human mic
C 717	6	42.9	171936	6	ABS55565	AbS55565 Human SUL	C 790	5	35.7	25	9	ACI42181	Act42181 Human mic
C 718	6	42.9	171936	12	ADN16205	Adn16205 Mouse sul	C 791	5	35.7	25	9	ACK26304	Ack26304 Human mic
C 719	6	42.9	172569	11	ACN44758	Acn44758 Human gen	C 792	5	35.7	25	9	ACK22633	Ack22633 Human mic
C 720	6	42.9	176771	12	ADQ97167	Adq97167 Human can	C 793	5	35.7	25	9	ACI31478	Act31478 Human mic
C 721	6	42.9	191284	12	ADQ97957	Adq97957 Mouse can	C 794	5	35.7	25	9	ACI09742	Act09742 Human mic
C 722	6	42.9	197997	10	AAH54074	Aah54074 Human tra	C 795	5	35.7	25	9	ACK25729	Ack25729 Human mic
C 723	6	42.9	203070	11	ACN44012	Acn44012 Mouse gen	C 796	5	35.7	25	9	ACI53347	Act53347 Human mic
C 724	6	42.9	207433	5	ABZ72040	Abz72040 Gene 216	C 797	5	35.7	25	9	ACI58441	Act58441 Human mic
C 725	6	42.9	207433	8	ABX74891	Abx74891 BAC1098L2	C 798	5	35.7	25	9	ACK24257	Ack24257 Human mic
C 726	6	42.9	207433	12	ADJ36614	Adj36614 Bacterial	C 799	5	35.7	25	9	ACK27260	Ack27260 Human mic
C 727	6	42.9	207433	12	ADL81193	Adl81193 BAC1098L2	C 800	5	35.7	25	9	ACI94194	Act94194 Human mic
C 728	6	42.9	210204	13	ABD32692	Abd32692 Human sof	C 801	5	35.7	25	9	ACI56987	Act56987 Human mic
C 729	6	42.9	219715	12	ABD32692	Abd32692 Mouse can	C 802	5	35.7	25	9	ACT159973	Act159973 Human mic
C 730	6	42.9	236246	12	ADQ97590	Adq97590 Mouse can	C 803	5	35.7	25	9	ACT158440	Act158440 Human mic
C 731	6	42.9	240823	10	ADD69391	Add69391 Human PG-	C 804	5	35.7	25	9	ACK03647	Ack03647 Human mic
C 732	6	42.9	240825	4	AAF24497	Aaf24497 Human PG-	C 805	5	35.7	25	9	ACK03647	Ack03647 Human mic
C 733	6	42.9	240825	6	ABQ81802	Abq81802 Human PG-	C 806	5	35.7	25	9	ACT103560	Act103560 Human mic
C 734	6	42.9	254366	8	ABZ23704	Abz23704 Human pho	C 807	5	35.7	25	9	ACT199839	Act199839 Human mic
C 735	6	42.9	256190	13	ABD33276	Abd33276 Human can	C 808	5	35.7	25	9	ACT179492	Act179492 Human mic

C 809	5	35.7	25	9	ACI82705	Ac182705 Human mic	882	5	35.7	51	4	AAL34292	Aal34292 Human SNP
C 810	5	35.7	25	9	ACI44763	Ac144763 Human mic	883	5	35.7	51	4	AAI74156	Aai74156 Human sil
C 811	5	35.7	25	9	ACI94195	Ac194195 Human mic	884	5	35.7	51	4	AAI74268	Aai74268 Human sil
C 812	5	35.7	25	9	ACI02924	Ac102924 Human mic	C 885	5	35.7	51	4	AAI78621	Aai78621 Human sil
C 813	5	35.7	25	9	ACI84193	Ac184193 Human mic	C 886	5	35.7	51	4	AAI78132	Aai78132 Human sil
C 814	5	35.7	25	9	ACI13266	Ac113266 Human mic	C 887	5	35.7	51	4	AAI78620	Aai78620 Human sil
C 815	5	35.7	25	9	ACK30734	Ac30734 Human mic	C 888	5	35.7	51	4	AAI74157	Aai74157 Human sil
C 816	5	35.7	25	9	ACH61126	Ac61126 DNA targe	889	5	35.7	54	2	AAQ86781	Aaq86781 SDI-1 mim
C 817	5	35.7	25	9	ACH61252	Ac61252 DNA targe	890	5	35.7	54	2	AAQ74004	Aaq74004 SDI-1 mim
C 818	5	35.7	25	9	ACH57727	Ac57727 DNA targe	C 891	5	35.7	59	2	AAV79267	Aav79267 Staphyloc
C 819	5	35.7	25	12	ADP13756	Adp13756 Renal cel	892	5	35.7	59	6	AAI33309	Aai33309 pEE14/NIF
C 820	5	35.7	27	2	AAQ10132	Aaq10132 Probe 165	893	5	35.7	60	6	ABN41624	Abn41624 Human spl
C 821	5	35.7	27	3	AA53628	Aa53628 Nested pr	894	5	35.7	60	6	ABN33030	Abn33030 Human spl
C 822	5	35.7	27	3	AA53648	Aa53648 Round two	C 895	5	35.7	60	6	ABN44783	Abn44783 Human spl
C 823	5	35.7	27	5	AA61784	Aa61784 B. brevis	C 896	5	35.7	60	6	ABN35375	Abn35375 Human spl
C 824	5	35.7	27	5	AA61806	Aa61806 B. brevis	C 897	5	35.7	60	6	ABN39481	Abn39481 Human spl
C 825	5	35.7	27	12	ADQ07396	Adq07396 Escherich	C 898	5	35.7	60	6	ABN41312	Abn41312 Human spl
C 826	5	35.7	28	2	AAQ63307	Aaq63307 Canine ho	C 899	5	35.7	60	6	ABN39698	Abn39698 Human spl
C 827	5	35.7	28	2	AAQ69066	Aaq69066 Primer fo	C 900	5	35.7	60	6	ABN58757	Abn58757 Human spl
C 828	5	35.7	28	2	AA85503	Aa85503 PCR prime	C 901	5	35.7	60	6	ABN32666	Abn32666 Human spl
C 829	5	35.7	28	12	ADJ27342	Adj27342 Mouse Lac	C 902	5	35.7	60	13	AD853261	Ad853261 Eucalyptu
C 830	5	35.7	30	2	AAQ40767	Aaq40767 Rat FCSR	903	5	35.7	60	13	AD854041	Ad854041 Eucalyptu
C 831	5	35.7	30	4	AAF90048	Aaf90048 PCR prime	C 904	5	35.7	60	13	AD852779	Ad852779 Eucalyptu
C 832	5	35.7	30	4	AAF90049	Aaf90049 PCR prime	905	5	35.7	64	10	ADG42035	Adg42035 Human N33
C 833	5	35.7	30	6	ABX67394	Abx67394 Novel Hel	906	5	35.7	65	2	AAT39538	Aat39538 Nucleotid
C 834	5	35.7	30	10	ADD22742	Add22742 Filamento	C 907	5	35.7	65	6	ABN28602	Abn28602 Rat spl
C 835	5	35.7	30	10	ADD22726	Add22726 Filamento	C 908	5	35.7	65	6	ABN30892	Abn30892 Rat spl
C 836	5	35.7	30	12	ADK15571	Adk15571 Hantaan h	C 909	5	35.7	65	6	ABN56813	Abn56813 Mouse spl
C 837	5	35.7	30	12	ADO79493	Ado79493 KIAA0783	C 910	5	35.7	65	6	ABN54059	Abn54059 Mouse spl
C 838	5	35.7	31	2	ACA03148	Aca03148 PCR prime	911	5	35.7	65	6	ABN54265	Abn54265 Mouse spl
C 839	5	35.7	32	8	ACA61966	Ac61966 Immunolog	C 912	5	35.7	74	9	ADA73848	Ada73848 Carcinoma
C 840	5	35.7	32	12	ADM48508	Adm48508 Human sub	913	5	35.7	76	10	ADG89178	Adg89178 Cancer de
C 841	5	35.7	32	13	ADS80909	Ads80909 Mammalian	914	5	35.7	77	6	ADA44074	Ada44074 VEGF 126
C 842	5	35.7	33	2	AAQ89881	Aaq89881 VEGF RNA	C 915	5	35.7	77	12	ADP85243	Adp85243 Ligand id
C 843	5	35.7	33	2	AAQ25751	Aaq25751 VEGF RNA	C 916	5	35.7	79	12	ACH88247	Ach88247 Human gen
C 844	5	35.7	33	2	AA16217	Aax16217 Serine pr	917	5	35.7	80	2	AAV33399	Aav33399 Group B c
C 845	5	35.7	33	3	AA16252	Aax16252 Serine pr	C 918	5	35.7	80	10	ADH06230	Adh06230 Cxsackie
C 846	5	35.7	33	3	AA16252	Aax16252 Serine pr	919	5	35.7	84	2	AAH87169	Aah87169 Chemokine
C 847	5	35.7	33	3	AA16252	Aax16252 Serine pr	C 920	5	35.7	85	2	AAV33398	Aav33398 Group B c
C 848	5	35.7	33	3	AA16252	Aax16252 Serine pr	921	5	35.7	85	10	ADH06229	Adh06229 Cxsackie
C 849	5	35.7	33	4	AAH45802	Aah45802 Human cel	C 922	5	35.7	87	2	AAH87168	Aah87168 Chemokine
C 850	5	35.7	33	4	AAI67556	Aai67556 Serine pr	923	5	35.7	89	4	AAI7941	Aai7941 Aspergill
C 851	5	35.7	33	4	AAI67517	Aai67517 Serine pr	C 924	5	35.7	90	2	AAI70934	Aai70934 Human gen
C 852	5	35.7	33	6	ABK12096	Abk12096 Phytochro	925	5	35.7	90	6	ABK36905	Abk36905 Human DNA
C 853	5	35.7	33	11	ADM44485	Adm44485 human zin	C 926	5	35.7	90	9	ADA02322	Ada02322 Mouse car
C 854	5	35.7	34	2	AAQ94578	Aaq94578 Antifunga	C 927	5	35.7	90	10	AD872061	Ad872061 Mouse car
C 855	5	35.7	34	2	AAQ89152	Aaq89152 VEGF trun	C 928	5	35.7	92	6	AAI33311	Aai33311 pEE14/NIF
C 856	5	35.7	35	2	ABL51944	Ab151944 Ankyrin r	C 929	5	35.7	99	3	AAH64308	Aah64308 PCR pimer
C 857	5	35.7	37	2	AA25753	Aax25753 VEGF RNA	C 930	5	35.7	100	2	AAV79171	Aav79171 Staphyloc
C 858	5	35.7	38	6	ABK86052	Abk86052 Protein C	C 931	5	35.7	100	2	AAH87176	Aah87176 Double ha
C 859	5	35.7	38	6	ABK86053	Abk86053 Protein C	932	5	35.7	100	8	ACD79500	Ac79500 E. coli K
C 860	5	35.7	41	2	AAV15337	Aav15337 GFP circ	C 933	5	35.7	100	8	ACD70381	Ac70381 E. coli K
C 861	5	35.7	41	2	AAV15337	Aav15337 Synthetic	934	5	35.7	100	8	ACD77616	Ac77616 E. coli K
C 862	5	35.7	41	2	AAV2530	Aav2530 Beta-MHC	935	5	35.7	100	8	ACD77615	Ac77615 E. coli K
C 863	5	35.7	41	2	AA86758	Aax86758 Oligonuc	C 936	5	35.7	100	8	ACD79501	Ac79501 E. coli K
C 864	5	35.7	41	6	AAV77363	Avv77363 Zinc fing	C 937	5	35.7	100	8	ACD74865	Ac74865 E. coli K
C 865	5	35.7	41	6	ABV75607	Abv75607 Human ret	C 938	5	35.7	100	8	ACD75503	Ac75503 E. coli K
C 866	5	35.7	41	6	ABK12098	Abk12098 Phytochro	939	5	35.7	101	3	AAI14387	Aai14387 Human sec
C 867	5	35.7	41	6	ABZ48060	Abz48060 Human ATP	C 940	5	35.7	102	2	AAV79142	Aav79142 Staphyloc
C 868	5	35.7	41	6	ABZ45685	Abz45685 Human ATP	C 941	5	35.7	103	6	ABL80662	Ab180662 Human ova
C 869	5	35.7	41	6	ABZ48021	Abz48021 Human ATP	942	5	35.7	103	8	ABX54766	Abx54766 Bovine ES
C 870	5	35.7	41	6	ABK48786	Abk48786 Oligonuc	943	5	35.7	104	2	AAV89599	Aav89599 EST clone
C 871	5	35.7	41	11	ADM64488	Adm64488 human zin	944	5	35.7	104	12	ACH88212	Ach88212 Human gen
C 872	5	35.7	41	11	ADM64489	Adm64489 human zin	945	5	35.7	105	4	AAH85481	Aah85481 Partial n
C 873	5	35.7	46	4	AAV77052	Aav77052 Primer #4	C 946	5	35.7	111	10	ABZ38510	Abz38510 N. gonorr
C 874	5	35.7	47	3	AAZ66386	Aaz66386 Human map	947	5	35.7	111	10	ABZ38356	Abz38356 N. gonorr
C 875	5	35.7	47	6	AAK40870	Aak40870 Human obe	948	5	35.7	111	10	ABZ41454	Abz41454 N. gonorr
C 876	5	35.7	50	4	AAI78133	Aai78133 Human sil	C 949	5	35.7	114	2	AAT97128	Aat97128 Human car
C 877	5	35.7	50	6	ABZ03620	Abz03620 Human leu	C 950	5	35.7	116	12	ADOI3487	Adoi3487 SNP targe
C 878	5	35.7	50	6	ABZ02784	Abz02784 Human leu	951	5	35.7	117	10	ADOI3487	Adoi3487 SNP targe
C 879	5	35.7	51	4	AAI32599	Aai32599 Human SNP	C 952	5	35.7	118	4	AAK22587	Aak22587 N. gonorr
C 880	5	35.7	51	4	AAI33008	Aai33008 Human SNP	C 953	5	35.7	119	10	AD801164	Ad801164 Verotoxin
C 881	5	35.7	51	4	AAI31770	Aai31770 Human SNP	C 954	5	35.7	121	12	ADK93490	Adk93490 Polynucle

```

955 5 35.7 121 12 ADK91018 Polynucle
956 5 35.7 121 12 ADK92261 Polynucle
957 5 35.7 121 12 ADK92268 Polynucle
c 958 5 35.7 121 12 ADK93848 Polynucle
959 5 35.7 124 4 AAI25295 Probe #15
c 960 5 35.7 124 4 ABA71214 Human foe
c 961 5 35.7 124 4 AAI51447 Probe #20
c 962 5 35.7 124 4 ABA37526 Probe #15
c 963 5 35.7 124 4 ABA45504 Human bon
c 964 5 35.7 124 4 AAK15913 Human bon
c 965 5 35.7 124 4 ABA45190 Human liv
c 966 5 35.7 124 6 ABA19772 Human gen
c 967 5 35.7 124 7 ADS66715 Corn seed
c 968 5 35.7 125 8 ABZ09285 Human oli
c 969 5 35.7 125 10 ABZ78738 Tumour su
c 970 5 35.7 126 4 ABL27169 Drosophil
c 971 5 35.7 128 2 AAT19739 Human gen
c 972 5 35.7 128 4 AAI23034 Probe #12
c 973 5 35.7 128 4 ABA68123 Human foe
c 974 5 35.7 128 4 AAI48335 Probe #17
c 975 5 35.7 128 4 ABA50188 Human bre
c 976 5 35.7 128 4 AAK42262 Human bon
c 977 5 35.7 128 4 AAK16509 Human bra
c 978 5 35.7 128 4 ABA41869 Human liv
c 979 5 35.7 128 5 AAI08693 Probe #86
c 980 5 35.7 128 6 ABA16313 Human gen
c 981 5 35.7 129 3 ABA45783 Human sec
c 982 5 35.7 129 4 ABA99473 Human pro
c 983 5 35.7 130 4 AAI26271 Probe #16
c 984 5 35.7 130 4 AAI2452 Probe #12
c 985 5 35.7 130 4 ABA74589 Human foe
c 986 5 35.7 130 4 ABA67528 Human foe
c 987 5 35.7 130 4 ABA73970 Human foe
c 988 5 35.7 130 4 AAI55071 Probe #23
c 989 5 35.7 130 4 AAI54419 Probe #23
c 990 5 35.7 130 4 AAI47744 Probe #16
c 991 5 35.7 130 4 ABA49625 Human bre
c 992 5 35.7 130 4 ABA39383 Probe #17
c 993 5 35.7 130 4 ABA39058 Probe #17
c 994 5 35.7 130 4 ABA34609 Probe #13
c 995 5 35.7 130 4 AAK49235 Human bon
c 996 5 35.7 130 4 AAK41699 Human bon
c 997 5 35.7 130 4 AAK48590 Human bon
c 998 5 35.7 130 4 AAK15954 Human bra
c 999 5 35.7 130 4 AAK23058 Human bra
c1000 5 35.7 130 4 AAK22423 Human bra

```

ALIGNMENTS

```

RESULT 1
AAQ76921
ID AAQ76921 standard; DNA; 136 BP.
AC AAQ76921;

```

```

XX AC
XX 25-MAR-2003 (revised)
DT 23-SEP-1994 (first entry)
XX XX
XX Human genome fragment.
DE

```

```

KW Brain; placenta; bone marrow; genetic analysis; gene mapping; detection;
KW homology; human; adrenal tissue; ds.
XX

```

```

OS Homo sapiens.
XX

```

```

XX WO9401548-A2.
XX

```

```

XX 20-JAN-1994.
XX

```

```

XX 13-JUL-1993; 93WO-GH001467.
XX

```

```

XX 13-JUL-1992; 92GB-00014857.
XX

```

```

XX (MEDI-) MEDICAL RES COUNCIL.
PA
XX Sibson DR, Gross J, Hadfield KM, Howells D, Starkey M, Kelly M;
PI Shaw D;
XX WPI; 1994-035056/04.
XX
XX New nucleic acid fragment encoding gene products - can be used for
PT genetic analysis and mapping.
XX
XX Claim 1; Page 272; 616pp; English.
XX
XX Human nucleic acid fragments, isolated from brain adrenal tissue, the
CC placenta or bone marrow comprise any of: (A) a sequence selected from
CC (AAQ76401-Q77613), (B) an allelic variation of a sequence as described in
CC (A), or (C) a sequence complementary to (A) or (B). (Updated on 25-MAR-
CC 2003 to correct PN field.)
XX
XX Sequence 136 BP; 36 A; 28 C; 29 G; 43 T; 0 U; 0 Other;
SQ

```

Alignment Scores:

Pred. No.:	8.94e-07	Length:	136
Score:	14.00	Matches:	14
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	2	Gaps:	0

US-09-736-250-5 (1-14) x AAQ76921 (1-136)

QY 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
|||||
DB 24 GAAGATAATCTCTCAGAAATGTCGTTCTGTTGTGGCACT 65

RESULT 2
AAD51549/c
ID AAD51549 standard; cDNA; 351 BP.

XX AC AAD51549;
XX
DT 16-APR-2003 (first entry)
XX
XX Human BCA7 cDNA.
XX
KW Human; breast cancer-associated gene; BCA-related disorder; lymphoma;
KW infectious disease; eating disorder; cancer; Ewing's tumour; allergy;
KW tumour; polycythaemia vera; forensic biology; gene therapy; leukaemia;
KW bone disease; sarcoma; vaccine; gene; ss.
XX
OS Homo sapiens.

XX XX
FH Key Location/Qualifiers
FT CDS 1..351
FT FT /*tag= a
FT FT /product= "BCA protein"
FT FT /transl_except= (pos:22..24, aa:Xaa)
FT FT /transl_except= (pos:28..30, aa:Xaa)
FT FT /transl_except= (pos:202..204, aa:Xaa)
FT FT /transl_except= (pos:313..315, aa:Xaa)
FT FT /transl_except= (pos:334..336, aa:Xaa)
FT FT /note= "Xaa corresponds to in-frame stop codon; No start
FT FT and stop codon"
FT FT /partial
XX
XX WO200287507-A2.
XX
XX 07-NOV-2002.
XX
XX 29-APR-2002; 2002WO-US013584.
XX
XX 27-APR-2001; 2001US-0287170P.
XX

compositions, such as vaccines, for the diagnosis, prevention, and treatment of colon cancer. Polynucleotide sequences may be used as hybridisation probes or primers, and in the design and preparation of ribozyme molecules for inhibiting expression of tumour polypeptides and proteins in tumour cells. The compositions are useful for stimulating an immune response against cancer, particularly for the immunotherapy of colon cancer, and as markers for the progression of cancer. ABK4450-ABK46237 represent coding sequences of human colon tumour proteins of the invention. Note: With the exception of SEQ ID No 1 and 2, the sequence data for this patent did not form part of the printed specification but was supplied by the European Patent Office

Sequence 444 BP; 134 A; 81 C; 74 G; 155 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2.52e-06 Length: 444
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-736-250-5 (1-14) x ABK45862 (1-444)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
|||||
Db 436 GAAGATAATGCTCAGAAATGGGTTCTGTGTGGCACT 395
|||||

RESULT 5

AAS25071
ID AAS25071 standard; cDNA; 447 BP.

XX AC AAS25071;

DT 07-NOV-2001 (first entry)

XX DE Human ovarian PCR-subtracted cDNA library clone #1252.

XX KW Immunogenic protein; cancer; ovarian tumour; T-cell stimulation; ss;
KW gene therapy; cytostatic; T-cell expansion; nucleic acid hybridisation;
KW primer; probe.

XX OS Homo sapiens.

XX PN WO200157207-A2.

XX PD 09-AUG-2001.

XX PF 05-FEB-2001; 2001WO-US003733.

XX PR 04-FEB-2000; 2000US-0180403P.

XX PR 28-MAR-2000; 2000US-0192745P.

XX PA (CORI-) CORIXA CORP.

XX PI Algate PA, Mannion J;

XX DR WPI; 2001-489879/53.

XX PT New polynucleotides encoding ovarian tumor proteins, useful for treating
PT ovarian cancer, and as probes, primers, and markers of cancer
PT progression.

XX PS Example 1; Page 304; 378pp; English.

XX CC The invention comprises compositions used for the therapy and diagnosis
CC of ovarian cancer. The compositions comprise one or more ovarian tumour
CC proteins, their associated polynucleotides, or immunogenic portions of
CC the proteins. The ovarian tumour polynucleotides and polypeptides are
CC useful for stimulating and/or expanding T cells specific for a tumour
CC protein. They are also useful for inhibiting the development of cancer in
CC a patient with an ovarian tumour DNA or protein by incubating isolated T-
CC cells allowing them to proliferate, and administering to the patient. The

CC sequences can be used as markers for cancer, for example, to monitor
CC ovarian cancer progression. Probes and primers are useful in nucleic acid
CC hybridisation, in detecting the presence of complementary sequences in a
CC given sample, for preparing mutant species and for preparing other
CC genetic constructions. Sequences AAS23820-AAS25231 and AAS25328-AAS25549
CC represent human ovarian tumour protein cDNA clones

XX SQ Sequence 447 BP; 157 A; 79 C; 92 G; 115 T; 0 U; 4 Other;

Alignment Scores:
Pred. No.: 2.53e-06 Length: 447
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-736-250-5 (1-14) x AAS25071 (1-447)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
|||||
Db 93 GAAGATAATGCTCAGAAATGGGTTCTGTGTGGCACT 134
|||||

RESULT 6

AAH83716
ID AAH83716 standard; cDNA; 447 BP.

XX AC AAH83716;

DT 25-SEP-2001 (first entry)

XX DE Human ovarian tumour associated polynucleotide sequence SEQ ID NO:1340.

XX KW Human; ovarian tumour; ovarian cancer; diagnosis; gene therapy;
KW immunogenic; vaccine; ss.

XX OS Homo sapiens.

XX PN WO200151513-A2.

XX PD 19-JUL-2001.

XX PF 16-JAN-2001; 2001WO-US001575.

XX PR 14-JAN-2000; 2000US-0176722P.

XX PA (CORI-) CORIXA CORP.

XX PI Algate PA;

XX DR WPI; 2001-425866/45.

XX FT Novel ovarian tumor proteins, and nucleic acids encoding them, used to
FT treat and diagnose cancers, particularly ovarian cancer.

XX PS Claim 5; Page 308; 338pp; English.

XX CC AAH82377 to AAH83878 represent human ovarian tumour-associated
CC polynucleotide sequences which encode ovarian tumour proteins. The
CC ovarian tumour protein and polynucleotide sequences have cytostatic
CC activity, and can be used in gene therapy and vaccine production. The
CC ovarian tumour proteins and polynucleotides can be used to inhibit the
CC development of cancer, particularly ovarian cancer. They can also be used
CC to diagnose the onset and progression of cancer

XX SQ Sequence 447 BP; 157 A; 79 C; 92 G; 115 T; 0 U; 4 Other;

Alignment Scores:
Pred. No.: 2.53e-06 Length: 447
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

```
DB: 5 Gaps: 0
US-09-736-250-5 (1-14) x AAH83716 (1-447)
Oy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
    |||||
Db 93 GAAGATAATGTCCTCAGAAATGTTGGTCTCTGTGTGGCACT 134

RESULT 7
ADK61065/c
ID ADK61065 standard; DNA; 597 BP.
XX AC ADK61065;
XX AC
XX DT 06-MAY-2004 (first entry)
XX DE
XX DE Ovarian cancer-related DNA #220 with altered ovarian cancer expression.
XX KW ds; gene; ovarian tumor; BRCA-1-like; BRCA-2-like; non-BRCA-like;
XX KW gene expression; primer; cancer.
XX OS Homo sapiens.
XX PN WO2003068054-A2.
XX PD 21-AUG-2003.
XX PF 13-FEB-2003; 2003WO-US004698.
XX PR 13-FEB-2002; 2002US-0357031P.
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PA (SLOK ) SLOAN KETTERING INST CANCER RES.
XX PI Jazaeri AA, Boyd J, Liu ET;
XX WPI; 2003-689589/65.
XX DR
XX PT Classifying an ovarian tumor as a BRCA-1-like or BRCA-2-like or non-BRCA-
XX PT like tumor by determining a pattern of expression in the ovarian tumor of
XX PT several markers.
XX PS Disclosure; SEQ ID NO 235; 137pp; English.
XX CC The invention relates to a method of classifying an ovarian tumor as a
XX CC BRCA-1-like or BRCA-2-like or non-BRCA-like tumor by: (1) determining a
XX CC pattern of expression in the ovarian tumor of several markers given in
XX CC the specification; and (2) comparing a similarity of the pattern of
XX CC expression of the markers in the ovarian tumor to a pattern of expression
XX CC of the markers in a comparison tissue of a known BRCA-1-like or BRCA-2-
XX CC like or non-BRCA-like tumor. The method is useful for classifying an
XX CC ovarian tumor as a BRCA-1-like or BRCA-2-like or non-BRCA-like tumor.
XX CC This sequence corresponds to an ovarian cancer -related gene having an
XX CC altered pattern of expression in ovarian cancer. (Note: The sequence data
XX CC for this patent did not form part of the printed specification but was
XX CC obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences).
XX SQ Sequence 597 BP; 152 A; 126 C; 143 G; 171 T; 0 U; 5 Other;

Alignment Scores:
Pred. No.: 3.26e-06 Length: 597
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-736-250-5 (1-14) x ADK61065 (1-597)
Oy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
    |||||
Db 303 GAAGATAATGTCCTCAGAAATGTTGGTCTCTGTGTGGCACT 262

RESULT 8
AAAX40003/c
ID AAAX40003 standard; DNA; 804 BP.
XX AC AAAX40003;
XX AC
XX DT 02-JUL-1999 (first entry)
XX DE
XX DE Prostate cancer associated gene.
XX KW Cancer associated antigen; diagnosis; research; treatment; human;
XX KW breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer;
XX KW prostate cancer; ss.
XX OS Homo sapiens.
XX PN WO9904265-A2.
XX PD 28-JAN-1999.
XX PF 15-JUL-1998; 98WO-US014679.
XX PR 17-JUL-1997; 97US-00896164.
XX PR 10-OCT-1997; 97US-0061599P.
XX PR 10-OCT-1997; 97US-0061765P.
XX PR 10-OCT-1997; 97US-00948705.
XX PR 11-OCT-1997; 97GB-00021697.
XX PR 22-JUN-1998; 98US-00102322.
XX PA (LUDW-) LUDWIG INST CANCER RES.
XX PI Old LJ, Scanlan MJ, Stockert E, Gure A, Chen Y, Gout I;
XX PI O'hare M, Obata Y, Pfreundschuh M, Tureci O, Sahin U;
XX WPI; 1999-132448/11.
XX DR
XX PT New isolated cancer associated nucleic acids and polypeptides - isolated
XX PT using sera from cancer patients, used to develop products for the
XX PT diagnosis, monitoring or treatment of cancers.
XX PS Claim 67; Page 630; 787pp; English.
XX CC The invention relates to a method for diagnosing a disorder characterised
XX CC by expression of a human cancer associated antigen precursor coded for by
XX CC a nucleic acid molecule (NAM). The method comprises: (a) contacting a
XX CC biological sample isolated from a subject with an agent that specifically
XX CC binds to the NAM, an expression product or a fragment of an expression
XX CC product complexed with an HLA molecule; and (b) determining the
XX CC interaction between the agent and the NAM or the expression product as a
XX CC determination of the disorder. The products and methods can be used in
XX CC the diagnosis, monitoring, research, or treatment of conditions
XX CC characterised by the expression of various cancer associated antigens.
XX CC The invention provides nucleic acid sequences and encoded polypeptides
XX CC which are cancer associated antigen precursors expressed in human breast
XX CC cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and
XX CC lung cancer
XX SQ Sequence 804 BP; 208 A; 172 C; 188 G; 222 T; 0 U; 14 Other;

Alignment Scores:
Pred. No.: 4.23e-06 Length: 804
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-736-250-5 (1-14) x AAAX40003 (1-804)
Oy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
    |||||
Db 301 GAAGATAATGTCCTCAGAAATGTTGGTCTCTGTGTGGCACT 260
```

RESULT 9
ADN01156
ID ADN01156 standard; DNA; 903 BP.
XX AC
XX ADN01156;
XX
XX 01-JUL-2004 (first entry)
XX
XX Human cell growth, differentiation, and death-associated coding seq #15.
XX
XX human; cell growth; cell differentiation; cell death; CGDD;
XX cell proliferative disorder; arteriosclerosis; atherosclerosis; bursitis;
XX cirrhosis; hepatitis; polycythemia vera; psoriasis; cancer;
XX developmental disorder; Cushing's syndrome; hypothyroidism;
XX neurological disorder; epilepsy; stroke; Alzheimer's disease;
XX Pick's disease; Huntington's disease; Parkinson's disease;
XX multiple sclerosis; autoimmune disorder; inflammatory disorder; AIDS;
XX allergy; anaemia; asthma; contact dermatitis; diabetes mellitus;
XX reproductive disorder; infertility; endometriosis; uterine fibroid; gene;
XX ds.
XX
XX Homo sapiens.
XX
XX WO2004031364-A2.
XX
XX 15-APR-2004.
XX
XX 03-OCT-2003; 2003WO-US031441.
XX
XX 03-OCT-2002; 2002US-0416205P.
XX 25-OCT-2002; 2002US-0421521P.
XX 21-NOV-2002; 2002US-0428376P.
XX 23-DEC-2002; 2002US-0436288P.
XX 10-JAN-2003; 2003US-0439292P.
XX 13-FEB-2003; 2003US-0447578P.
XX
XX (INCY-) INCYTE CORP.
XX (BURR/) BURRILL J D.
XX
XX Elliott VS, Swarnakar A, Tang YT, Yue H, Lu DAM, Khare R;
XX Chawla NK, Richardson TW, Marquis JP, Lal PG, Nguyen DB, Lee SY;
XX Tran UK, Bhatia UG, Lee S, Blake JJ, Ho A, Zheng W, Gao J, Tran B;
XX Yang YG, Gietzen KJ, Hatalia AJA;
XX
XX WPI; 2004-330172/30.
XX P-PSDB; ADN01131.
XX
XX New isolated polypeptides associated with cell growth, differentiation
XX and death, useful for diagnosing, treating or preventing e.g.
XX atherosclerosis, psoriasis, cancers, Alzheimer's disease, AIDS, anemia,
XX diabetes mellitus or infertility.
XX
XX Claim 5; SEQ ID NO 40; 213pp; English.

The invention comprises the amino acid and coding sequences of human proteins that are associated with cell growth, differentiation, and death (CGDD). The DNA and protein sequences of the invention are useful for diagnosing, treating or preventing disorders associated with aberrant expression of CGDD, such as: cell proliferative disorders (e.g. arteriosclerosis, atherosclerosis, bursitis, cirrhosis, hepatitis, polycythemia vera, psoriasis and cancers), developmental disorders (e.g. Cushing's syndrome and hypothyroidism), neurological disorders (e.g. epilepsy, stroke, Alzheimer's disease, Pick's disease, Huntington's disease, Parkinson's disease and multiple sclerosis), autoimmune/inflammatory disorders (e.g. AIDS, allergies, anaemia, asthma, contact dermatitis and diabetes mellitus), and reproductive disorders (e.g. infertility, endometriosis and uterine fibroid). The present DNA sequence encodes a human CGDD-associated protein of the invention.

SQ Sequence 903 BP; 247 A; 202 C; 201 G; 253 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 4.68e-06 Length: 903
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-09-736-250-5 (1-14) x ADN01156 (1-903)

QY 1 GLUASPASVValSerGluHsnValGlySerValCysGlyThr 14
DB 797 GAAGATAATCTCAGAAAATGGGTCTGTGTGTGGCACT 838

RESULT 10
AAZ37836
ID AAZ37836 standard; DNA; 1260 BP.
XX AAZ37836;
XX AC
XX 09-FEB-2000 (first entry)
XX
XX Human cyclin I nucleotide sequence.
XX
XX Cyclin-dependent kinase 2; CDK2; hReq; hReq*-1; hReq*-2; cyclin I;
XX ERH; cell cycle; proliferation; cancer; hyperproliferative disorder;
XX atherosclerosis; tumour; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 1..1134
XX FT /*tag= a
XX FT /product= "Cyclin_I"
XX
XX W09925829-A2.
XX
XX 27-MAY-1999.
XX
XX 12-NOV-1998; 98WO-US024095.
XX
XX 13-NOV-1997; 97US-00969106.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Yang M, Nandabalan K, Schulz VP;
XX
XX WPI; 2000-061923/05.
XX P-PSDB; AAY52185.
XX
XX New complexes of the cyclin-dependent kinase 2 protein with its
XX interacting proteins, used to treat, e.g. atherosclerosis.
XX
XX Example; Fig 2; 90pp; English.

This sequence is the human Cyclin I nucleotide sequence. Cyclin I is expressed at almost constant levels throughout the cell cycle, and is implicated in controlling cell cycle progression and transcriptional control. Cyclins form complexes with cyclin-dependent kinases. CDK2, cyclin-dependent kinase 2, is used in the invention which relates to complexes of the CDK2 protein with other proteins, selected from cyclin I, ERH, hReq, hReq*-1 and hReq*-2 (AAY52185-YS2188). CDK2 is expressed late in G1 or early in S phase of the cell cycle, and is pivotal for G1/S transition. Compositions containing a CDK2 complex, an antibody targeting the complex, and nucleotide sequences encoding CDK2 or its derivatives can be used therapeutically. The complexes and their nucleotide sequences can be used to treat diseases or disorders associated with increased or decreased levels of the complex. Screening the complex, or a derivative or a modulator of the complex for neoplastic activity by measuring the survival or proliferation of cells from a malignant cell line when in contact with the complex can be used to indicate if the complex has anti-neoplastic activity. Screening for molecules that modulate the formation of the complexes can be used for treating or preventing atherosclerosis or atherosclerosis-associated disease by contacting cells

or using a test animal, in which tumour growth or regression is measured to test whether anti-neoplastic activity is displayed. Diseases which can be treated or prevented by molecule/s which modulate the function of the complex include cancer, hyperproliferative disorders and atherosclerosis

Sequence 1260 BP; 352 A; 283 C; 274 G; 351 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	6.26e-06	Length:	1260
Score:	14.00	Matches:	14
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	3	Gaps:	0

US-09-736-250-5 (1-14) x AA237836 (1-1260)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14

Db 1027 GAAGATAATGCTCAGAAAATGTGGTTCGTGTGGCACT 1068

RESULT 11

ID ABK83672 standard; cDNA; 1260 BP.

XX ABK83672;

XX 14-AUG-2002 (first entry)

XX Human cDNA differentially expressed in granulocytic cells #243.

XX Human; ss; granulocytic cell; DNA chip; bacterial infection;

XX viral infection; parasitic infection; protozoal infection;

XX fungal infection; sterile inflammatory disease; psoriasis;

XX rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;

XX cardiac reperfusion injury; renal reperfusion injury; ARDS;

XX adult respiratory distress syndrome; inflammatory bowel disease;

XX Crohn's disease; ulcerative colitis; periodontal disease;

XX granulocyte activation; chronic inflammation; allergy.

OS Homo sapiens.

XX WO200228999-A2.

XX 11-APR-2002.

XX 03-OCT-2001; 2001WO-US030821.

XX 03-OCT-2000; 2000US-0237189P.

XX (GENE-) GENE LOGIC INC.

XX Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;

XX WPI; 2002-435328/46.

XX Claim 1; SEQ ID NO 243; 114pp; English.

XX The invention relates to detecting (M1) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (Gs) identified by DNA chip analysis as given in the specification, and comparing the expression level to an expression level in an unactivated GC, where differential expression of Gs is indicative of GCA. Also included are modulating (M2) GA by contacting GC with an agent that alters the expression of at least one gene in Gs; (2) screening (M3) for an agent capable of modulating GCA or an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the gene expression profile; (3) detecting (M4) an inflammation (especially chronic) in a

CC tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the level of expression in a sample of the tissue of gene(s) from Gs, where the level of expression of the gene is indicative of inflammation; (4) treating (M5) an inflammation (especially chronic) or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by contacting a tissue having inflammation with an agent that modulates the expression of gene(s) from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for modulating GA; M3 is useful for screening an agent capable of modulating GCA preferably in an inflammation in a tissue; M4 is useful for detecting an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease (e.g. psoriasis, rheumatoid arthritis, glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal reperfusion injury, ARDS, adult respiratory distress syndrome, inflammatory bowel disease, Crohn's disease, ulcerative colitis, periodontal disease; also bacterial infection, viral infection, parasitic infection, protozoal infection, fungal infection and M5 is useful for treating one of the above conditions. The present sequence represents a gene differentially expressed in granulocytes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 1260 BP; 352 A; 283 C; 274 G; 351 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	6.26e-06	Length:	1260
Score:	14.00	Matches:	14
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-09-736-250-5 (1-14) x ABK83672 (1-1260)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14

Db 1027 GAAGATAATGCTCAGAAAATGTGGTTCGTGTGGCACT 1068

RESULT 12

ID ADK61064 standard; DNA; 1260 BP.

XX ADK61064;

XX 06-MAY-2004 (first entry)

XX Ovarian cancer-related DNA #219 with altered ovarian cancer expression.

XX ds; gene; ovarian tumor; BRCA-1-like; BRCA-2-like; non-BRCA-like; gene expression; primer; cancer.

XX Homo sapiens.

XX WO2003068054-A2.

XX 21-AUG-2003.

XX 13-FEB-2003; 2003WO-US004688.

XX 13-FEB-2002; 2002US-0357031P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX (SLOK) SLOAN KETTERING INST CANCER RES.

XX Jazaeri AA, Boyd J, Liu ET;

XX WPI; 2003-689589/65.

XX Classifying an ovarian tumor as a BRCA-1-like or BRCA-2-like or non-BRCA-like tumor by determining a pattern of expression in the ovarian tumor of

PT several markers.
XX
PS Disclosure; SEQ ID NO 234; 137pp; English.
XX
CC The invention relates to a method of classifying an ovarian tumor as a
CC BRCA-1-like or BRCA-2-like or non-BRCA-like tumor by: (1) determining a
CC pattern of expression in the ovarian tumor of several markers given in
CC the specification; and (2) comparing a similarity of the pattern of
CC expression of the markers in the ovarian tumor to a pattern of expression
CC of the markers in a comparison tissue of a known BRCA-1-like or BRCA-2-
CC like or non-BRCA-like tumor. The method is useful for classifying an
CC ovarian tumor as a BRCA-1-like or BRCA-2-like or non-BRCA-like tumor.
CC This sequence corresponds to an ovarian cancer -related gene having an
CC altered pattern of expression in ovarian cancer. (Note: The sequence data
CC for this patent did not form part of the printed specification but was
CC obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences).
XX
SQ Sequence 1260 BP; 352 A; 283 C; 274 G; 351 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6.26e-06 Length: 1260
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-736-250-5 (1-14) x ADK61064 (1-1260)

Qy 1 GluAspAenValSerGluAenValGlySerValCysGlyThr 14
Db 1027 GAAGATAATGCTCAGAAAATGGGTCTCTGTGTGGCACT 1068

RESULT 13
ADI31573
ID ADI31573 standard; cDNA; 1260 BP.
XX
AC ADI31573;
XX
DT 17-JUN-2004 (first entry)
XX
DE Human cDNA #899.
XX
KW Human; gene; ss; immunological response; immunopathological condition;
KW Crohn's disease; asthma; ulcerative colitis; hypereosinophilia;
KW irritable bowel syndrome; osteoarthritis; rheumatoid arthritis;
KW acute monocytic leukaemia; antiinflammatory; antiasthmatic; antiulcer;
KW osteopathic; antiarthritic; antirheumatic; cytostatic.
XX
OS Homo sapiens.
XX
FN US6607879-B1.
XX
PD 19-AUG-2003.
XX
PF 09-FEB-1998; 98US-00023655.
XX
PR 09-FEB-1998; 98US-00023655.
XX
PA (INCY-) INCYTE CORP.
XX
PI Cocks BG, Stuart SG, Seilhamer JJ;
XX
WPI; 2003-895307/82.
XX
DR A composition comprising a plurality of cDNAs, useful for detecting
PT altered expression of genes in an immunological response or for
PT diagnosing and treating an immunopathology, e.g. Crohn's disease, asthma
PT or osteoarthritis.
XX
PS Claim 1; SEQ ID NO 899; 50pp; English.
XX

CC The invention relates to a composition comprising a plurality of cDNAs
CC for detecting the altered expression of genes in an immunological
CC response. The invention also relates to a method of diagnosing or
CC monitoring the treatment of an immunopathological condition in a sample,
CC comprising obtaining nucleic acids from a sample, contacting the nucleic
CC acids of the sample with an array comprising the plurality of cDNAs under
CC conditions to form one or more hybridisation complexes, detecting the
CC hybridisation complexes and comparing the levels of the detected
CC hybridisation complexes with the level of hybridisation complexes
CC detected in a non-diseased sample, where an altered level of the detected
CC hybridisation complexes correlates with the presence of an
CC immunopathological condition. Also disclosed are an expression profile
CC comprising a microarray and a plurality of detectable complexes and a
CC method for identifying a plurality of polynucleotide probes. The cDNAs
CC are useful as hybridisable array elements in a microarray for monitoring
CC the expression of target polynucleotides. The microarray can be used in
CC the diagnosis of an immunopathology, such as Crohn's disease, asthma,
CC ulcerative colitis, hypereosinophilia, irritable bowel syndrome,
CC osteoarthritis, rheumatoid arthritis or acute monocytic leukaemia, and in
CC identifying agents for the treatment of the diseases. The microarray may
CC also be used in drug discovery and development, toxicological and
CC carcinogenicity studies, forensics or pharmacogenomics. The composition
CC may also be used in purification of a subpopulation of mRNAs, cDNAs or
CC genomic fragments. This sequence represents a human cDNA of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification but was obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 1260 BP; 352 A; 283 C; 274 G; 351 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6.26e-06 Length: 1260
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 11 Gaps: 0

US-09-736-250-5 (1-14) x ADI31573 (1-1260)

Qy 1 GluAspAenValSerGluAenValGlySerValCysGlyThr 14
Db 1027 GAAGATAATGCTCAGAAAATGGGTCTCTGTGTGGCACT 1068

RESULT 14
ADR25465
ID ADR25465 standard; DNA; 1260 BP.
XX
AC ADR25465;
XX
DT 21-OCT-2004 (first entry)
XX
DE Breast cancer prognosis marker #1326.
XX
KW ds; breast cancer; prognosis; gene expression; diagnosis.
XX
OS Homo sapiens.
XX
FN WO2004065545-A2.
XX
PD 05-AUG-2004.
XX
PF 15-JAN-2004; 2004WO-US001100.
XX
PR 15-JAN-2003; 2003US-00342887.
XX
PA (ROSE-) ROSETTA INPHARMATICS LLC.
PA (NECA-) NETHERLANDS CANCER INST.
XX
PI Van't Veer LJ, He Y;
XX
DR WPI; 2004-593473/57.
XX

PT Classifying a breast cancer patient according to prognosis comprises
PT determining the similarity between the level of expression of each of
PT five genes in a cell sample taken from patient, to control levels.
XX
XX
PS Disclosure; SEQ ID NO 1326; 226pp; English.

XX The invention relates to a method of classifying a breast cancer patient
CC according to prognosis by determining the similarity between the level of
CC expression of each of five genes for which markers are listed in the
CC specification, in a cell sample taken from the breast cancer patient, to
CC control levels of expression for each respective five genes to obtain a
CC patient similarity value. The methods are useful for classifying a breast
CC cancer patient according to prognosis. Kits and computer program products
CC are useful for data analysis using the diagnostic, prognostic and
CC statistical methods of the invention. This sequence corresponds to a
CC marker used in the method of the invention.

XX
SQ Sequence 1260 BP; 352 A; 283 C; 274 G; 351 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6.26e-06 Length: 1260
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-09-736-250-5 (1-14) x ADR25465 (1-1260)

Oy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 1027 GAAGATAATGTCCTCAGAAAATGGGTTCTGTGTGGCACT 1068

RESULT 15

AAT73937
ID AAT73937 standard; DNA; 1328 BP.

XX
AC AAT73937;

XX 02-DEC-1997 (first entry)

XX DNA encoding human cyclin I.

XX human; cyclin I; antisense; probe; neurone; cancer; antibody; ds.

XX Homo sapiens.

XX Key Location/Qualifiers
XX CDS 69..1202
XX /*tag= a

XX WO9712973-A1.

XX 10-APR-1997.

XX 07-OCT-1996; 96WO-JP002905.

XX 05-OCT-1995; 95JP-00284663.

XX (SUME) SUMITOMO ELECTRIC IND CO.

XX Nakamura T;

XX WPI; 1997-226217/20.

XX P-PSDB; AAW21965.

XX Human cyclin I protein and related (anti:sense) DNA - used for neuron
PT labelling method and cancer cell detection.

XX Example 1; Fig 1; 45pp; Japanese.

XX This sequence encodes human cyclin I. Antisense polynucleotides are
XX useful for as probes and can be labelled and used for detection of

CC neurones by hybridisation with mRNA for cyclin I (contained in the
CC neurones and arising by the expression of the cyclin I gene in these
CC cells). The gene can be used for detection of cancer cells by detecting
CC the expression of the cyclin I gene in these cells. Also antibodies
CC specific for the fragments of the protein (especially AAW21966) can be
CC used for detection

XX
SQ Sequence 1328 BP; 376 A; 292 C; 302 G; 358 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6.56e-06 Length: 1328
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-736-250-5 (1-14) x AAT73937 (1-1328)

Oy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 1095 GAAGATAATGTCCTCAGAAAATGGGTTCTGTGTGGCACT 1136

Search completed: February 11, 2005, 10:39:48

Job time : 104.197 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 11, 2005, 09:52:50 ; Search time 11.1356 Seconds
(without alignments)
2057.184 Million cell updates/sec

Title: US-09-736-250-5

Perfect score: 14

Sequence: 1 EDNVSENVGVCGT 14

Scoring table:

OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Word size: 1

Total number of hits satisfying chosen parameters: 2395371

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO.spool/US09736250/runat_07022005_154942_20670/app.query.fasta_1.718
-DB=Issued Patents_NA -QWMT=fastap -SUFFIX=oligo.rn1 -MINMATCH=0.1 -LOOPCUI=0
-LOOPEXT=0 -UNITS=Dits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.ccd
-LIST=1000 -DOCALLIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09736250@cgn 1 1 93 @runat_07022005_154942_20670 -NCPU=6 -ICPU=3
-NO MMAP -LARGQUERY -NEG_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	14	100.0	1133	3	US-09-054-492B-2	Sequence 2, Appli
2	14	100.0	1260	2	US-08-969-106-5	Sequence 5, Appli
3	14	100.0	1260	4	US-09-338-125-5	Sequence 5, Appli
4	14	100.0	1260	4	US-09-023-655-899	Sequence 899, App
5	13	92.9	304	4	US-09-513-999C-29894	Sequence 29894, A
C 6	7	50.0	601	4	US-09-949-016-187337	Sequence 187337,
C 7	7	50.0	601	4	US-09-949-016-187338	Sequence 187338,
C 8	7	50.0	601	4	US-09-949-016-187339	Sequence 187339,
C 9	7	50.0	601	4	US-09-949-016-187340	Sequence 187340,
10	7	50.0	1226	4	US-09-976-594-1110	Sequence 1110, Ap
C 11	7	50.0	76563	4	US-09-949-016-17099	Sequence 17099, A
C 12	7	50.0	78269	4	US-09-949-016-12497	Sequence 12497, A

c	13	6	42.9	19	4	US-09-422-978-6641	Sequence 6641, Ap
c	14	6	42.9	201	4	US-09-489-039A-3894	Sequence 3894, Ap
c	15	6	42.9	256	4	US-09-513-999C-27371	Sequence 27371, A
c	16	6	42.9	293	4	US-09-702-705-538	Sequence 538, App
c	17	6	42.9	293	4	US-09-736-457-538	Sequence 538, App
c	18	6	42.9	293	4	US-09-614-124B-538	Sequence 538, App
c	19	6	42.9	293	4	US-09-671-325-538	Sequence 538, App
c	20	6	42.9	293	4	US-09-589-184-538	Sequence 538, App
c	21	6	42.9	293	4	US-09-658-824-538	Sequence 538, App
c	22	6	42.9	343	5	PCT-US95-08295-13	Sequence 13, Appl
c	23	6	42.9	480	3	US-09-188-930-39	Sequence 39, Appl
c	24	6	42.9	480	3	US-09-188-930-208	Sequence 208, App
c	25	6	42.9	480	4	US-09-312-283C-39	Sequence 39, Appl
c	26	6	42.9	480	4	US-09-312-283C-208	Sequence 208, App
c	27	6	42.9	498	3	US-09-328-111-252	Sequence 252, App
c	28	6	42.9	601	4	US-09-949-016-18756	Sequence 18756, A
c	29	6	42.9	601	4	US-09-949-016-33007	Sequence 33007, A
c	30	6	42.9	601	4	US-09-949-016-33008	Sequence 33008, A
c	31	6	42.9	601	4	US-09-949-016-71298	Sequence 71298, A
c	32	6	42.9	601	4	US-09-949-016-107870	Sequence 107870, A
c	33	6	42.9	601	4	US-09-949-016-133721	Sequence 133721, A
c	34	6	42.9	601	4	US-09-949-016-130929	Sequence 130929, A
c	35	6	42.9	601	4	US-09-949-016-140783	Sequence 140783, A
c	36	6	42.9	601	4	US-09-949-016-164103	Sequence 164103, A
c	37	6	42.9	601	4	US-09-949-016-175780	Sequence 175780, A
c	38	6	42.9	601	4	US-09-949-016-186703	Sequence 186703, A
c	39	6	42.9	639	4	US-09-489-039A-3940	Sequence 3940, Ap
c	40	6	42.9	708	4	US-09-543-681A-2551	Sequence 2551, Ap
c	41	6	42.9	823	4	US-09-949-016-1025	Sequence 1025, Ap
c	42	6	42.9	823	4	US-09-949-016-2692	Sequence 2692, Ap
c	43	6	42.9	830	4	US-09-976-594-858	Sequence 858, App
c	44	6	42.9	862	3	US-09-149-476-73	Sequence 73, Appl
c	45	6	42.9	932	3	US-09-149-476-237	Sequence 237, App
c	46	6	42.9	962	1	US-08-324-301-14	Sequence 14, Appl
c	47	6	42.9	1001	4	US-09-671-317-17	Sequence 17, Appl
c	48	6	42.9	1001	4	US-09-671-317-18	Sequence 18, Appl
c	49	6	42.9	1236	4	US-09-252-991A-1087	Sequence 1087, Ap
c	50	6	42.9	1512	3	US-08-476-509B-1	Sequence 1, Appli
c	51	6	42.9	1626	3	US-08-348-518-1	Sequence 1, Appli
c	52	6	42.9	1731	4	US-09-540-236-366	Sequence 366, App
c	53	6	42.9	1765	4	US-09-270-767-11023	Sequence 11023, A
c	54	6	42.9	1842	4	US-09-016-434-46	Sequence 46, Appl
c	55	6	42.9	1933	4	US-09-023-655-739	Sequence 739, App
c	56	6	42.9	1947	4	US-09-252-991A-1048	Sequence 1048, Ap
c	57	6	42.9	2253	6	5457037-2	Patent No. 5457037
c	58	6	42.9	2253	6	5457037-2	Patent No. 5457037
c	59	6	42.9	2256	4	US-09-949-016-2427	Sequence 2427, Ap
c	60	6	42.9	2256	4	US-09-949-016-2428	Sequence 2428, Ap
c	61	6	42.9	2437	1	US-07-795-859B-5	Sequence 5, Appli
c	62	6	42.9	2437	1	US-08-457-616-5	Sequence 5, Appli
c	63	6	42.9	2437	3	US-09-235-538-1	Sequence 1, Appli
c	64	6	42.9	2455	4	US-09-949-016-1570	Sequence 1570, Ap
c	65	6	42.9	2625	6	5457037-4	Patent No. 5457037
c	66	6	42.9	2625	6	5457037-4	Patent No. 5457037
c	67	6	42.9	2715	4	US-09-543-681A-392	Sequence 392, App
c	68	6	42.9	2980	4	US-09-799-451-373	Sequence 373, App
c	69	6	42.9	2994	4	US-09-976-594-398	Sequence 398, App
c	70	6	42.9	3189	4	US-09-447-399-1	Sequence 1, Appli
c	71	6	42.9	3336	6	5457037-1	Patent No. 5457037
c	72	6	42.9	3336	6	5457037-1	Patent No. 5457037
c	73	6	42.9	3420	4	US-09-447-399-3	Sequence 3, Appli
c	74	6	42.9	3464	3	US-09-318-448-30	Sequence 30, Appl
c	75	6	42.9	3502	4	US-09-976-594-659	Sequence 659, App
c	76	6	42.9	3546	1	US-07-951-715A-27	Sequence 27, Appl
c	77	6	42.9	3546	2	US-08-459-448A-27	Sequence 27, Appl
c	78	6	42.9	3546	3	US-08-459-595A-27	Sequence 27, Appl
c	79	6	42.9	3546	3	US-08-459-504B-27	Sequence 27, Appl
c	80	6	42.9	3546	3	US-08-459-444-27	Sequence 27, Appl
c	81	6	42.9	3546	3	US-09-547-422-27	Sequence 27, Appl
c	82	6	42.9	3546	4	US-09-968-462-27	Sequence 27, Appl
c	83	6	42.9	3709	3	US-09-541-782-7	Sequence 7, Appli
c	84	6	42.9	3709	3	US-09-723-820-7	Sequence 7, Appli
c	85	6	42.9	3709	4	US-10-270-085-7	Sequence 7, Appli

86	6	42.9	3887	4	US-09-976-594-660	Sequence 660, App	159	6	42.9	1664976	4	US-09-692-570-1	Sequence 1, Appl
87	6	42.9	3934	4	US-09-023-655-1066	Sequence 1966, App	160	5	35.7	17	3	US-08-584-040-4276	Sequence 4276, Ap
88	6	42.9	4248	4	US-09-252-991A-9867	Sequence 9867, Ap	c 161	5	35.7	17	4	US-09-371-728-2043	Sequence 2043, Ap
89	6	42.9	4530	4	US-09-566-921-134	Sequence 134, App	c 162	5	35.7	17	4	US-09-685-664B-2043	Sequence 2043, Ap
90	6	42.9	4530	4	US-09-939-039-358	Sequence 358, App	163	5	35.7	20	4	US-09-596-248D-50	Sequence 50, Appl
c 91	6	42.9	4628	4	US-09-799-451-85	Sequence 85, Appl	164	5	35.7	21	3	US-09-061-273-10	Sequence 10, Appl
c 92	6	42.9	4819	4	US-09-774-528-72	Sequence 72, Appl	165	5	35.7	22	3	US-09-009-913-251	Sequence 251, App
c 93	6	42.9	5595	1	US-07-841-655-1	Sequence 1, Appl	c 166	5	35.7	23	4	US-09-520-538-15	Sequence 15, Appl
c 94	6	42.9	5595	1	US-07-635-965C-1	Sequence 1, Appl	c 167	5	35.7	25	1	US-08-427-862-5	Sequence 5, Appl
c 95	6	42.9	6574	3	US-08-221-017B-1097	Sequence 1097, Ap	168	5	35.7	25	4	US-09-396-196G-13143	Sequence 13143, A
c 96	6	42.9	7497	4	US-08-949-016-3114	Sequence 3114, Ap	169	5	35.7	25	4	US-09-396-196G-23216	Sequence 23216, A
c 97	6	42.9	16448	4	US-09-902-540-9686	Sequence 9686, Ap	170	5	35.7	25	4	US-09-396-196G-29217	Sequence 29217, A
c 98	6	42.9	16450	4	US-09-902-540-1098	Sequence 1098, Ap	171	5	35.7	25	4	US-09-396-196G-29218	Sequence 29218, A
99	6	42.9	18471	4	US-09-902-540-1167	Sequence 1167, Ap	c 172	5	35.7	25	4	US-09-396-196G-31171	Sequence 31171, A
100	6	42.9	21513	4	US-09-949-016-16695	Sequence 16695, A	c 173	5	35.7	25	4	US-09-396-196G-31172	Sequence 31172, A
101	6	42.9	21513	4	US-09-949-016-16696	Sequence 16696, A	c 174	5	35.7	25	4	US-09-396-196G-32009	Sequence 32009, A
102	6	42.9	21513	4	US-09-949-016-16697	Sequence 16697, A	c 175	5	35.7	25	4	US-09-396-196G-48676	Sequence 48676, A
c 103	6	42.9	21721	4	US-08-269-939A-41	Sequence 41, Appl	c 176	5	35.7	25	4	US-09-396-196G-64202	Sequence 64202, A
c 104	6	42.9	22976	4	US-08-269-939A-19	Sequence 19, Appl	c 177	5	35.7	25	4	US-09-396-196G-64204	Sequence 64204, A
c 105	6	42.9	23187	4	US-09-499-522-1	Sequence 1, Appl	c 178	5	35.7	25	4	US-09-396-196G-64205	Sequence 64205, A
106	6	42.9	34312	4	US-09-949-016-12352	Sequence 12352, A	c 179	5	35.7	25	4	US-09-396-196G-68388	Sequence 68388, A
107	6	42.9	38575	4	US-09-949-016-12876	Sequence 12876, A	c 180	5	35.7	25	4	US-09-396-196G-70793	Sequence 70793, A
108	6	42.9	38575	4	US-09-949-016-13871	Sequence 13871, A	c 181	5	35.7	25	4	US-09-396-196G-76419	Sequence 76419, A
c 109	6	42.9	39003	4	US-09-596-002-21	Sequence 21, Appl	c 182	5	35.7	25	4	US-09-396-196G-76430	Sequence 76430, A
c 110	6	42.9	39293	4	US-09-949-016-12556	Sequence 12556, A	183	5	35.7	25	4	US-09-396-196G-102778	Sequence 102778, A
c 111	6	42.9	39295	4	US-09-949-016-16078	Sequence 16078, A	184	5	35.7	25	4	US-09-396-196G-102779	Sequence 102779, A
c 112	6	42.9	41639	4	US-09-949-016-15471	Sequence 15471, A	c 185	5	35.7	25	4	US-09-396-196G-106684	Sequence 106684, A
c 113	6	42.9	46902	4	US-09-949-016-13844	Sequence 13844, A	c 186	5	35.7	25	4	US-09-396-196G-106685	Sequence 106685, A
114	6	42.9	49526	4	US-09-949-016-12959	Sequence 12959, A	c 187	5	35.7	25	4	US-09-396-196G-114606	Sequence 114606, A
115	6	42.9	50269	4	US-09-949-016-17598	Sequence 17598, A	c 188	5	35.7	25	4	US-09-396-196G-124308	Sequence 124308, A
c 116	6	42.9	60417	4	US-09-949-016-13312	Sequence 13312, A	c 189	5	35.7	25	4	US-09-396-196G-124309	Sequence 124309, A
117	6	42.9	61399	4	US-09-949-016-14386	Sequence 14386, A	c 190	5	35.7	27	3	US-09-245-248B-39	Sequence 25, Appl
118	6	42.9	65042	3	US-09-784-316-3	Sequence 3, Appl	191	5	35.7	28	1	US-08-173-510B-12	Sequence 33, Appl
119	6	42.9	65042	4	US-10-229-124-3	Sequence 3, Appl	c 192	5	35.7	28	1	US-08-458-218-12	Sequence 12, Appl
120	6	42.9	66213	4	US-08-949-016-11803	Sequence 11803, A	c 193	5	35.7	28	1	US-08-458-218-12	Sequence 12, Appl
121	6	42.9	66213	4	US-09-949-016-16739	Sequence 16739, A	c 194	5	35.7	28	2	US-08-450-433C-9	Sequence 9, Appl
122	6	42.9	67899	4	US-09-949-016-15432	Sequence 15432, A	c 195	5	35.7	28	4	US-08-060-433C-9	Sequence 12, Appl
123	6	42.9	67902	4	US-09-949-016-11870	Sequence 11870, A	c 196	5	35.7	28	4	US-08-450-482B-12	Sequence 2, Appl
c 124	6	42.9	79578	4	US-09-949-016-16339	Sequence 16339, A	197	5	35.7	30	1	US-08-232-144-2	Sequence 101, App
125	6	42.9	85665	4	US-09-949-016-17345	Sequence 17345, A	c 198	5	35.7	30	3	US-09-442-349A-101	Sequence 102, App
c 126	6	42.9	85956	4	US-09-949-016-12994	Sequence 12994, A	199	5	35.7	31	3	US-09-442-349A-102	Sequence 20, Appl
c 127	6	42.9	87567	4	US-09-949-016-13335	Sequence 13335, A	200	5	35.7	31	4	US-10-062-848-20	Sequence 6, Appl
128	6	42.9	89220	4	US-09-949-016-12655	Sequence 12655, A	201	5	35.7	34	1	US-08-627-706-6	Sequence 6, Appl
129	6	42.9	89224	4	US-09-949-016-15572	Sequence 15572, A	202	5	35.7	34	3	US-09-103-489-6	Sequence 6, Appl
c 130	6	42.9	90472	4	US-09-949-016-14038	Sequence 14038, A	203	5	35.7	34	3	US-09-829-381D-6	Sequence 56, Appl
c 131	6	42.9	96690	4	US-09-949-016-17103	Sequence 17103, A	204	5	35.7	35	1	US-08-447-169A-56	Sequence 56, Appl
c 132	6	42.9	101951	4	US-09-949-016-15648	Sequence 15648, A	205	5	35.7	35	2	US-08-233-012C-56	Sequence 56, Appl
c 133	6	42.9	107140	4	US-09-949-016-14834	Sequence 14834, A	206	5	35.7	35	4	US-09-860-474-56	Sequence 56, Appl
134	6	42.9	109159	4	US-09-949-016-14169	Sequence 14169, A	c 207	5	35.7	35	4	US-08-327-874A-33	Sequence 33, Appl
c 135	6	42.9	109159	4	US-09-949-016-14170	Sequence 14170, A	c 208	5	35.7	40	3	US-10-008-960-33	Sequence 33, Appl
c 136	6	42.9	124884	4	US-09-661-596A-76	Sequence 76, Appl	c 209	5	35.7	40	5	PCT-US94-09700-35	Sequence 35, Appl
c 137	6	42.9	124884	4	US-09-913-514-1	Sequence 1, Appl	c 210	5	35.7	40	5	PCT-US94-09700-35	Sequence 35, Appl
c 138	6	42.9	125157	4	US-09-913-514-2	Sequence 2, Appl	211	5	35.7	41	1	US-08-330-638D-10	Sequence 10, Appl
c 139	6	42.9	125778	4	US-09-949-016-12191	Sequence 12191, A	212	5	35.7	41	2	US-08-306-746A-10	Sequence 10, Appl
c 140	6	42.9	129778	4	US-09-949-016-17075	Sequence 17075, A	c 213	5	35.7	47	4	US-09-422-978-733	Sequence 733, App
c 141	6	42.9	132778	4	US-09-949-016-12554	Sequence 12524, A	214	5	35.7	54	3	US-08-327-874A-35	Sequence 35, Appl
142	6	42.9	133358	4	US-09-949-016-16964	Sequence 16964, A	215	5	35.7	54	4	US-10-008-960-35	Sequence 35, Appl
143	6	42.9	133360	4	US-09-949-016-12651	Sequence 12651, A	216	5	35.7	54	5	PCT-US94-09700-35	Sequence 35, Appl
c 144	6	42.9	152524	4	US-09-949-016-12683	Sequence 12683, A	c 217	5	35.7	59	4	US-08-956-171B-4956	Sequence 4956, Ap
c 145	6	42.9	152524	4	US-09-949-016-13194	Sequence 13194, A	c 218	5	35.7	59	4	US-08-781-986A-4956	Sequence 4956, Ap
c 146	6	42.9	154605	4	US-09-949-016-11894	Sequence 11894, A	219	5	35.7	63	1	US-07-967-693-8	Sequence 8, Appl
c 147	6	42.9	221545	4	US-09-949-016-13875	Sequence 13875, A	220	5	35.7	63	1	US-08-195-072-6	Sequence 6, Appl
c 148	6	42.9	222452	4	US-09-949-016-12968	Sequence 12968, A	221	5	35.7	63	1	US-08-195-735-6	Sequence 6, Appl
149	6	42.9	254286	4	US-09-949-016-15497	Sequence 15497, A	222	5	35.7	63	1	US-08-195-747-6	Sequence 6, Appl
c 150	6	42.9	254366	4	US-09-822-871-3	Sequence 3, Appl	223	5	35.7	63	1	US-08-446-884-6	Sequence 6, Appl
c 151	6	42.9	264358	4	US-09-949-016-15725	Sequence 15725, A	224	5	35.7	63	1	US-08-195-073-6	Sequence 6, Appl
152	6	42.9	276237	4	US-09-949-016-17504	Sequence 17504, A	225	5	35.7	63	1	US-08-198-175-6	Sequence 6, Appl
153	6	42.9	312957	4	US-09-949-001-31	Sequence 31, Appl	226	5	35.7	63	2	US-08-443-153-6	Sequence 6, Appl
154	6	42.9	312972	4	US-09-949-001-34	Sequence 34, Appl	227	5	35.7	63	3	US-08-442-807-6	Sequence 17, Appl
155	6	42.9	346112	4	US-09-949-016-13165	Sequence 13165, A	228	5	35.7	65	3	US-09-191-852-17	Sequence 17, Appl
c 156	6	42.9	390890	4	US-09-949-016-14720	Sequence 14720, A	229	5	35.7	65	3	US-08-817-906-17	Sequence 17, Appl
157	6	42.9	421118	4	US-09-949-016-16297	Sequence 16297, A	230	5	35.7	65	5	PCT-US95-13376-17	Sequence 17, Appl
158	6	42.9	1664976	4	US-08-916-421B-1	Sequence 1, Appl	231	5	35.7	77	1	US-08-447-169A-38	Sequence 38, Appl

232	5	35.7	77	2	US-08-233-012C-38	Sequence 38, Appl	305	5	35.7	276	4	US-09-489-039A-7135	Sequence 7135, Ap
233	5	35.7	77	4	US-09-860-474-38	Sequence 2, Appl	306	5	35.7	278	4	US-09-270-767-28010	Sequence 28010, A
234	5	35.7	80	3	US-08-812-121-2	Sequence 38, Appl	c 307	5	35.7	279	3	US-09-615-192A-262	Sequence 262, A
235	5	35.7	80	3	US-09-403-672-2	Sequence 2, Appl	308	5	35.7	280	4	US-09-513-999C-10084	Sequence 10084, A
236	5	35.7	85	3	US-08-812-121-1	Sequence 1, Appl	309	5	35.7	285	4	US-09-976-594-932	Sequence 932, App
237	5	35.7	85	3	US-09-403-672-1	Sequence 1, Appl	c 310	5	35.7	287	4	US-09-270-767-25944	Sequence 25944, A
238	5	35.7	100	4	US-08-956-171E-4860	Sequence 460, Ap	c 311	5	35.7	287	4	US-09-513-999C-3402	Sequence 3402, Ap
c 239	5	35.7	100	4	US-08-781-986A-4860	Sequence 460, Ap	c 312	5	35.7	288	4	US-08-956-171E-4433	Sequence 4433, Ap
c 240	5	35.7	101	4	US-09-513-999C-18462	Sequence 18462, A	c 313	5	35.7	288	4	US-08-781-986A-4433	Sequence 4433, Ap
c 241	5	35.7	102	4	US-08-956-171E-4831	Sequence 4831, Ap	c 314	5	35.7	290	4	US-09-513-999C-30616	Sequence 30616, A
c 242	5	35.7	102	4	US-08-781-986A-4831	Sequence 4831, Ap	c 315	5	35.7	293	4	US-09-313-294A-6856	Sequence 6856, Ap
c 243	5	35.7	114	4	US-08-850-348A-3	Sequence 3, Appl	c 316	5	35.7	294	4	US-09-313-294A-4234	Sequence 4234, Ap
c 244	5	35.7	153	4	US-09-930-803-24	Sequence 24, Appl	c 317	5	35.7	294	4	US-09-107-532A-3243	Sequence 3243, Ap
c 245	5	35.7	153	4	US-09-513-999C-17528	Sequence 17528, A	c 318	5	35.7	294	4	US-09-489-039A-3664	Sequence 3664, Ap
c 246	5	35.7	157	4	US-08-956-171E-3163	Sequence 3163, Ap	c 319	5	35.7	295	4	US-09-313-294A-7316	Sequence 7316, Ap
c 247	5	35.7	157	4	US-08-781-986A-3163	Sequence 3163, Ap	c 320	5	35.7	296	4	US-09-313-294A-2877	Sequence 2877, Ap
c 248	5	35.7	159	4	US-09-513-999C-27073	Sequence 27073, Ap	c 321	5	35.7	296	4	US-09-313-294A-4432	Sequence 4432, Ap
c 249	5	35.7	165	4	US-09-513-999C-22235	Sequence 22235, A	c 322	5	35.7	297	4	US-09-543-681A-3109	Sequence 3109, Ap
c 250	5	35.7	171	4	US-09-621-976-10885	Sequence 10885, A	c 323	5	35.7	300	2	US-08-351-316A-9	Sequence 9, Appl
c 251	5	35.7	175	4	US-09-513-999C-13879	Sequence 13879, A	c 324	5	35.7	300	4	US-09-471-276-699	Sequence 699, App
c 252	5	35.7	183	4	US-09-248-796A-12054	Sequence 12054, A	c 325	5	35.7	301	3	US-09-439-313-292	Sequence 292, App
c 253	5	35.7	186	4	US-09-540-236-1147	Sequence 1147, Ap	c 326	5	35.7	301	3	US-09-352-616A-292	Sequence 292, App
c 254	5	35.7	189	4	US-09-248-796A-7486	Sequence 7486, Ap	c 327	5	35.7	301	3	US-09-232-149A-292	Sequence 292, App
c 255	5	35.7	192	4	US-09-107-532A-1014	Sequence 1014, Ap	c 328	5	35.7	301	4	US-09-159-612-292	Sequence 292, App
c 256	5	35.7	192	4	US-09-489-039A-7126	Sequence 7126, Ap	c 329	5	35.7	301	4	US-09-636-215-292	Sequence 292, App
c 257	5	35.7	195	4	US-09-107-433-2343	Sequence 2343, Ap	c 330	5	35.7	301	4	US-09-685-166A-292	Sequence 292, App
c 258	5	35.7	198	4	US-09-107-433-2344	Sequence 2344, Ap	c 331	5	35.7	301	4	US-09-688-489-292	Sequence 292, App
c 259	5	35.7	207	4	US-09-248-796A-11439	Sequence 11439, A	c 332	5	35.7	301	4	US-09-679-426-292	Sequence 292, App
c 260	5	35.7	209	4	US-09-513-999C-27245	Sequence 27245, A	c 333	5	35.7	301	4	US-09-759-143-292	Sequence 292, App
c 261	5	35.7	210	4	US-09-248-796A-12381	Sequence 12381, A	c 334	5	35.7	301	4	US-09-651-216-292	Sequence 292, App
c 262	5	35.7	210	4	US-09-513-999C-9765	Sequence 9765, Ap	c 335	5	35.7	302	4	US-09-513-999C-2676	Sequence 2676, Ap
c 263	5	35.7	210	4	US-09-471-276-328	Sequence 328, App	c 336	5	35.7	305	4	US-09-513-999C-14109	Sequence 14109, A
c 264	5	35.7	212	4	US-09-513-999C-2823	Sequence 2823, Ap	c 337	5	35.7	306	3	US-09-134-001C-1107	Sequence 1107, Ap
c 265	5	35.7	213	4	US-09-313-294A-6651	Sequence 6651, Ap	c 338	5	35.7	307	4	US-09-621-976-8362	Sequence 8362, Ap
c 266	5	35.7	213	4	US-09-107-532A-938	Sequence 938, App	c 339	5	35.7	307	4	US-09-513-999C-10738	Sequence 10738, A
c 267	5	35.7	213	4	US-09-107-532A-938	Sequence 938, App	c 340	5	35.7	309	4	US-09-513-999C-13129	Sequence 13129, A
c 268	5	35.7	214	4	US-09-513-999C-23018	Sequence 23018, A	c 341	5	35.7	312	3	US-09-191-852-20	Sequence 20, Appl
c 269	5	35.7	219	4	US-09-252-991A-13341	Sequence 13341, A	c 342	5	35.7	312	3	US-08-817-906-20	Sequence 20, Appl
c 270	5	35.7	222	4	US-09-270-767-30143	Sequence 30143, A	c 343	5	35.7	312	4	US-09-513-999C-10993	Sequence 10993, A
c 271	5	35.7	228	4	US-08-956-171E-2523	Sequence 2523, Ap	c 344	5	35.7	312	5	PCT-US95-13376-20	Sequence 20, Appl
c 272	5	35.7	228	4	US-08-781-986A-2523	Sequence 2523, Ap	c 345	5	35.7	314	4	US-09-513-999C-1998	Sequence 1998, Ap
c 273	5	35.7	230	4	US-09-270-767-31075	Sequence 31075, A	c 346	5	35.7	316	4	US-08-956-171E-4288	Sequence 4288, Ap
c 274	5	35.7	231	1	US-08-065-845-8	Sequence 8, Appl	c 347	5	35.7	316	4	US-08-781-986A-4288	Sequence 4288, Ap
c 275	5	35.7	231	1	US-08-429-523-8	Sequence 8, Appl	c 348	5	35.7	321	3	US-09-222-575-54	Sequence 54, Appl
c 276	5	35.7	231	1	US-08-429-523-8	Sequence 8, Appl	c 349	5	35.7	321	4	US-09-389-681-54	Sequence 54, Appl
c 277	5	35.7	231	1	US-08-429-523-8	Sequence 8, Appl	c 350	5	35.7	321	4	US-09-620-4058-54	Sequence 54, Appl
c 278	5	35.7	231	1	US-08-429-520-8	Sequence 8, Appl	c 351	5	35.7	321	4	US-09-339-338-54	Sequence 54, Appl
c 279	5	35.7	231	3	US-09-065-474-126	Sequence 126, App	c 352	5	35.7	321	4	US-09-433-826B-54	Sequence 54, Appl
c 280	5	35.7	231	3	US-09-065-474-127	Sequence 127, App	c 353	5	35.7	321	4	US-09-604-287A-54	Sequence 54, Appl
c 281	5	35.7	231	3	US-09-269-136B-8	Sequence 8, Appl	c 354	5	35.7	321	4	US-09-285-480-54	Sequence 54, Appl
c 282	5	35.7	231	3	US-09-557-034-126	Sequence 126, App	c 355	5	35.7	321	4	US-09-834-759-54	Sequence 54, Appl
c 283	5	35.7	231	3	US-09-557-034-127	Sequence 127, App	c 356	5	35.7	321	4	US-09-590-751A-54	Sequence 54, Appl
c 284	5	35.7	233	4	US-09-513-999C-25651	Sequence 25651, A	c 357	5	35.7	321	4	US-09-551-621-54	Sequence 54, Appl
c 285	5	35.7	234	4	US-09-489-039A-3465	Sequence 3465, Ap	c 358	5	35.7	324	4	US-08-956-171E-4259	Sequence 4259, Ap
c 286	5	35.7	234	4	US-09-107-532A-364	Sequence 364, App	c 359	5	35.7	324	4	US-08-956-171E-4337	Sequence 4337, Ap
c 287	5	35.7	239	4	US-09-016-434-106	Sequence 106, App	c 360	5	35.7	324	4	US-08-781-986A-4259	Sequence 4259, Ap
c 288	5	35.7	239	4	US-09-513-999C-3102	Sequence 3102, Ap	c 361	5	35.7	324	4	US-08-781-986A-4337	Sequence 4337, Ap
c 289	5	35.7	243	4	US-08-956-171E-4515	Sequence 4515, Ap	c 362	5	35.7	325	4	US-09-513-999C-31954	Sequence 31954, A
c 290	5	35.7	243	4	US-08-781-986A-4515	Sequence 4515, Ap	c 363	5	35.7	328	4	US-09-270-767-8036	Sequence 8036, Ap
c 291	5	35.7	243	4	US-09-513-999C-24203	Sequence 24203, A	c 364	5	35.7	328	4	US-09-270-767-23318	Sequence 23318, A
c 292	5	35.7	243	4	US-09-513-999C-26106	Sequence 26106, A	c 365	5	35.7	329	4	US-09-513-999C-34427	Sequence 34427, A
c 293	5	35.7	244	4	US-09-910-009A-282	Sequence 282, App	c 366	5	35.7	330	4	US-09-902-540-8238	Sequence 8238, Ap
c 294	5	35.7	258	4	US-09-248-796A-13421	Sequence 13421, A	c 367	5	35.7	332	1	US-09-985-799-65	Sequence 65, Appl
c 295	5	35.7	260	4	US-09-513-999C-32662	Sequence 32662, A	c 368	5	35.7	332	1	US-09-977-371-65	Sequence 65, Appl
c 296	5	35.7	261	4	US-08-956-171E-4484	Sequence 4484, Ap	c 369	5	35.7	332	1	US-08-594-031-65	Sequence 65, Appl
c 297	5	35.7	261	4	US-09-543-681A-3859	Sequence 3859, Ap	c 370	5	35.7	339	4	US-09-543-681A-3103	Sequence 3103, Ap
c 298	5	35.7	261	4	US-08-781-986A-4484	Sequence 4484, Ap	c 371	5	35.7	340	4	US-08-956-171E-4403	Sequence 4403, Ap
c 299	5	35.7	264	4	US-09-328-352-17	Sequence 17, Appl	c 372	5	35.7	342	3	US-09-306-042-4	Sequence 4, Appl
c 300	5	35.7	264	4	US-09-270-767-27570	Sequence 27570, A	c 373	5	35.7	342	4	US-09-489-039A-6535	Sequence 6535, Ap
c 301	5	35.7	269	4	US-09-016-434-141	Sequence 141, App	c 374	5	35.7	342	4	US-08-956-171E-4301	Sequence 4301, Ap
c 302	5	35.7	272	4	US-09-544-398B-57	Sequence 57, Appl	c 375	5	35.7	348	4	US-08-781-986A-4301	Sequence 4301, Ap
c 303	5	35.7	272	4	US-09-543-771B-57	Sequence 57, Appl	c 376	5	35.7	348	4	US-09-513-999C-13928	Sequence 13928, A
c 304	5	35.7	275	4	US-09-513-999C-12140	Sequence 12140, A	c 377	5	35.7	348	4		

C 378	5	35.7	351	4	US-08-956-171E-793	Sequence 793, App	C 451	417	4	US-09-513-999C-11315	Sequence 11315, A
C 379	5	35.7	351	4	US-08-956-171E-4341	Sequence 4341, App	C 452	419	4	US-09-513-999C-31472	Sequence 31472, A
C 380	5	35.7	351	4	US-08-781-986A-793	Sequence 793, App	C 453	420	4	US-09-270-767-28106	Sequence 28106, A
C 381	5	35.7	351	4	US-08-781-986A-4341	Sequence 4341, App	C 454	422	3	US-09-397-787-229	Sequence 229, App
C 382	5	35.7	355	4	US-07-988-945-2	Sequence 2, Appl	C 455	422	4	US-09-270-767-2619	Sequence 2619, App
C 383	5	35.7	355	4	US-09-621-935A-41	Sequence 41, Appl	C 456	422	4	US-09-270-767-24901	Sequence 24901, A
C 384	5	35.7	355	4	US-09-621-976-18286	Sequence 18286, A	C 457	424	3	US-09-132-316-26	Sequence 26, Appl
C 385	5	35.7	355	4	US-09-513-999C-1716	Sequence 1716, App	C 458	426	4	US-09-270-767-6880	Sequence 6880, App
C 386	5	35.7	356	4	US-09-513-999C-8231	Sequence 8231, App	C 459	426	4	US-09-270-767-22162	Sequence 22162, A
C 387	5	35.7	358	4	US-09-401-064-234	Sequence 234, App	C 460	427	4	US-09-621-976-11351	Sequence 11351, A
C 388	5	35.7	358	4	US-09-401-064-246	Sequence 246, App	C 461	427	4	US-09-919-172-14	Sequence 14, Appl
C 389	5	35.7	360	4	US-09-621-976-8395	Sequence 8395, App	C 462	428	4	US-09-270-767-3723	Sequence 3723, App
C 390	5	35.7	360	4	US-09-107-433-2334	Sequence 2334, App	C 463	428	4	US-09-270-767-19005	Sequence 19005, A
C 391	5	35.7	363	4	US-09-543-681A-3090	Sequence 3090, App	C 464	432	3	US-09-252-991A-9405	Sequence 9405, App
C 392	5	35.7	365	3	US-09-439-313-389	Sequence 389, App	C 465	432	3	US-09-132-316-22	Sequence 22, Appl
C 393	5	35.7	365	3	US-09-352-616A-389	Sequence 389, App	C 466	435	4	US-09-621-976-16911	Sequence 16911, A
C 394	5	35.7	365	4	US-09-636-215-389	Sequence 389, App	C 467	435	4	US-09-134-000C-717	Sequence 717, App
C 395	5	35.7	365	4	US-09-685-166A-389	Sequence 389, App	C 468	438	4	US-09-513-999C-12012	Sequence 12012, A
C 396	5	35.7	365	4	US-09-679-426-389	Sequence 389, App	C 469	439	4	US-09-179-221D-12	Sequence 12, Appl
C 397	5	35.7	365	4	US-09-759-143-389	Sequence 389, App	C 470	440	4	US-09-621-976-12872	Sequence 12872, A
C 398	5	35.7	365	4	US-09-651-236-389	Sequence 389, App	C 471	441	4	US-09-252-991A-14798	Sequence 14798, A
C 399	5	35.7	369	1	US-09-083-945-3	Sequence 3, Appl	C 472	442	4	US-09-513-999C-9397	Sequence 9397, App
C 400	5	35.7	371	4	US-09-702-705-1141	Sequence 1141, App	C 473	443	4	US-09-621-976-13951	Sequence 13951, A
C 401	5	35.7	371	4	US-09-736-457-1141	Sequence 1141, App	C 474	444	4	US-08-956-171E-4006	Sequence 4006, App
C 402	5	35.7	371	4	US-09-614-124B-1141	Sequence 1141, App	C 475	444	4	US-08-781-986A-4006	Sequence 4006, App
C 403	5	35.7	371	4	US-09-671-325-1141	Sequence 1141, App	C 476	447	4	US-09-764-325A-5	Sequence 5, Appl
C 404	5	35.7	371	4	US-09-658-824-1141	Sequence 1141, App	C 477	447	4	US-09-912-935-5	Sequence 17291, A
C 405	5	35.7	374	4	US-09-270-767-14825	Sequence 14825, A	C 478	450	4	US-09-621-976-17291	Sequence 17291, A
C 406	5	35.7	375	4	US-09-328-352-1161	Sequence 1161, App	C 479	451	4	US-09-513-999C-32355	Sequence 32355, A
C 407	5	35.7	375	4	US-09-302-626B-13	Sequence 13, Appl	C 480	452	4	US-09-302-540-1485	Sequence 1485, App
C 408	5	35.7	375	4	US-09-302-626B-15	Sequence 15, Appl	C 481	452	4	US-09-270-767-12871	Sequence 12271, A
C 409	5	35.7	376	4	US-09-023-655-395	Sequence 395, App	C 482	457	4	US-09-270-767-7059	Sequence 7059, App
C 410	5	35.7	378	4	US-09-248-796A-1918	Sequence 1918, App	C 483	460	4	US-09-270-767-22341	Sequence 22341, A
C 411	5	35.7	378	4	US-09-248-796A-12752	Sequence 12752, App	C 484	460	4	US-09-513-999C-13651	Sequence 13651, A
C 412	5	35.7	381	3	US-09-615-192A-174	Sequence 174, App	C 485	462	4	US-09-401-064-214	Sequence 214, App
C 413	5	35.7	381	4	US-09-169-789-174	Sequence 174, App	C 486	462	4	US-09-621-976-17211	Sequence 17211, A
C 414	5	35.7	383	3	US-08-888-998-3	Sequence 3, Appl	C 487	467	4	US-09-270-767-11335	Sequence 11335, A
C 415	5	35.7	383	3	US-09-362-633-3	Sequence 3, Appl	C 488	468	3	US-09-132-316-9	Sequence 9, Appl
C 416	5	35.7	384	4	US-09-270-767-7395	Sequence 7395, App	C 489	469	4	US-09-621-976-18497	Sequence 18497, A
C 417	5	35.7	384	4	US-09-270-767-22677	Sequence 22677, A	C 490	469	4	US-09-513-999C-10642	Sequence 10642, A
C 418	5	35.7	385	4	US-09-270-767-6580	Sequence 6580, App	C 491	476	4	US-09-252-991A-2464	Sequence 2464, App
C 419	5	35.7	385	4	US-09-270-767-21862	Sequence 21862, A	C 492	476	4	US-09-596-248D-4	Sequence 2440, App
C 420	5	35.7	391	4	US-09-902-540-1553	Sequence 1553, App	C 493	472	4	US-09-621-976-2240	Sequence 3, Appl
C 421	5	35.7	392	4	US-09-270-767-6358	Sequence 6358, App	C 494	472	4	US-09-596-248D-3	Sequence 3, Appl
C 422	5	35.7	392	4	US-09-270-767-21640	Sequence 21640, A	C 495	474	4	US-09-270-767-11907	Sequence 11907, A
C 423	5	35.7	393	4	US-09-621-976-16211	Sequence 16211, A	C 496	478	4	US-09-270-767-1345	Sequence 1345, App
C 424	5	35.7	398	4	US-09-513-999C-3548	Sequence 3548, App	C 497	478	4	US-09-270-767-16627	Sequence 16627, A
C 425	5	35.7	399	4	US-09-107-532A-936	Sequence 936, App	C 498	478	4	US-09-513-999C-561	Sequence 561, App
C 426	5	35.7	399	4	US-09-489-039A-4573	Sequence 4573, App	C 499	479	3	US-08-936-165A-37	Sequence 37, Appl
C 427	5	35.7	399	4	US-09-513-999C-11884	Sequence 11884, A	C 500	480	4	US-08-956-171E-3734	Sequence 3734, App
C 428	5	35.7	399	4	US-08-956-171E-3568	Sequence 3568, App	C 501	480	4	US-08-781-986A-3734	Sequence 3734, App
C 429	5	35.7	400	4	US-08-956-171E-3773	Sequence 3773, App	C 502	484	2	US-08-783-395-1	Sequence 1, Appl
C 430	5	35.7	400	4	US-08-956-171E-3842	Sequence 3842, App	C 503	484	2	US-08-924-838-7	Sequence 7, Appl
C 431	5	35.7	400	4	US-08-956-171E-3867	Sequence 3867, App	C 504	484	4	US-09-621-976-15154	Sequence 11034, A
C 432	5	35.7	400	4	US-08-956-171E-3881	Sequence 3881, App	C 505	484	4	US-09-621-976-15154	Sequence 15154, A
C 433	5	35.7	400	4	US-08-956-171E-4140	Sequence 4140, App	C 506	486	4	US-09-252-991A-5896	Sequence 5896, App
C 434	5	35.7	400	4	US-08-956-171E-4153	Sequence 4153, App	C 507	486	4	US-09-621-976-879	Sequence 879, App
C 435	5	35.7	400	4	US-08-956-171E-4174	Sequence 4174, App	C 508	487	4	US-09-621-976-17089	Sequence 17089, A
C 436	5	35.7	400	4	US-08-956-171E-4346	Sequence 4346, App	C 509	489	3	US-08-078-271B-7	Sequence 5, Appl
C 437	5	35.7	400	4	US-08-956-171E-3568	Sequence 3568, App	C 510	489	3	US-08-078-271B-5	Sequence 7, Appl
C 438	5	35.7	400	4	US-08-781-986A-3773	Sequence 3773, App	C 511	492	3	US-08-600-430-1	Sequence 1, Appl
C 439	5	35.7	400	4	US-08-781-986A-3842	Sequence 3842, App	C 512	492	3	US-08-600-430-3	Sequence 3, Appl
C 440	5	35.7	400	4	US-08-781-986A-3867	Sequence 3867, App	C 513	492	4	US-09-621-976-1760	Sequence 1760, App
C 441	5	35.7	400	4	US-08-781-986A-3881	Sequence 3881, App	C 514	492	4	US-09-621-976-17517	Sequence 1517, A
C 442	5	35.7	400	4	US-08-781-986A-4140	Sequence 4140, App	C 515	494	4	US-09-513-999C-1395	Sequence 1395, App
C 443	5	35.7	400	4	US-08-781-986A-4153	Sequence 4153, App	C 516	495	1	US-08-406-248-1	Sequence 1, Appl
C 444	5	35.7	400	4	US-08-781-986A-4174	Sequence 4174, App	C 517	495	1	US-08-075-505-4	Sequence 4, Appl
C 445	5	35.7	400	4	US-08-781-986A-4346	Sequence 4346, App	C 518	495	4	US-09-270-767-111	Sequence 111, App
C 446	5	35.7	400	4	US-09-513-999C-10114	Sequence 10114, A	C 519	495	4	US-09-270-767-15393	Sequence 15393, A
C 447	5	35.7	407	4	US-09-513-999C-30663	Sequence 30663, A	C 520	495	4	US-09-221-268D-4	Sequence 4, Appl
C 448	5	35.7	408	4	US-09-513-999C-9630	Sequence 9630, App	C 521	495	4	US-09-248-796A-5258	Sequence 5258, App
C 449	5	35.7	414	4	US-09-328-352-3589	Sequence 3589, App	C 522	497	4	US-09-621-976-17681	Sequence 17681, A
C 450	5	35.7	414	4	US-09-134-000C-1924	Sequence 1924, App	C 523	497	4	US-09-640-211A-1863	Sequence 1863, App

524	5	35.7	501	4	US-09-621-976-18972	Sequence 18972, A	597	5	35.7	601	4	US-09-949-016-20913	Sequence 20913, A
525	5	35.7	502	4	US-09-544-358B-635	Sequence 635, App	598	5	35.7	601	4	US-09-949-016-20914	Sequence 20914, A
526	5	35.7	503	4	US-09-543-771B-635	Sequence 635, App	c 599	5	35.7	601	4	US-09-949-016-21716	Sequence 21716, A
527	5	35.7	504	4	US-09-270-767-2408	Sequence 2408, App	c 600	5	35.7	601	4	US-09-949-016-21767	Sequence 21767, A
528	5	35.7	505	4	US-09-270-767-17690	Sequence 17690, A	c 601	5	35.7	601	4	US-09-949-016-21896	Sequence 21896, A
c 529	5	35.7	506	4	US-09-270-767-4931	Sequence 4931, App	c 602	5	35.7	601	4	US-09-949-016-22573	Sequence 22573, A
c 530	5	35.7	507	4	US-09-270-767-20213	Sequence 20213, App	c 603	5	35.7	601	4	US-09-949-016-23252	Sequence 23252, A
531	5	35.7	507	4	US-09-621-976-16214	Sequence 16214, A	c 604	5	35.7	601	4	US-09-949-016-23559	Sequence 23559, A
c 532	5	35.7	507	4	US-09-513-999C-1552	Sequence 1552, App	c 605	5	35.7	601	4	US-09-949-016-23600	Sequence 23600, A
c 533	5	35.7	509	4	US-08-956-171E-3590	Sequence 3590, App	c 606	5	35.7	601	4	US-09-949-016-23626	Sequence 23626, A
c 534	5	35.7	509	4	US-08-781-986A-3590	Sequence 3590, App	c 607	5	35.7	601	4	US-09-949-016-23747	Sequence 23747, A
c 535	5	35.7	509	4	US-09-809-665A-53	Sequence 53, Appl	c 608	5	35.7	601	4	US-09-949-016-24577	Sequence 24577, A
c 536	5	35.7	510	4	US-09-621-976-17682	Sequence 17682, A	c 609	5	35.7	601	4	US-09-949-016-24729	Sequence 24729, A
537	5	35.7	510	4	US-09-248-756A-13488	Sequence 13488, A	c 610	5	35.7	601	4	US-09-949-016-24798	Sequence 24798, A
538	5	35.7	511	4	US-09-513-999C-11935	Sequence 11935, A	c 611	5	35.7	601	4	US-09-949-016-24799	Sequence 24799, A
c 539	5	35.7	516	4	US-09-621-976-18600	Sequence 18600, A	c 612	5	35.7	601	4	US-09-949-016-24888	Sequence 24888, A
c 540	5	35.7	520	4	US-09-621-976-1040	Sequence 1040, App	c 613	5	35.7	601	4	US-09-949-016-25436	Sequence 25436, A
541	5	35.7	525	4	US-09-270-767-1441	Sequence 1441, App	614	5	35.7	601	4	US-09-949-016-25437	Sequence 25437, A
542	5	35.7	525	4	US-09-270-767-16723	Sequence 16723, App	615	5	35.7	601	4	US-09-949-016-25438	Sequence 25438, A
c 543	5	35.7	526	4	US-09-023-655-236	Sequence 236, App	616	5	35.7	601	4	US-09-949-016-25765	Sequence 25765, A
544	5	35.7	527	4	US-09-451-651-20	Sequence 20, Appl	c 617	5	35.7	601	4	US-09-949-016-26121	Sequence 26121, A
545	5	35.7	529	4	US-09-270-767-7961	Sequence 7961, App	c 618	5	35.7	601	4	US-09-949-016-26122	Sequence 26122, A
546	5	35.7	531	4	US-09-270-767-23243	Sequence 23243, App	619	5	35.7	601	4	US-09-949-016-26351	Sequence 26351, A
547	5	35.7	531	4	US-09-902-540-2095	Sequence 2095, App	620	5	35.7	601	4	US-09-949-016-26899	Sequence 26899, A
c 548	5	35.7	532	4	US-09-270-767-10526	Sequence 10526, A	621	5	35.7	601	4	US-09-949-016-26900	Sequence 26900, A
549	5	35.7	535	3	US-09-465-558-23	Sequence 23, Appl	c 622	5	35.7	601	4	US-09-949-016-27257	Sequence 27257, A
c 550	5	35.7	537	4	US-10-101-464A-358	Sequence 358, App	c 623	5	35.7	601	4	US-09-949-016-27587	Sequence 27587, A
c 551	5	35.7	538	4	US-09-621-976-9313	Sequence 9313, App	c 624	5	35.7	601	4	US-09-949-016-27588	Sequence 27588, A
552	5	35.7	542	3	US-09-465-558-19	Sequence 19, Appl	c 625	5	35.7	601	4	US-09-949-016-27589	Sequence 27589, A
553	5	35.7	549	4	US-09-583-110-2023	Sequence 2023, App	c 626	5	35.7	601	4	US-09-949-016-28121	Sequence 28121, A
c 554	5	35.7	550	3	US-09-306-042-2	Sequence 2, Appl	c 627	5	35.7	601	4	US-09-949-016-28122	Sequence 28122, A
c 555	5	35.7	550	4	US-10-101-464A-308	Sequence 308, App	c 628	5	35.7	601	4	US-09-949-016-28123	Sequence 28123, A
556	5	35.7	553	4	US-09-513-999C-180	Sequence 180, App	629	5	35.7	601	4	US-09-949-016-28815	Sequence 28815, A
557	5	35.7	556	4	US-09-513-999C-3747	Sequence 3747, App	630	5	35.7	601	4	US-09-949-016-29352	Sequence 29352, A
558	5	35.7	558	4	US-09-543-681A-2277	Sequence 2277, App	631	5	35.7	601	4	US-09-949-016-29353	Sequence 29353, A
559	5	35.7	558	4	US-09-134-000C-2786	Sequence 2786, App	c 632	5	35.7	601	4	US-09-949-016-29399	Sequence 29399, A
560	5	35.7	558	4	US-09-107-433-2030	Sequence 2030, App	c 633	5	35.7	601	4	US-09-949-016-30102	Sequence 30102, A
561	5	35.7	561	4	US-09-252-991A-10905	Sequence 10905, A	634	5	35.7	601	4	US-09-949-016-30189	Sequence 30189, A
c 562	5	35.7	561	4	US-09-513-999C-8229	Sequence 8229, App	635	5	35.7	601	4	US-09-949-016-30190	Sequence 30190, A
c 563	5	35.7	566	3	US-09-171-209-30	Sequence 30, Appl	c 636	5	35.7	601	4	US-09-949-016-30394	Sequence 30394, A
c 564	5	35.7	570	3	US-08-646-273-13	Sequence 13, Appl	c 637	5	35.7	601	4	US-09-949-016-30395	Sequence 30395, A
c 565	5	35.7	576	4	US-09-543-681A-860	Sequence 860, App	c 638	5	35.7	601	4	US-09-949-016-30396	Sequence 30396, A
c 566	5	35.7	579	4	US-09-270-767-2617	Sequence 2617, App	c 639	5	35.7	601	4	US-09-949-016-31382	Sequence 31382, A
567	5	35.7	579	4	US-09-270-767-17899	Sequence 17899, A	640	5	35.7	601	4	US-09-949-016-31675	Sequence 31675, A
568	5	35.7	582	4	US-09-270-767-583	Sequence 583, App	c 641	5	35.7	601	4	US-09-949-016-31902	Sequence 31902, A
569	5	35.7	582	4	US-09-270-767-15865	Sequence 15865, A	c 642	5	35.7	601	4	US-09-949-016-31903	Sequence 31903, A
c 570	5	35.7	585	4	US-09-248-756A-490	Sequence 490, App	c 643	5	35.7	601	4	US-09-949-016-32237	Sequence 32237, A
571	5	35.7	585	4	US-09-561-077C-8	Sequence 8, Appl	c 644	5	35.7	601	4	US-09-949-016-32276	Sequence 32276, A
572	5	35.7	596	4	US-09-221-014-8	Sequence 8, Appl	c 645	5	35.7	601	4	US-09-949-016-33637	Sequence 33637, A
c 573	5	35.7	597	4	US-09-489-039A-5146	Sequence 5146, App	c 646	5	35.7	601	4	US-09-949-016-33826	Sequence 33826, A
574	5	35.7	600	4	US-09-023-655-922	Sequence 922, App	c 647	5	35.7	601	4	US-09-949-016-33827	Sequence 33827, A
575	5	35.7	600	4	US-09-461-912A-22	Sequence 22, Appl	c 648	5	35.7	601	4	US-09-949-016-33838	Sequence 33838, A
576	5	35.7	601	4	US-09-811-825A-27	Sequence 27, Appl	c 649	5	35.7	601	4	US-09-949-016-34026	Sequence 34026, A
c 577	5	35.7	601	4	US-09-949-016-17836	Sequence 17836, A	650	5	35.7	601	4	US-09-949-016-34061	Sequence 34061, A
c 578	5	35.7	601	4	US-09-949-016-17837	Sequence 17837, A	c 651	5	35.7	601	4	US-09-949-016-34201	Sequence 34201, A
c 579	5	35.7	601	4	US-09-949-016-17967	Sequence 17967, A	652	5	35.7	601	4	US-09-949-016-35071	Sequence 35071, A
580	5	35.7	601	4	US-09-949-016-17968	Sequence 17968, A	c 653	5	35.7	601	4	US-09-949-016-35072	Sequence 35072, A
581	5	35.7	601	4	US-09-949-016-18250	Sequence 18250, A	c 654	5	35.7	601	4	US-09-949-016-35073	Sequence 35073, A
c 582	5	35.7	601	4	US-09-949-016-18251	Sequence 18251, A	c 655	5	35.7	601	4	US-09-949-016-35074	Sequence 35074, A
c 583	5	35.7	601	4	US-09-949-016-18252	Sequence 18252, A	c 656	5	35.7	601	4	US-09-949-016-36186	Sequence 36186, A
c 584	5	35.7	601	4	US-09-949-016-18253	Sequence 18253, A	c 657	5	35.7	601	4	US-09-949-016-36187	Sequence 36187, A
c 585	5	35.7	601	4	US-09-949-016-18844	Sequence 18844, A	c 658	5	35.7	601	4	US-09-949-016-36365	Sequence 36365, A
586	5	35.7	601	4	US-09-949-016-19245	Sequence 19245, A	c 659	5	35.7	601	4	US-09-949-016-36367	Sequence 36367, A
587	5	35.7	601	4	US-09-949-016-19246	Sequence 19246, A	660	5	35.7	601	4	US-09-949-016-37613	Sequence 37613, A
588	5	35.7	601	4	US-09-949-016-19247	Sequence 19247, A	661	5	35.7	601	4	US-09-949-016-38037	Sequence 38037, A
589	5	35.7	601	4	US-09-949-016-19386	Sequence 19386, A	c 662	5	35.7	601	4	US-09-949-016-38037	Sequence 38037, A
c 590	5	35.7	601	4	US-09-949-016-19387	Sequence 19387, A	c 663	5	35.7	601	4	US-09-949-016-38463	Sequence 38463, A
c 591	5	35.7	601	4	US-09-949-016-19388	Sequence 19388, A	c 664	5	35.7	601	4	US-09-949-016-38753	Sequence 38753, A
c 592	5	35.7	601	4	US-09-949-016-19389	Sequence 19389, A	c 665	5	35.7	601	4	US-09-949-016-38754	Sequence 38754, A
c 593	5	35.7	601	4	US-09-949-016-19573	Sequence 19573, A	c 666	5	35.7	601	4	US-09-949-016-38755	Sequence 38755, A
c 594	5	35.7	601	4	US-09-949-016-19902	Sequence 19902, A	c 667	5	35.7	601	4	US-09-949-016-38756	Sequence 38756, A
c 595	5	35.7	601	4	US-09-949-016-20239	Sequence 20239, A	c 668	5	35.7	601	4	US-09-949-016-38757	Sequence 38757, A
c 596	5	35.7	601	4			c 669	5	35.7	601	4		

C 816	5	35.7	601	4	US-09-949-016-77629	Sequence 77629, A	C 889	5	35.7	601	4	US-09-949-016-98019	Sequence 98019, A
C 817	5	35.7	601	4	US-09-949-016-77630	Sequence 77630, A	C 890	5	35.7	601	4	US-09-949-016-98285	Sequence 98285, A
C 818	5	35.7	601	4	US-09-949-016-77631	Sequence 77631, A	C 891	5	35.7	601	4	US-09-949-016-98551	Sequence 98551, A
C 819	5	35.7	601	4	US-09-949-016-78113	Sequence 78113, A	C 892	5	35.7	601	4	US-09-949-016-98817	Sequence 98817, A
C 820	5	35.7	601	4	US-09-949-016-78117	Sequence 78117, A	C 893	5	35.7	601	4	US-09-949-016-99083	Sequence 99083, A
C 821	5	35.7	601	4	US-09-949-016-78496	Sequence 78496, A	C 894	5	35.7	601	4	US-09-949-016-99349	Sequence 99349, A
C 822	5	35.7	601	4	US-09-949-016-78497	Sequence 78497, A	C 895	5	35.7	601	4	US-09-949-016-99615	Sequence 99615, A
C 823	5	35.7	601	4	US-09-949-016-78819	Sequence 78819, A	C 896	5	35.7	601	4	US-09-949-016-99881	Sequence 99881, A
C 824	5	35.7	601	4	US-09-949-016-78820	Sequence 78820, A	C 897	5	35.7	601	4	US-09-949-016-100147	Sequence 100147, A
C 825	5	35.7	601	4	US-09-949-016-78821	Sequence 78821, A	C 898	5	35.7	601	4	US-09-949-016-100413	Sequence 100413, A
C 826	5	35.7	601	4	US-09-949-016-78822	Sequence 78822, A	C 899	5	35.7	601	4	US-09-949-016-100679	Sequence 100679, A
C 827	5	35.7	601	4	US-09-949-016-79020	Sequence 79020, A	C 900	5	35.7	601	4	US-09-949-016-100983	Sequence 100983, A
C 828	5	35.7	601	4	US-09-949-016-79021	Sequence 79021, A	C 901	5	35.7	601	4	US-09-949-016-101249	Sequence 101249, A
C 829	5	35.7	601	4	US-09-949-016-79626	Sequence 79626, A	C 902	5	35.7	601	4	US-09-949-016-101515	Sequence 101515, A
C 830	5	35.7	601	4	US-09-949-016-79627	Sequence 79627, A	C 903	5	35.7	601	4	US-09-949-016-101781	Sequence 101781, A
C 831	5	35.7	601	4	US-09-949-016-79628	Sequence 79628, A	C 904	5	35.7	601	4	US-09-949-016-102593	Sequence 102593, A
C 832	5	35.7	601	4	US-09-949-016-79948	Sequence 79948, A	C 905	5	35.7	601	4	US-09-949-016-102705	Sequence 102705, A
C 833	5	35.7	601	4	US-09-949-016-79949	Sequence 79949, A	C 906	5	35.7	601	4	US-09-949-016-103229	Sequence 103229, A
C 834	5	35.7	601	4	US-09-949-016-80182	Sequence 80182, A	C 907	5	35.7	601	4	US-09-949-016-103242	Sequence 103242, A
C 835	5	35.7	601	4	US-09-949-016-80183	Sequence 80183, A	C 908	5	35.7	601	4	US-09-949-016-103255	Sequence 103255, A
C 836	5	35.7	601	4	US-09-949-016-80462	Sequence 80462, A	C 909	5	35.7	601	4	US-09-949-016-103268	Sequence 103268, A
C 837	5	35.7	601	4	US-09-949-016-80793	Sequence 80793, A	C 910	5	35.7	601	4	US-09-949-016-103281	Sequence 103281, A
C 838	5	35.7	601	4	US-09-949-016-80940	Sequence 80940, A	C 911	5	35.7	601	4	US-09-949-016-103294	Sequence 103294, A
C 839	5	35.7	601	4	US-09-949-016-81042	Sequence 81042, A	C 912	5	35.7	601	4	US-09-949-016-103422	Sequence 103422, A
C 840	5	35.7	601	4	US-09-949-016-81053	Sequence 81053, A	C 913	5	35.7	601	4	US-09-949-016-103423	Sequence 103423, A
C 841	5	35.7	601	4	US-09-949-016-81054	Sequence 81054, A	C 914	5	35.7	601	4	US-09-949-016-103424	Sequence 103424, A
C 842	5	35.7	601	4	US-09-949-016-81259	Sequence 81259, A	C 915	5	35.7	601	4	US-09-949-016-103776	Sequence 103776, A
C 843	5	35.7	601	4	US-09-949-016-83012	Sequence 83012, A	C 916	5	35.7	601	4	US-09-949-016-104081	Sequence 104081, A
C 844	5	35.7	601	4	US-09-949-016-83528	Sequence 83528, A	C 917	5	35.7	601	4	US-09-949-016-104803	Sequence 104803, A
C 845	5	35.7	601	4	US-09-949-016-83529	Sequence 83529, A	C 918	5	35.7	601	4	US-09-949-016-104804	Sequence 104804, A
C 846	5	35.7	601	4	US-09-949-016-84096	Sequence 84096, A	C 919	5	35.7	601	4	US-09-949-016-104805	Sequence 104805, A
C 847	5	35.7	601	4	US-09-949-016-84147	Sequence 84147, A	C 920	5	35.7	601	4	US-09-949-016-107402	Sequence 107402, A
C 848	5	35.7	601	4	US-09-949-016-86273	Sequence 86273, A	C 921	5	35.7	601	4	US-09-949-016-107411	Sequence 107411, A
C 849	5	35.7	601	4	US-09-949-016-86645	Sequence 86645, A	C 922	5	35.7	601	4	US-09-949-016-107412	Sequence 107412, A
C 850	5	35.7	601	4	US-09-949-016-86647	Sequence 86647, A	C 923	5	35.7	601	4	US-09-949-016-107413	Sequence 107413, A
C 851	5	35.7	601	4	US-09-949-016-87176	Sequence 87176, A	C 924	5	35.7	601	4	US-09-949-016-107463	Sequence 107463, A
C 852	5	35.7	601	4	US-09-949-016-87177	Sequence 87177, A	C 925	5	35.7	601	4	US-09-949-016-107532	Sequence 107532, A
C 853	5	35.7	601	4	US-09-949-016-87178	Sequence 87178, A	C 926	5	35.7	601	4	US-09-949-016-103960	Sequence 103960, A
C 854	5	35.7	601	4	US-09-949-016-87301	Sequence 87301, A	C 927	5	35.7	601	4	US-09-949-016-103960	Sequence 103960, A
C 855	5	35.7	601	4	US-09-949-016-87302	Sequence 87302, A	C 928	5	35.7	601	4	US-09-949-016-110041	Sequence 110041, A
C 856	5	35.7	601	4	US-09-949-016-87303	Sequence 87303, A	C 929	5	35.7	601	4	US-09-949-016-110146	Sequence 110146, A
C 857	5	35.7	601	4	US-09-949-016-88289	Sequence 88289, A	C 930	5	35.7	601	4	US-09-949-016-110273	Sequence 110273, A
C 858	5	35.7	601	4	US-09-949-016-88681	Sequence 88681, A	C 931	5	35.7	601	4	US-09-949-016-110303	Sequence 110303, A
C 859	5	35.7	601	4	US-09-949-016-88727	Sequence 88727, A	C 932	5	35.7	601	4	US-09-949-016-110318	Sequence 110318, A
C 860	5	35.7	601	4	US-09-949-016-88728	Sequence 88728, A	C 933	5	35.7	601	4	US-09-949-016-110333	Sequence 110333, A
C 861	5	35.7	601	4	US-09-949-016-89043	Sequence 89043, A	C 934	5	35.7	601	4	US-09-949-016-110348	Sequence 110348, A
C 862	5	35.7	601	4	US-09-949-016-89244	Sequence 89244, A	C 935	5	35.7	601	4	US-09-949-016-110363	Sequence 110363, A
C 863	5	35.7	601	4	US-09-949-016-89244	Sequence 89244, A	C 936	5	35.7	601	4	US-09-949-016-110378	Sequence 110378, A
C 864	5	35.7	601	4	US-09-949-016-90135	Sequence 90135, A	C 937	5	35.7	601	4	US-09-949-016-110393	Sequence 110393, A
C 865	5	35.7	601	4	US-09-949-016-91300	Sequence 91300, A	C 938	5	35.7	601	4	US-09-949-016-110408	Sequence 110408, A
C 866	5	35.7	601	4	US-09-949-016-91404	Sequence 91404, A	C 939	5	35.7	601	4	US-09-949-016-110423	Sequence 110423, A
C 867	5	35.7	601	4	US-09-949-016-93209	Sequence 93209, A	C 940	5	35.7	601	4	US-09-949-016-110438	Sequence 110438, A
C 868	5	35.7	601	4	US-09-949-016-93210	Sequence 93210, A	C 941	5	35.7	601	4	US-09-949-016-110483	Sequence 110483, A
C 869	5	35.7	601	4	US-09-949-016-93522	Sequence 93522, A	C 942	5	35.7	601	4	US-09-949-016-110528	Sequence 110528, A
C 870	5	35.7	601	4	US-09-949-016-94578	Sequence 94578, A	C 943	5	35.7	601	4	US-09-949-016-110573	Sequence 110573, A
C 871	5	35.7	601	4	US-09-949-016-94579	Sequence 94579, A	C 944	5	35.7	601	4	US-09-949-016-110618	Sequence 110618, A
C 872	5	35.7	601	4	US-09-949-016-94580	Sequence 94580, A	C 945	5	35.7	601	4	US-09-949-016-110663	Sequence 110663, A
C 873	5	35.7	601	4	US-09-949-016-94581	Sequence 94581, A	C 946	5	35.7	601	4	US-09-949-016-110661	Sequence 110661, A
C 874	5	35.7	601	4	US-09-949-016-95315	Sequence 95315, A	C 947	5	35.7	601	4	US-09-949-016-110862	Sequence 110862, A
C 875	5	35.7	601	4	US-09-949-016-95316	Sequence 95316, A	C 948	5	35.7	601	4	US-09-949-016-111022	Sequence 111022, A
C 876	5	35.7	601	4	US-09-949-016-95493	Sequence 95493, A	C 949	5	35.7	601	4	US-09-949-016-111023	Sequence 111023, A
C 877	5	35.7	601	4	US-09-949-016-95494	Sequence 95494, A	C 950	5	35.7	601	4	US-09-949-016-111183	Sequence 111183, A
C 878	5	35.7	601	4	US-09-949-016-95671	Sequence 95671, A	C 951	5	35.7	601	4	US-09-949-016-111184	Sequence 111184, A
C 879	5	35.7	601	4	US-09-949-016-95672	Sequence 95672, A	C 952	5	35.7	601	4	US-09-949-016-111344	Sequence 111344, A
C 880	5	35.7	601	4	US-09-949-016-95849	Sequence 95849, A	C 953	5	35.7	601	4	US-09-949-016-111345	Sequence 111345, A
C 881	5	35.7	601	4	US-09-949-016-95850	Sequence 95850, A	C 954	5	35.7	601	4	US-09-949-016-112661	Sequence 112661, A
C 882	5	35.7	601	4	US-09-949-016-96268	Sequence 96268, A	C 955	5	35.7	601	4	US-09-949-016-113500	Sequence 113500, A
C 883	5	35.7	601	4	US-09-949-016-96423	Sequence 96423, A	C 956	5	35.7	601	4	US-09-949-016-113501	Sequence 113501, A
C 884	5	35.7	601	4	US-09-949-016-96423	Sequence 96423, A	C 957	5	35.7	601	4	US-09-949-016-115237	Sequence 115237, A
C 885	5	35.7	601	4	US-09-949-016-96859	Sequence 96859, A	C 958	5	35.7	601	4	US-09-949-016-115238	Sequence 115238, A
C 886	5	35.7	601	4	US-09-949-016-96955	Sequence 96955, A	C 959	5	35.7	601	4	US-09-949-016-115239	Sequence 115239, A
C 887	5	35.7	601	4	US-09-949-016-97221	Sequence 97221, A	C 960	5	35.7	601	4	US-09-949-016-115535	Sequence 115535, A
C 888	5	35.7	601	4	US-09-949-016-97487	Sequence 97487, A	C 961	5	35.7	601	4	US-09-949-016-115536	Sequence 115536, A
					Sequence 97753, A								

Sequence 115570, 601 4 US-09-949-016-115570
Sequence 115628, 5 35.7 601 4 US-09-949-016-115628
Sequence 115629, 5 35.7 601 4 US-09-949-016-115629
Sequence 115633, 5 35.7 601 4 US-09-949-016-115633
Sequence 115721, 5 35.7 601 4 US-09-949-016-115721
Sequence 115722, 5 35.7 601 4 US-09-949-016-115722
Sequence 115756, 5 35.7 601 4 US-09-949-016-115756
Sequence 115814, 5 35.7 601 4 US-09-949-016-115814
Sequence 115815, 5 35.7 601 4 US-09-949-016-115815
Sequence 115849, 5 35.7 601 4 US-09-949-016-115849
Sequence 115907, 5 35.7 601 4 US-09-949-016-115907
Sequence 115908, 5 35.7 601 4 US-09-949-016-115908
Sequence 115942, 5 35.7 601 4 US-09-949-016-115942
Sequence 116000, 5 35.7 601 4 US-09-949-016-116000
Sequence 116001, 5 35.7 601 4 US-09-949-016-116001
Sequence 116035, 5 35.7 601 4 US-09-949-016-116035
Sequence 116093, 5 35.7 601 4 US-09-949-016-116093
Sequence 116094, 5 35.7 601 4 US-09-949-016-116094
Sequence 116128, 5 35.7 601 4 US-09-949-016-116128
Sequence 116186, 5 35.7 601 4 US-09-949-016-116186
Sequence 116187, 5 35.7 601 4 US-09-949-016-116187
Sequence 116221, 5 35.7 601 4 US-09-949-016-116221
Sequence 116279, 5 35.7 601 4 US-09-949-016-116279
Sequence 116280, 5 35.7 601 4 US-09-949-016-116280
Sequence 116314, 5 35.7 601 4 US-09-949-016-116314
Sequence 116372, 5 35.7 601 4 US-09-949-016-116372
Sequence 116373, 5 35.7 601 4 US-09-949-016-116373
Sequence 116407, 5 35.7 601 4 US-09-949-016-116407
Sequence 116887, 5 35.7 601 4 US-09-949-016-116887
Sequence 117778, 5 35.7 601 4 US-09-949-016-117778
Sequence 118095, 5 35.7 601 4 US-09-949-016-118095
Sequence 119488, 5 35.7 601 4 US-09-949-016-119488
Sequence 120402, 5 35.7 601 4 US-09-949-016-120402
Sequence 120891, 5 35.7 601 4 US-09-949-016-120891
Sequence 122063, 5 35.7 601 4 US-09-949-016-122063
Sequence 122134, 5 35.7 601 4 US-09-949-016-122134
Sequence 122186, 5 35.7 601 4 US-09-949-016-122186
Sequence 122384, 5 35.7 601 4 US-09-949-016-122384
Sequence 122831, 5 35.7 601 4 US-09-949-016-122831

ALIGNMENTS

RESULT 1
US-09-054-492B-2
; Sequence 2, Application US/09054492B
; Patent No. 6218115
; GENERAL INFORMATION:
; APPLICANT: TAKESHI NAKAMURA
; TITLE OF INVENTION: HUMAN CYCLIN I AND GENES ENCODING SAME
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY, MADISON & SUTRO
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/054,492B
; FILING DATE: APRIL 3, 1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: PAUL E. WHITE, JR.
; REGISTRATION NUMBER: 32,011
; REFERENCE/DOCKET NUMBER: 7898/252159
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000

TELEFAX: (202) 822-0944
TELEX: 6714627CUSH
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1133
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-054-492B-2
Alignment Scores:
Pred. No.: 5.61e-07 Length: 1133
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0
US-09-736-250-5 (1-14) x US-09-054-492B-2 (1-1133)
Qy 1 GLUAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 1027 GAAGATAATGCTCAGAAATGGGTTCGTGTGGCACT 1068
RESULT 2
US-08-969-106-5
; Sequence 5, Application US/08969106
; Patent No. 5986055
; GENERAL INFORMATION:
; APPLICANT: Yang, M.
; APPLICANT: Nandabalan, K.
; APPLICANT: Schulz, V.
; TITLE OF INVENTION: CDK2 INTERACTIONS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/969,106
; FILING DATE: 13-NOV-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7934-057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1260 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...1131
; OTHER INFORMATION:
US-08-969-106-5
Alignment Scores:

Pred. No.: 6.18e-07 Length: 1260
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-736-250-5 (1-14) x US-08-969-106-5 (1-1260)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 1027 GAAGATAATGCTCAGAAAATGGGTTCTGTGTGGCACT 1068

RESULT 3

US-09-338-125-5
; Sequence 5, Application US/09338125
; Patent No. 6521412
; GENERAL INFORMATION:
; APPLICANT: Yang, M.
; APPLICANT: Nandabalan, K.
; APPLICANT: Schulz, V.
; TITLE OF INVENTION: CDK2 INTERACTIONS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/338,125
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/969,106
; FILING DATE: 13-NOV-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7934-057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1260 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1..1131
; OTHER INFORMATION:
US-09-338-125-5

Alignment Scores:
Pred. No.: 6.18e-07 Length: 1260
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-736-250-5 (1-14) x US-09-338-125-5 (1-1260)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 1027 GAAGATAATGCTCAGAAAATGGGTTCTGTGTGGCACT 1068

RESULT 4

US-09-023-655-899
; Sequence 899, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 895-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 899:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1260 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g1183161
US-09-023-655-899

Alignment Scores:
Pred. No.: 6.18e-07 Length: 1260
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-736-250-5 (1-14) x US-09-023-655-899 (1-1260)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 1027 GAAGATAATGCTCAGAAAATGGGTTCTGTGTGGCACT 1068

RESULT 5

US-09-513-999C-29894
; Sequence 29894, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.

APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 29894
LENGTH: 304
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 230
OTHER INFORMATION: m-a or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: 231
OTHER INFORMATION: n-a, g, c or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: 268
OTHER INFORMATION: w-a or t
US-09-513-999C-29894

Alignment Scores:
Pred. No.: 2,19e-06 Length: 304
Score: 13.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 92.86% Indels: 0
DB: 4 Gaps: 0

US-09-736-250-5 (1-14) x US-09-513-999C-29894 (1-304)
QY 2 AsnValSerGluAsnValGlySerValCysGlyThr 14
DB 2 GATATGTCAGAAATGGGTTCTGTGTGGCACT 40

RESULT 6
US-09-949-016-187337/c
Sequence 187337, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 187337
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-187337

Alignment Scores:
Pred. No.: 19 Length: 601
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 50.00% Indels: 0
DB: 4 Gaps: 0

US-09-736-250-5 (1-14) x US-09-949-016-187338 (1-601)
QY 7 AsnValGlySerValCysGly 13
DB 339 AATGTGGGTTCAAGTTTGTGGC 319

RESULT 8
US-09-949-016-187339/c
Sequence 187339, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 187339
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-187339

Query Match: 50.00% Indels: 0
DB: 4 Gaps: 0

US-09-736-250-5 (1-14) x US-09-949-016-187337 (1-601)
QY 7 AsnValGlySerValCysGly 13
DB 600 AATGTGGGTTCAAGTTTGTGGC 580

RESULT 7
US-09-949-016-187338/c
Sequence 187338, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 187338
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-187338

Alignment Scores:
Pred. No.: 19 Length: 601
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 50.00% Indels: 0
DB: 4 Gaps: 0

US-09-736-250-5 (1-14) x US-09-949-016-187338 (1-601)
QY 7 AsnValGlySerValCysGly 13
DB 339 AATGTGGGTTCAAGTTTGTGGC 319

RESULT 8
US-09-949-016-187339/c
Sequence 187339, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 187339
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-187339

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12497
; LENGTH: 78269
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12497

Alignment Scores:
Pred. No.: 1.61e+03 Length: 78269
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 50.00% Indels: 0
DB: 4 Gaps: 0

US-09-736-250-5 (1-14) x US-09-949-016-12497 (1-78269)

Qy 7 AsnValGlySerValCysGly 13
Db 16283 AATGTGGGTTTCAGTTTGTGGC 16263

RESULT 13

US-09-422-978-6641/c
; Sequence 6641, Application US/09422978
; Patent No. 6537751

GENERAL INFORMATION:

; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilva
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1998-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 6641
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..19
; OTHER INFORMATION: upstream amplification primer 99-14949 for SEQ 2707,
US-09-422-978-6641

Alignment Scores:
Pred. No.: 10.6 Length: 19
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 42.86% Indels: 0
DB: 4 Gaps: 0

US-09-736-250-5 (1-14) x US-09-422-978-6641 (1-19)

Qy 1 GluAspAsnValSerGlu 6
Db 19 GAGGATAATGTGAGTGAA 2

RESULT 14

US-09-489-039A-3894
; Sequence 3894, Application US/09489039A
; Patent No. 6610836

; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 3894
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-3894

Alignment Scores:
Pred. No.: 90.7 Length: 201
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 42.86% Indels: 0
DB: 4 Gaps: 0

US-09-736-250-5 (1-14) x US-09-489-039A-3894 (1-201)

Qy 8 ValGlySerValCysGly 13
Db 44 GTAGGCTCTGTTGCGT 61

RESULT 15

US-09-513-999C-27371/c
; Sequence 27371, Application US/09513999C
; Patent No. 6783961

GENERAL INFORMATION:

; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 27371
; LENGTH: 256
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 18
; OTHER INFORMATION: k=g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 55
; OTHER INFORMATION: r=a or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 173
; OTHER INFORMATION: h=a or c or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 227
; OTHER INFORMATION: y=c or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 228
; OTHER INFORMATION: d=a or g or t

US-09-513-999C-27371

Alignment Scores: 113 Length: 256
 Pred. No.: 6.00 Matches: 6
 Score: 100.00% Conservative: 0
 Percent Similarity: 100.00% Mismatches: 0
 Best Local Similarity: 42.86% Indels: 0
 Query Match: 4 Gaps: 0
 DB: 4

US-09-736-250-5 (1-14) x US-09-513-999C-27371 (1-256)

Qy 5 SerGluAsnValGlySer 10
 |||||
 Db 156 TCTGAAACGTGGGCTCT 139

Search completed: February 11, 2005, 14:37:45
 Job time : 34.1356 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 11, 2005, 12:22:06 ; Search time 36.665 Seconds
(without alignments)
2253.008 Million cell updates/sec

Title: US-09-736-250-5

Perfect score: 14

Sequence: 1 EDNVSENVGVCVT 14

Scoring table:

Gapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5378673 seqs, 2950229984 residues

Word size: 1

Total number of hits satisfying chosen parameters: 10734570

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US09736250/runat_07022005_154944_20748/app_query.fasta_1.718
-DB=Published Applications NA -QEXT=fastap -SUFFIX=oligo.rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo
-TRANS=human40.cdi -LIST=1000 -DOCLIGN=200 -THR_SCORE=quality -THR_MIN=1
-ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09736250 @CGN 1 1.582 @runat_07022005_154944_20748
-NCPU=6 -ICPU=3 -NO MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

Published Applications NA:
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:
18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:
19: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:
20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:
21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:
22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	14	100.0	288	17	US-10-242-535A-57578	Sequence 57578, A
2	14	100.0	288	17	US-10-085-783A-57578	Sequence 57578, A
3	14	100.0	350	17	US-10-242-535A-20816	Sequence 20816, A
4	14	100.0	350	17	US-10-085-783A-20816	Sequence 20816, A
5	14	100.0	444	9	US-09-920-300A-1413	Sequence 1413, Ap
6	14	100.0	444	13	US-10-033-528-1413	Sequence 1413, Ap
7	14	100.0	444	16	US-10-099-926-1413	Sequence 1413, Ap
8	14	100.0	447	9	US-09-777-564-1252	Sequence 1252, Ap
9	14	100.0	447	14	US-10-015-219-1252	Sequence 1252, Ap
10	14	100.0	1134	12	US-09-736-250-2	Sequence 2, Appl1
11	14	100.0	1260	17	US-10-172-118-1326	Sequence 1326, Ap
12	14	100.0	1260	17	US-10-342-887-1326	Sequence 1326, Ap
13	14	100.0	1260	17	US-10-641-643-899	Sequence 899, App
14	14	100.0	1889	9	US-09-867-701-10907	Sequence 10907, A
15	14	100.0	2146	10	US-09-814-353-21294	Sequence 21294, A
16	14	100.0	2755	10	US-09-814-353-21586	Sequence 21586, A
17	13	92.9	308	17	US-10-242-535A-41781	Sequence 41781, A
18	13	92.9	308	17	US-10-085-783A-41781	Sequence 41781, A
19	9	64.3	200	17	US-10-242-535A-5568	Sequence 5568, Ap
20	9	64.3	200	17	US-10-085-783A-5568	Sequence 5568, Ap
21	8	57.1	791	18	US-10-363-345A-23639	Sequence 23639, A
22	8	57.1	791	18	US-10-363-345A-23640	Sequence 23640, A
23	8	57.1	796	18	US-10-363-345A-20749	Sequence 20749, A
24	8	57.1	796	18	US-10-363-345A-20750	Sequence 20750, A
25	7	50.0	25	19	US-10-719-900-712383	Sequence 712383, A
26	7	50.0	82	13	US-10-027-632-177870	Sequence 177870, A
27	7	50.0	82	17	US-10-027-632-177870	Sequence 177870, A
28	7	50.0	283	17	US-10-424-599-66605	Sequence 66605, A
29	7	50.0	293	18	US-10-723-860-2410	Sequence 2410, Ap
30	7	50.0	420	9	US-09-960-352-9810	Sequence 9810, Ap
31	7	50.0	578	16	US-10-029-386-12911	Sequence 12911, A
32	7	50.0	622	17	US-10-424-599-54530	Sequence 54530, A
33	7	50.0	642	17	US-10-424-599-114534	Sequence 114534, A
34	7	50.0	1044	18	US-10-437-963-27914	Sequence 27914, A
35	7	50.0	1210	17	US-10-425-114-6115	Sequence 6115, Ap
36	7	50.0	1226	13	US-10-071-766-25	Sequence 25, Appl
37	7	50.0	1265	13	US-10-027-632-254386	Sequence 254386, A
38	7	50.0	1265	17	US-10-027-632-254386	Sequence 254386, A
39	7	50.0	1338	17	US-10-149-310-279	Sequence 279, App
40	7	50.0	1428	18	US-10-489-425-673	Sequence 63, Appl
41	7	50.0	1682	16	US-10-247-671-110	Sequence 110, App
42	7	50.0	1696	17	US-10-424-599-114535	Sequence 114535, A
43	7	50.0	2321	13	US-10-071-766-34	Sequence 34, Appl
44	7	50.0	3573	17	US-10-369-493-42233	Sequence 42233, A
45	7	50.0	92563	11	US-09-997-722-70	Sequence 70, Appl
46	6	42.9	19	17	US-10-349-143-6641	Sequence 6641, Ap
47	6	42.9	25	15	US-10-098-263B-50944	Sequence 50944, A
48	6	42.9	25	18	US-10-717-597-493	Sequence 493, App
49	6	42.9	25	19	US-10-719-900-128648	Sequence 128648, A
50	6	42.9	25	19	US-10-719-900-40668	Sequence 40668, A
51	6	42.9	60	10	US-09-908-975-16123	Sequence 16123, A
52	6	42.9	108	9	US-09-864-761-25163	Sequence 25163, A
53	6	42.9	157	18	US-10-425-115-176491	Sequence 176491, A
54	6	42.9	159	18	US-10-809-824-2	Sequence 2, Appl1
55	6	42.9	164	18	US-10-425-115-135453	Sequence 135453, A
56	6	42.9	174	17	US-10-242-535A-40314	Sequence 40314, A
57	6	42.9	174	17	US-10-085-783A-40314	Sequence 40314, A
58	6	42.9	181	18	US-10-674-124A-28543	Sequence 28543, A
59	6	42.9	193	17	US-10-424-599-92176	Sequence 92176, A
60	6	42.9	201	17	US-10-424-599-9266	Sequence 9266, Ap
61	6	42.9	201	18	US-10-741-601-21451	Sequence 21451, A
62	6	42.9	201	18	US-10-741-601-25686	Sequence 25686, A
63	6	42.9	201	18	US-10-719-993-83393	Sequence 83393, Ap
64	6	42.9	201	18	US-10-719-993-48999	Sequence 48999, A
65	6	42.9	201	19	US-10-741-600-3477	Sequence 3477, Ap
66	6	42.9	201	19	US-10-741-600-20861	Sequence 20861, A
67	6	42.9	201	19	US-10-741-600-60742	Sequence 60742, A
68	6	42.9	201	19	US-10-741-600-70375	Sequence 70375, A
69	6	42.9	216	18	US-10-425-115-184546	Sequence 184546, A

C	70	6	42.9	228	18	US-10-437-963-26997	Sequence 26997, A	C 143	6	42.9	446	9	US-09-967-768A-273	Sequence 273, App
	71	6	42.9	233	17	US-10-424-599-12090	Sequence 12090, A	C 144	6	42.9	450	18	US-10-357-930-324	Sequence 9324, App
	72	6	42.9	235	14	US-10-062-727-864	Sequence 864, App	C 145	6	42.9	455	18	US-10-425-115-72260	Sequence 72260, A
	73	6	42.9	241	18	US-10-674-124A-3318	Sequence 3318, App	C 146	6	42.9	458	10	US-09-918-995-11290	Sequence 11290, A
	74	6	42.9	263	17	US-10-242-535A-16597	Sequence 16597, A	C 147	6	42.9	465	10	US-09-918-995-11236	Sequence 11236, A
	75	6	42.9	263	17	US-10-085-783A-16597	Sequence 16597, A	C 148	6	42.9	465	10	US-09-918-995-11236	Sequence 11236, A
	76	6	42.9	279	9	US-09-983-965-1356	Sequence 1356, App	C 149	6	42.9	469	9	US-09-770-444-224	Sequence 224, App
	77	6	42.9	279	17	US-10-242-535A-12199	Sequence 12199, A	C 150	6	42.9	471	17	US-10-242-535A-16761	Sequence 16761, A
	78	6	42.9	279	17	US-10-085-783A-12199	Sequence 12199, A	C 151	6	42.9	471	17	US-10-085-783A-16761	Sequence 16761, A
	79	6	42.9	287	18	US-10-425-115-67525	Sequence 67525, A	C 152	6	42.9	472	10	US-09-866-050A-429	Sequence 429, App
	80	6	42.9	287	18	US-10-425-115-67525	Sequence 67525, A	C 153	6	42.9	472	10	US-09-866-050A-429	Sequence 429, App
	81	6	42.9	289	17	US-10-437-963-77425	Sequence 77425, A	C 154	6	42.9	476	17	US-10-424-599-141472	Sequence 141472, A
	82	6	42.9	289	17	US-10-437-963-77425	Sequence 77425, A	C 155	6	42.9	476	17	US-10-424-599-141472	Sequence 141472, A
	83	6	42.9	291	18	US-10-085-783A-15501	Sequence 15501, A	C 156	6	42.9	477	18	US-09-864-761-5825	Sequence 5825, App
	84	6	42.9	291	18	US-10-437-963-83648	Sequence 83648, A	C 157	6	42.9	478	18	US-10-357-930-30527	Sequence 30527, A
	85	6	42.9	293	9	US-09-736-457-538	Sequence 538, App	C 158	6	42.9	480	10	US-09-866-050A-208	Sequence 208, App
	86	6	42.9	293	9	US-09-902-941-538	Sequence 538, App	C 159	6	42.9	480	10	US-09-866-050A-208	Sequence 208, App
	87	6	42.9	293	9	US-09-849-626-538	Sequence 538, App	C 160	6	42.9	480	10	US-09-866-050A-208	Sequence 208, App
	88	6	42.9	293	14	US-10-017-754-538	Sequence 538, App	C 161	6	42.9	480	14	US-10-152-661-39	Sequence 39, Appl
	89	6	42.9	293	16	US-10-113-872-538	Sequence 538, App	C 162	6	42.9	482	13	US-10-027-632-324416	Sequence 324416, A
	90	6	42.9	293	17	US-10-283-017-538	Sequence 538, App	C 163	6	42.9	482	17	US-10-027-632-324416	Sequence 324416, A
	91	6	42.9	304	9	US-09-960-352-8963	Sequence 8963, App	C 164	6	42.9	482	18	US-10-425-115-75654	Sequence 75654, A
	92	6	42.9	306	17	US-10-425-114-25753	Sequence 25753, A	C 165	6	42.9	483	9	US-09-728-445-337	Sequence 337, App
	93	6	42.9	309	17	US-10-242-535A-42634	Sequence 42634, A	C 166	6	42.9	495	18	US-10-437-963-66930	Sequence 66930, A
	94	6	42.9	309	17	US-10-085-783A-42634	Sequence 42634, A	C 167	6	42.9	498	9	US-09-879-536-252	Sequence 252, App
	95	6	42.9	318	17	US-10-424-599-101178	Sequence 101178, A	C 168	6	42.9	500	10	US-09-918-995-130	Sequence 130, App
	96	6	42.9	336	18	US-10-425-115-94724	Sequence 94724, A	C 169	6	42.9	505	10	US-09-918-995-20170	Sequence 20170, A
	97	6	42.9	337	18	US-10-674-124A-23764	Sequence 23764, A	C 170	6	42.9	508	9	US-09-823-245A-381	Sequence 381, App
	98	6	42.9	343	14	US-10-267-849-13	Sequence 13, Appl	C 171	6	42.9	510	17	US-10-369-493-41048	Sequence 41048, A
	99	6	42.9	343	15	US-10-106-698-3396	Sequence 3396, App	C 172	6	42.9	519	13	US-10-027-632-269991	Sequence 269991, A
	100	6	42.9	344	17	US-10-062-674-926	Sequence 926, App	C 173	6	42.9	519	17	US-10-027-632-269991	Sequence 269991, A
	101	6	42.9	346	17	US-10-242-535A-34937	Sequence 34937, A	C 174	6	42.9	520	9	US-09-864-761-8435	Sequence 8435, App
	102	6	42.9	346	17	US-10-242-535A-34937	Sequence 34937, A	C 175	6	42.9	526	17	US-10-276-774-333	Sequence 333, App
	103	6	42.9	346	17	US-10-085-783A-1042	Sequence 1042, App	C 176	6	42.9	526	17	US-10-276-774-333	Sequence 333, App
	104	6	42.9	346	17	US-10-085-783A-34937	Sequence 34937, A	C 177	6	42.9	532	13	US-10-027-632-43849	Sequence 43849, A
	105	6	42.9	347	17	US-10-242-535A-36276	Sequence 36276, A	C 178	6	42.9	532	13	US-10-027-632-43850	Sequence 43850, A
	106	6	42.9	347	17	US-10-085-783A-36276	Sequence 36276, A	C 179	6	42.9	532	13	US-10-027-632-43849	Sequence 43849, A
	107	6	42.9	348	14	US-10-062-727-705	Sequence 705, App	C 180	6	42.9	532	17	US-10-027-632-43850	Sequence 43850, A
	108	6	42.9	351	14	US-10-062-727-461	Sequence 461, App	C 181	6	42.9	533	11	US-09-801-944B-105	Sequence 105, App
	109	6	42.9	353	10	US-09-918-995-7552	Sequence 7552, App	C 182	6	42.9	534	14	US-10-424-599-7219	Sequence 7219, App
	110	6	42.9	354	17	US-10-369-493-29172	Sequence 29172, A	C 183	6	42.9	534	14	US-10-060-036-4027	Sequence 4027, App
	111	6	42.9	357	17	US-10-398-221-998	Sequence 998, App	C 184	6	42.9	542	13	US-10-027-632-206700	Sequence 206700, A
	112	6	42.9	357	17	US-10-398-221-2790	Sequence 2790, App	C 185	6	42.9	542	17	US-10-027-632-206700	Sequence 206700, A
	113	6	42.9	358	13	US-10-040-739-45	Sequence 45, Appl	C 186	6	42.9	543	14	US-10-066-543-1953	Sequence 1953, App
	114	6	42.9	360	10	US-09-918-995-7574	Sequence 7574, App	C 187	6	42.9	549	17	US-10-425-115-84809	Sequence 84809, A
	115	6	42.9	361	17	US-10-424-599-6767	Sequence 6767, App	C 188	6	42.9	549	18	US-10-425-115-84809	Sequence 84809, A
	116	6	42.9	368	9	US-09-924-401-28	Sequence 28, Appl	C 189	6	42.9	549	18	US-10-363-345A-24469	Sequence 24469, A
	117	6	42.9	386	14	US-10-062-727-405	Sequence 405, App	C 190	6	42.9	549	18	US-10-363-345A-24470	Sequence 24470, A
	118	6	42.9	391	18	US-10-437-963-99409	Sequence 99409, A	C 191	6	42.9	554	9	US-09-878-178-2080	Sequence 2080, App
	119	6	42.9	392	17	US-10-296-115-42	Sequence 42, Appl	C 192	6	42.9	554	13	US-10-046-503-2080	Sequence 2080, App
	120	6	42.9	393	18	US-10-767-795-2576	Sequence 2576, App	C 193	6	42.9	554	14	US-10-146-503-2080	Sequence 2080, App
	121	6	42.9	398	17	US-10-242-535A-20017	Sequence 20017, A	C 194	6	42.9	561	9	US-09-998-598-1340	Sequence 1340, App
	122	6	42.9	398	17	US-10-085-783A-20017	Sequence 20017, A	C 195	6	42.9	561	18	US-10-425-115-175172	Sequence 175172, A
	123	6	42.9	399	10	US-09-918-995-36734	Sequence 36734, A	C 196	6	42.9	563	9	US-09-796-692-352	Sequence 352, App
	124	6	42.9	401	9	US-09-864-761-14172	Sequence 14172, A	C 197	6	42.9	563	9	US-09-796-692-352	Sequence 352, App
	125	6	42.9	406	17	US-10-264-049-1711	Sequence 1711, App	C 198	6	42.9	563	9	US-09-796-692-352	Sequence 352, App
	126	6	42.9	410	13	US-10-027-632-13506	Sequence 13506, A	C 199	6	42.9	563	14	US-10-040-862-480	Sequence 480, App
	127	6	42.9	410	17	US-10-027-632-13506	Sequence 13506, A	C 200	6	42.9	563	14	US-10-040-862-480	Sequence 480, App
	128	6	42.9	411	18	US-10-437-963-56648	Sequence 56648, A	C 201	6	42.9	563	14	US-10-040-862-480	Sequence 480, App
	129	6	42.9	412	17	US-10-424-599-24907	Sequence 24907, A	C 202	6	42.9	563	17	US-10-040-862-481	Sequence 481, App
	130	6	42.9	414	9	US-09-974-300-7520	Sequence 7520, App	C 203	6	42.9	563	17	US-10-057-475B-480	Sequence 480, App
	131	6	42.9	416	18	US-10-425-115-43376	Sequence 43376, A	C 204	6	42.9	563	17	US-10-057-475B-480	Sequence 480, App
	132	6	42.9	427	18	US-10-437-963-17379	Sequence 17379, A	C 205	6	42.9	563	17	US-10-057-475B-481	Sequence 481, App
	133	6	42.9	433	18	US-10-357-930-155	Sequence 155, App	C 206	6	42.9	563	17	US-10-057-475B-481	Sequence 481, App
	134	6	42.9	433	18	US-10-425-115-72773	Sequence 72773, A	C 207	6	42.9	563	17	US-10-057-475B-481	Sequence 481, App
	135	6	42.9	436	17	US-10-242-535A-15995	Sequence 15995, A	C 208	6	42.9	563	17	US-10-057-475B-481	Sequence 481, App
	136	6	42.9	436	17	US-10-085-783A-15995	Sequence 15995, A	C 209	6	42.9	563	17	US-10-057-475B-481	Sequence 481, App
	137	6	42.9	441	10	US-09-918-995-28803	Sequence 28803, A	C 210	6	42.9	563	17	US-10-057-475B-481	Sequence 481, App
	138	6	42.9	441	17	US-10-424-599-93340	Sequence 93340, A	C 211	6	42.9	563	17	US-10-057-475B-481	Sequence 481, App
	139	6	42.9	445	17	US-10-242-535A-56459	Sequence 56459, A	C 212	6	42.9	563	18	US-10-764-324-480	Sequence 324, App
	140	6	42.9	445	17	US-10-085-783A-56459	Sequence 56459, A	C 213	6	42.9	563	18	US-10-764-324-480	Sequence 324, App
	141	6	42.9	446	9	US-09-954-456-436	Sequence 436, App	C 214	6	42.9	563	18	US-10-764-324-480	Sequence 324, App
	142	6	42.9	446	9	US-09-954-456-2188	Sequence 2188, App	C 215	6	42.9	563	18	US-10-764-324-481	Sequence 481, App

C 216	6	42.9	565	18	US-10-363-345A-23725	Sequence 23725, A	C 289	6	42.9	724	17	US-10-027-632-19999	Sequence 19999, A
C 217	6	42.9	565	18	US-10-363-345A-23726	Sequence 23726, A	C 290	6	42.9	724	17	US-10-027-632-20000	Sequence 20000, A
C 218	6	42.9	572	13	US-10-027-632-246195	Sequence 246195, A	C 291	6	42.9	724	17	US-10-027-632-110992	Sequence 110992, A
C 219	6	42.9	572	13	US-10-027-632-246195	Sequence 246195, A	C 292	6	42.9	731	18	US-10-027-632-110992	Sequence 110992, A
C 220	6	42.9	580	17	US-10-027-632-246195	Sequence 246195, A	C 293	6	42.9	731	18	US-10-027-632-110992	Sequence 110992, A
C 221	6	42.9	583	18	US-10-425-115-132819	Sequence 132819, A	C 294	6	42.9	741	18	US-10-027-632-136087	Sequence 136087, A
C 222	6	42.9	583	18	US-10-027-632-246195	Sequence 246195, A	C 295	6	42.9	741	18	US-10-027-632-136087	Sequence 136087, A
C 223	6	42.9	585	13	US-10-027-632-254275	Sequence 254275, A	C 296	6	42.9	741	18	US-10-027-632-136087	Sequence 136087, A
C 224	6	42.9	585	13	US-10-027-632-254275	Sequence 254275, A	C 297	6	42.9	742	13	US-10-027-632-131667	Sequence 131667, A
C 225	6	42.9	588	17	US-10-156-761-2784	Sequence 2784, A	C 298	6	42.9	742	13	US-10-027-632-131667	Sequence 131667, A
C 226	6	42.9	588	17	US-10-424-599-114315	Sequence 114315, A	C 299	6	42.9	760	13	US-10-027-632-141860	Sequence 141860, A
C 227	6	42.9	594	9	US-09-974-300-6194	Sequence 6194, A	C 300	6	42.9	760	13	US-10-027-632-141860	Sequence 141860, A
C 228	6	42.9	597	13	US-10-027-632-34768	Sequence 34768, A	C 301	6	42.9	771	18	US-10-027-632-141860	Sequence 141860, A
C 229	6	42.9	597	13	US-10-027-632-69817	Sequence 69817, A	C 302	6	42.9	772	15	US-10-211-079-27	Sequence 27, Appl
C 230	6	42.9	597	13	US-10-027-632-208832	Sequence 208832, A	C 303	6	42.9	772	16	US-10-356-708-26	Sequence 26, Appl
C 231	6	42.9	597	13	US-10-027-632-297417	Sequence 297417, A	C 304	6	42.9	772	18	US-10-280-913A-26	Sequence 26, Appl
C 232	6	42.9	597	17	US-10-027-632-34768	Sequence 34768, A	C 305	6	42.9	772	18	US-10-684-134-26	Sequence 26, Appl
C 233	6	42.9	597	17	US-10-027-632-69817	Sequence 69817, A	C 306	6	42.9	772	18	US-10-637-758-26	Sequence 26, Appl
C 234	6	42.9	597	17	US-10-027-632-208832	Sequence 208832, A	C 307	6	42.9	773	18	US-10-027-632-7857	Sequence 7857, Ap
C 235	6	42.9	597	17	US-10-027-632-297417	Sequence 297417, A	C 308	6	42.9	773	18	US-10-027-632-7857	Sequence 7857, Ap
C 236	6	42.9	599	18	US-10-437-963-64879	Sequence 64879, A	C 309	6	42.9	818	13	US-10-027-632-7858	Sequence 7858, Ap
C 237	6	42.9	601	18	US-10-437-963-81476	Sequence 81476, A	C 310	6	42.9	818	17	US-10-027-632-7858	Sequence 7858, Ap
C 238	6	42.9	609	13	US-10-027-632-229528	Sequence 229528, A	C 311	6	42.9	825	13	US-10-027-632-165286	Sequence 165286, A
C 239	6	42.9	609	13	US-10-027-632-229529	Sequence 229529, A	C 312	6	42.9	825	13	US-10-027-632-165286	Sequence 165286, A
C 240	6	42.9	609	17	US-10-027-632-229529	Sequence 229529, A	C 313	6	42.9	839	17	US-10-027-632-121935	Sequence 121935, A
C 241	6	42.9	613	13	US-10-027-632-26413	Sequence 26413, A	C 314	6	42.9	846	9	US-09-770-445-636	Sequence 636, App
C 242	6	42.9	613	13	US-10-027-632-26413	Sequence 26413, A	C 315	6	42.9	852	13	US-10-027-632-161712	Sequence 161712, A
C 243	6	42.9	615	13	US-10-027-632-234018	Sequence 234018, A	C 316	6	42.9	852	17	US-10-027-632-161712	Sequence 161712, A
C 244	6	42.9	615	17	US-10-027-632-234018	Sequence 234018, A	C 317	6	42.9	862	10	US-09-809-391-73	Sequence 73, Appl
C 245	6	42.9	622	18	US-10-486-401-1	Sequence 1, Appli	C 318	6	42.9	862	10	US-09-882-171-73	Sequence 73, Appl
C 246	6	42.9	624	18	US-10-425-115-165891	Sequence 165891, A	C 319	6	42.9	862	14	US-10-150-469-3	Sequence 3, Appli
C 247	6	42.9	629	13	US-10-027-632-261710	Sequence 261710, A	C 320	6	42.9	862	17	US-10-164-861-73	Sequence 73, Appl
C 248	6	42.9	632	17	US-10-027-632-261710	Sequence 261710, A	C 321	6	42.9	867	18	US-10-425-115-96582	Sequence 96582, A
C 249	6	42.9	632	13	US-10-027-632-261620	Sequence 261620, A	C 322	6	42.9	867	17	US-10-398-221-1754	Sequence 1754, Ap
C 250	6	42.9	632	17	US-10-027-632-261620	Sequence 261620, A	C 323	6	42.9	880	17	US-10-282-122A-41803	Sequence 41803, A
C 251	6	42.9	638	18	US-10-363-345A-8853	Sequence 8853, Ap	C 324	6	42.9	892	18	US-09-814-353-21426	Sequence 21426, A
C 252	6	42.9	638	18	US-10-363-345A-8854	Sequence 8854, Ap	C 325	6	42.9	892	18	US-10-357-930-22319	Sequence 22319, A
C 253	6	42.9	640	13	US-10-027-632-144439	Sequence 144439, A	C 326	6	42.9	892	18	US-10-357-930-28779	Sequence 28779, A
C 254	6	42.9	640	17	US-10-027-632-144439	Sequence 144439, A	C 327	6	42.9	894	18	US-10-653-047-316	Sequence 316, App
C 255	6	42.9	642	13	US-10-027-632-272446	Sequence 272446, A	C 328	6	42.9	920	10	US-09-776-724A-25	Sequence 25, Appl
C 256	6	42.9	642	17	US-10-027-632-272446	Sequence 272446, A	C 329	6	42.9	920	17	US-10-425-114-34605	Sequence 34605, A
C 257	6	42.9	645	13	US-10-027-632-232463	Sequence 232463, A	C 330	6	42.9	932	10	US-09-809-391-237	Sequence 237, App
C 258	6	42.9	645	17	US-10-027-632-232463	Sequence 232463, A	C 331	6	42.9	932	10	US-09-882-171-237	Sequence 237, App
C 259	6	42.9	648	18	US-10-425-115-53977	Sequence 53977, A	C 332	6	42.9	932	17	US-10-164-861-237	Sequence 237, App
C 260	6	42.9	650	13	US-10-027-632-236680	Sequence 236680, A	C 333	6	42.9	935	17	US-10-398-221-3087	Sequence 3087, Ap
C 261	6	42.9	650	17	US-10-027-632-236680	Sequence 236680, A	C 334	6	42.9	970	18	US-10-437-963-77528	Sequence 77528, A
C 262	6	42.9	651	18	US-10-437-963-22273	Sequence 22273, A	C 335	6	42.9	976	11	US-09-876-143-1395	Sequence 1395, Ap
C 263	6	42.9	654	18	US-10-841-316-12	Sequence 12, Appl	C 336	6	42.9	993	18	US-10-425-115-75306	Sequence 75306, A
C 264	6	42.9	654	18	US-10-841-316-14	Sequence 14, Appl	C 337	6	42.9	1001	17	US-10-294-934-17	Sequence 17, Appl
C 265	6	42.9	655	13	US-10-027-632-200620	Sequence 200620, A	C 338	6	42.9	1001	17	US-10-294-934-18	Sequence 18, Appl
C 266	6	42.9	655	13	US-10-027-632-200621	Sequence 200621, A	C 339	6	42.9	1034	18	US-10-425-115-177527	Sequence 177527, A
C 267	6	42.9	655	13	US-10-027-632-200621	Sequence 200621, A	C 340	6	42.9	1070	17	US-10-425-114-22394	Sequence 22394, A
C 268	6	42.9	655	17	US-10-027-632-200620	Sequence 200620, A	C 341	6	42.9	1083	9	US-09-764-870-575	Sequence 575, App
C 269	6	42.9	655	17	US-10-027-632-200621	Sequence 200621, A	C 342	6	42.9	1083	9	US-09-764-853-928	Sequence 928, App
C 270	6	42.9	655	17	US-10-027-632-200622	Sequence 200622, A	C 343	6	42.9	1083	14	US-10-125-540-575	Sequence 575, App
C 271	6	42.9	657	13	US-10-027-632-150788	Sequence 150788, A	C 344	6	42.9	1083	14	US-10-103-313-646	Sequence 646, App
C 272	6	42.9	657	13	US-10-027-632-150788	Sequence 150788, A	C 345	6	42.9	1083	17	US-10-158-057-379	Sequence 379, App
C 273	6	42.9	657	17	US-10-027-632-150789	Sequence 150789, A	C 346	6	42.9	1096	18	US-10-363-345A-3425	Sequence 3425, Ap
C 274	6	42.9	657	17	US-10-027-632-150789	Sequence 150789, A	C 347	6	42.9	1096	18	US-10-363-345A-3426	Sequence 3426, Ap
C 275	6	42.9	663	18	US-10-437-963-95404	Sequence 95404, A	C 348	6	42.9	1112	13	US-10-044-090-464	Sequence 464, App
C 276	6	42.9	692	13	US-10-027-632-136088	Sequence 136088, A	C 349	6	42.9	1112	13	US-10-369-493-40316	Sequence 40316, A
C 277	6	42.9	692	13	US-10-027-632-136089	Sequence 136089, A	C 350	6	42.9	1113	17	US-10-424-599-119601	Sequence 119601, A
C 278	6	42.9	692	17	US-10-027-632-136088	Sequence 136088, A	C 351	6	42.9	1122	9	US-09-738-626-2278	Sequence 2278, Ap
C 279	6	42.9	692	17	US-10-027-632-136089	Sequence 136089, A	C 352	6	42.9	1124	17	US-10-424-599-50646	Sequence 50646, A
C 280	6	42.9	702	17	US-10-282-122A-24614	Sequence 24614, A	C 353	6	42.9	1130	18	US-10-767-701-12252	Sequence 12252, A
C 281	6	42.9	712	18	US-10-363-345A-22403	Sequence 22403, A	C 354	6	42.9	1136	17	US-10-425-114-32056	Sequence 32056, A
C 282	6	42.9	712	18	US-10-363-345A-22404	Sequence 22404, A	C 355	6	42.9	1140	9	US-09-764-893-131	Sequence 131, App
C 283	6	42.9	717	18	US-10-767-701-23882	Sequence 23882, A	C 356	6	42.9	1140	9	US-09-764-886-82	Sequence 82, Appl
C 284	6	42.9	723	18	US-10-425-115-95839	Sequence 95839, A	C 357	6	42.9	1140	9	US-09-764-853-893	Sequence 893, App
C 285	6	42.9	723	18	US-10-767-701-5420	Sequence 5420, Ap	C 358	6	42.9	1140	9	US-09-938-842A-2000	Sequence 2000, Ap
C 286	6	42.9	724	13	US-10-027-632-19999	Sequence 19999, A	C 359	6	42.9	1140	9	US-09-860-670-149	Sequence 149, App
C 287	6	42.9	724	13	US-10-027-632-20000	Sequence 20000, A	C 360	6	42.9	1140	10	US-09-989-442-158	Sequence 158, App
C 288	6	42.9	724	13	US-10-027-632-110992	Sequence 110992, A	C 361	6	42.9	1140	10	US-09-764-886-82	Sequence 82, Appl

362	6	42.9	1140	11	US-09-938-8428-2000	Sequence 2000, App	435	18	US-10-425-115-65532	Sequence 65532, A
363	6	42.9	1140	11	US-09-764-875-1214	Sequence 1214, App	436	18	US-09-822-846-200	Sequence 200, App
364	6	42.9	1140	14	US-10-073-865-131	Sequence 131, App	437	18	US-10-723-860-8157	Sequence 8157, App
365	6	42.9	1140	14	US-10-103-313-602	Sequence 602, App	438	14	US-10-073-885-15	Sequence 15, Appl
366	6	42.9	1140	17	US-10-227-646-149	Sequence 149, App	c 439	17	US-10-369-493-26651	Sequence 26651, A
367	6	42.9	1146	17	US-10-282-122A-24149	Sequence 24149, A	6	42.9	US-10-276-774-881	Sequence 881, App
368	6	42.9	1148	17	US-10-424-599-1403	Sequence 1403, App	6	42.9	US-10-437-963-94941	Sequence 94941, A
369	6	42.9	1157	17	US-10-425-114-31746	Sequence 31746, A	6	42.9	US-10-260-238-1860	Sequence 1860, App
c 370	6	42.9	1160	17	US-10-424-599-26547	Sequence 26547, A	6	42.9	US-10-437-963-43011	Sequence 43011, A
371	6	42.9	1160	18	US-10-841-796-21	Sequence 27, Appl	6	42.9	US-10-087-192-1985	Sequence 1985, App
372	6	42.9	1163	17	US-10-398-221-3047	Sequence 3047, App	6	42.9	US-10-425-114-7566	Sequence 7566, App
373	6	42.9	1175	18	US-10-653-047-5924	Sequence 5924, App	6	42.9	US-10-104-047-1712	Sequence 1712, App
374	6	42.9	1178	18	US-10-821-273-79	Sequence 79, Appl	6	42.9	US-10-282-122A-41296	Sequence 41296, A
375	6	42.9	1198	16	US-10-006-285-312	Sequence 312, App	6	42.9	US-10-282-122A-40201	Sequence 40201, A
c 376	6	42.9	1202	18	US-10-425-115-13573	Sequence 13573, A	6	42.9	US-10-156-761-3059	Sequence 3059, App
377	6	42.9	1215	18	US-10-363-345A-28505	Sequence 28505, A	6	42.9	US-09-906-226-33	Sequence 33, Appl
c 378	6	42.9	1215	18	US-10-363-345A-28506	Sequence 28506, A	6	42.9	US-10-027-632-101709	Sequence 101709, A
c 379	6	42.9	1236	13	US-10-027-632-101099	Sequence 101099, A	6	42.9	US-10-027-632-101709	Sequence 101709, A
c 380	6	42.9	1236	17	US-10-027-632-101099	Sequence 101099, A	6	42.9	US-09-974-300-1541	Sequence 1541, App
381	6	42.9	1238	17	US-10-424-599-108037	Sequence 108037, A	6	42.9	US-10-191-997-92	Sequence 92, Appl
382	6	42.9	1239	17	US-10-282-122A-14579	Sequence 14579, A	6	42.9	US-10-027-632-110396	Sequence 110396, A
c 383	6	42.9	1286	18	US-10-767-701-13663	Sequence 13663, A	6	42.9	US-10-027-632-110397	Sequence 110397, A
c 384	6	42.9	1309	17	US-10-374-780A-1873	Sequence 1873, App	6	42.9	US-10-027-632-110398	Sequence 110398, A
c 385	6	42.9	1310	18	US-10-739-565-3	Sequence 3, Appl	6	42.9	US-10-027-632-110396	Sequence 110396, A
c 386	6	42.9	1336	9	US-09-799-777-114	Sequence 114, App	6	42.9	US-10-027-632-110397	Sequence 110397, A
c 387	6	42.9	1341	18	US-10-363-345A-1641	Sequence 1641, App	6	42.9	US-10-027-632-110398	Sequence 110398, A
c 388	6	42.9	1341	18	US-10-363-345A-1642	Sequence 1642, App	6	42.9	US-09-960-706-955	Sequence 955, App
c 389	6	42.9	1351	18	US-10-494-672-243	Sequence 243, App	6	42.9	US-09-873-319-624	Sequence 624, App
c 390	6	42.9	1378	13	US-10-001-843-90	Sequence 90, Appl	6	42.9	US-10-094-749-1141	Sequence 1141, App
391	6	42.9	1383	18	US-10-437-963-17062	Sequence 17062, A	6	42.9	US-10-087-192-611	Sequence 611, App
392	6	42.9	1412	18	US-10-437-963-61052	Sequence 61052, A	6	42.9	US-10-282-122A-16623	Sequence 16623, A
393	6	42.9	1413	9	US-09-764-893-16	Sequence 16, Appl	6	42.9	US-10-282-122A-17111	Sequence 17111, A
394	6	42.9	1413	9	US-09-764-886-17	Sequence 17, Appl	6	42.9	US-10-282-122A-17097	Sequence 17097, A
395	6	42.9	1413	9	US-09-764-853-101	Sequence 101, App	6	42.9	US-10-282-122A-32581	Sequence 32581, A
c 396	6	42.9	1413	9	US-09-860-670-12	Sequence 12, Appl	6	42.9	US-10-425-115-107095	Sequence 107095, A
c 397	6	42.9	1413	10	US-09-989-442-25	Sequence 25, Appl	6	42.9	US-10-104-047-1867	Sequence 1867, App
c 398	6	42.9	1413	10	US-09-764-886-17	Sequence 17, Appl	6	42.9	US-10-437-963-81151	Sequence 81151, A
c 399	6	42.9	1413	11	US-09-764-875-103	Sequence 103, App	6	42.9	US-10-425-115-73560	Sequence 73560, A
c 400	6	42.9	1413	14	US-10-073-865-16	Sequence 16, Appl	6	42.9	US-10-398-221-3473	Sequence 3473, App
c 401	6	42.9	1413	14	US-10-103-313-53	Sequence 53, Appl	6	42.9	US-10-302-172-373	Sequence 373, App
c 402	6	42.9	1413	17	US-10-073-885-43	Sequence 43, Appl	6	42.9	US-10-094-749-974	Sequence 974, App
c 403	6	42.9	1413	17	US-10-227-646-12	Sequence 12, Appl	6	42.9	US-09-781-693A-3	Sequence 3, Appl
c 404	6	42.9	1420	18	US-10-425-115-63513	Sequence 63513, A	6	42.9	US-10-723-860-5853	Sequence 5853, App
c 405	6	42.9	1451	18	US-10-425-115-118516	Sequence 118516, A	6	42.9	US-10-425-115-78456	Sequence 78456, A
c 406	6	42.9	1502	17	US-10-424-599-11856	Sequence 11856, A	6	42.9	US-10-425-115-78456	Sequence 2471, App
c 407	6	42.9	1536	18	US-10-425-115-12456	Sequence 12456, A	6	42.9	US-10-739-930-2471	Sequence 34971, A
c 408	6	42.9	1563	18	US-10-425-115-73567	Sequence 73567, A	6	42.9	US-10-425-114-34971	Sequence 34971, A
c 409	6	42.9	1567	18	US-10-425-115-151250	Sequence 151250, A	6	42.9	US-09-957-763-1	Sequence 1, Appl
c 410	6	42.9	1572	18	US-10-425-115-150505	Sequence 150505, A	6	42.9	US-09-957-763-3	Sequence 3, Appl
c 411	6	42.9	1601	17	US-10-425-114-25599	Sequence 25599, A	6	42.9	US-10-424-599-81828	Sequence 81828, A
c 412	6	42.9	1618	9	US-09-925-300-271	Sequence 271, App	6	42.9	US-10-172-573-1	Sequence 1, Appl
c 413	6	42.9	1646	9	US-09-815-828-3	Sequence 3, Appl	6	42.9	US-10-425-115-33058	Sequence 33058, A
c 414	6	42.9	1716	17	US-10-425-114-3299	Sequence 3299, App	6	42.9	US-10-425-115-21515	Sequence 21515, A
c 415	6	42.9	1726	17	US-10-369-493-29967	Sequence 29967, A	6	42.9	US-10-374-780A-1861	Sequence 1861, App
c 416	6	42.9	1754	17	US-10-425-114-28227	Sequence 28227, A	6	42.9	US-10-320-797-262	Sequence 262, App
c 417	6	42.9	1782	9	US-09-925-298-233	Sequence 233, App	6	42.9	US-10-206-566-1	Sequence 1, Appl
c 418	6	42.9	1802	14	US-10-102-806-233	Sequence 233, App	6	42.9	US-10-172-573-3	Sequence 3, Appl
c 419	6	42.9	1802	15	US-10-425-114-28027	Sequence 28027, A	6	42.9	US-10-739-930-1001	Sequence 3, Appl
c 420	6	42.9	1802	15	US-10-273-517-5	Sequence 5, Appl	6	42.9	US-10-108-260A-419	Sequence 419, App
c 421	6	42.9	1802	17	US-10-311-104-5	Sequence 5, Appl	6	42.9	US-09-988-462-27	Sequence 27, Appl
c 422	6	42.9	1807	17	US-10-425-114-24720	Sequence 24720, A	6	42.9	US-10-437-963-9728	Sequence 9728, App
c 423	6	42.9	1809	17	US-10-282-122A-12055	Sequence 12055, A	6	42.9	US-10-437-963-9728	Sequence 10076, A
c 424	6	42.9	1811	18	US-10-425-115-120743	Sequence 120743, A	6	42.9	US-09-764-891-10076	Sequence 291, App
c 425	6	42.9	1816	18	US-10-425-115-147226	Sequence 147226, A	6	42.9	US-10-205-428-986	Sequence 986, App
c 426	6	42.9	1842	17	US-10-305-720-46	Sequence 46, Appl	6	42.9	US-10-283-975A-291	Sequence 1066, App
c 427	6	42.9	1844	18	US-10-425-115-10679	Sequence 10679, A	6	42.9	US-10-641-643-1066	Sequence 48, Appl
c 428	6	42.9	1850	18	US-10-425-115-94481	Sequence 94481, A	6	42.9	US-10-741-600-48	Sequence 1, Appl
c 429	6	42.9	1853	17	US-10-425-114-31477	Sequence 31477, A	6	42.9	US-10-620-532-1	Sequence 1, Appl
c 430	6	42.9	1866	18	US-10-437-963-68132	Sequence 68132, A	6	42.9	US-09-968-007A-377	Sequence 377, App
c 431	6	42.9	1888	17	US-10-369-493-37743	Sequence 37743, A	6	42.9	US-09-919-039-358	Sequence 358, App
c 432	6	42.9	1890	17	US-10-094-749-742	Sequence 742, App	6	42.9	US-10-044-090-357	Sequence 357, App
c 433	6	42.9	1902	17	US-10-282-122A-12718	Sequence 12718, A	6	42.9	US-10-302-172-85	Sequence 85, Appl
c 434	6	42.9	1933	17	US-10-641-643-739	Sequence 739, App	6	42.9	US-10-241-220-25	Sequence 25, Appl

508	6	42.9	4709	18	US-10-872-972-25	Sequence 25, Appl	c 581	6	42.9	31946	13	US-10-087-192-1909	Sequence 1909, Ap
509	6	42.9	4709	18	US-10-872-991-25	Sequence 25, Appl	c 582	6	42.9	33486	16	US-10-085-959-143	Sequence 143, App
510	6	42.9	4722	18	US-10-602-494-146	Sequence 146, App	c 583	6	42.9	39003	17	US-10-672-781-21	Sequence 21, Appl
511	6	42.9	4736	17	US-10-398-221-3763	Sequence 3763, Ap	c 584	6	42.9	41322	15	US-10-024-396-13	Sequence 13, Appl
512	6	42.9	4819	17	US-10-120-988-72	Sequence 72, Appl	c 585	6	42.9	41936	9	US-09-967-768A-116	Sequence 116, App
c 513	6	42.9	4974	15	US-10-156-761-2487	Sequence 2487, Ap	c 586	6	42.9	45845	9	US-09-927-091-6	Sequence 6, Appli
514	6	42.9	5047	18	US-10-717-597-11	Sequence 11, Appl	c 587	6	42.9	45862	13	US-10-216-355-3	Sequence 3, Appli
515	6	42.9	5159	17	US-10-334-143-111	Sequence 111, App	c 588	6	42.9	49088	13	US-10-087-192-13	Sequence 13, Appl
c 516	6	42.9	5567	17	US-10-361-522-2	Sequence 2, Appli	c 589	6	42.9	50460	13	US-10-087-192-1633	Sequence 1633, Ap
517	6	42.9	5989	17	US-10-221-714A-257	Sequence 257, App	c 590	6	42.9	55005	18	US-10-719-993-6968	Sequence 6968, Ap
518	6	42.9	6343	18	US-10-473-126-334	Sequence 334, App	c 591	6	42.9	56773	18	US-10-331-053-47	Sequence 47, Appli
519	6	42.9	6436	15	US-10-311-455-1665	Sequence 1665, Ap	c 592	6	42.9	57082	18	US-10-715-066-1	Sequence 1, Appli
c 520	6	42.9	6574	13	US-10-194-163-1097	Sequence 1097, Ap	c 593	6	42.9	65042	9	US-09-784-316-3	Sequence 3, Appli
521	6	42.9	7069	15	US-10-311-455-1325	Sequence 1325, Ap	c 594	6	42.9	65042	14	US-10-229-124-3	Sequence 3, Appli
522	6	42.9	7069	17	US-10-221-613-179	Sequence 179, App	c 595	6	42.9	65042	18	US-10-778-301-3	Sequence 3, Appli
523	6	42.9	7069	17	US-10-221-714A-375	Sequence 375, App	c 596	6	42.9	66765	18	US-10-715-066-4	Sequence 4, Appli
524	6	42.9	7069	18	US-10-433-793-13	Sequence 13, Appl	c 597	6	42.9	66916	18	US-10-741-601-5708	Sequence 5708, Ap
525	6	42.9	7431	15	US-10-311-455-54	Sequence 54, Appl	c 598	6	42.9	66916	19	US-10-741-600-17810	Sequence 17810, A
526	6	42.9	7518	18	US-10-437-963-68129	Sequence 68129, A	c 599	6	42.9	85915	18	US-10-647-196-1	Sequence 1, Appli
c 527	6	42.9	7538	17	US-10-062-674-1996	Sequence 1996, Ap	c 600	6	42.9	86111	18	US-10-741-601-5665	Sequence 5665, Ap
528	6	42.9	7695	18	US-10-437-963-68125	Sequence 68125, A	c 601	6	42.9	86131	19	US-10-741-600-17895	Sequence 17895, A
529	6	42.9	8325	17	US-10-369-493-33563	Sequence 33563, A	c 602	6	42.9	88398	18	US-10-810-788A-5	Sequence 5, Appli
530	6	42.9	8530	15	US-10-311-455-406	Sequence 406, App	c 603	6	42.9	99957	11	US-09-997-722-298	Sequence 298, App
531	6	42.9	8776	17	US-10-257-166-149	Sequence 149, App	c 604	6	42.9	100534	18	US-10-367-094-160	Sequence 160, App
c 532	6	42.9	9393	16	US-10-085-959-22	Sequence 22, Appl	c 605	6	42.9	106938	18	US-10-322-281-566	Sequence 566, App
533	6	42.9	9631	15	US-10-017-161-1569	Sequence 1569, App	c 606	6	42.9	109977	18	US-10-719-993-6870	Sequence 6870, Ap
534	6	42.9	9935	18	US-10-489-242-9	Sequence 9, Appli	c 607	6	42.9	114111	18	US-10-723-860-3910	Sequence 3910, Ap
535	6	42.9	10464	9	US-09-957-974-1	Sequence 1, Appli	c 608	6	42.9	115284	13	US-10-087-192-673	Sequence 673, App
536	6	42.9	11473	15	US-10-311-455-1328	Sequence 1328, Ap	c 609	6	42.9	121410	19	US-10-741-600-17733	Sequence 17733, A
537	6	42.9	11473	17	US-10-257-166-112	Sequence 112, App	c 610	6	42.9	124884	10	US-09-913-514-1	Sequence 1, Appli
c 538	6	42.9	11809	17	US-10-280-183A-2	Sequence 2, Appli	c 611	6	42.9	124884	16	US-10-288-823-76	Sequence 76, Appl
539	6	42.9	12192	9	US-09-764-860-629	Sequence 629, App	c 612	6	42.9	125157	10	US-09-913-514-2	Sequence 2, Appli
540	6	42.9	12192	14	US-10-074-095-629	Sequence 629, App	c 613	6	42.9	126872	18	US-10-741-601-5738	Sequence 5738, Ap
541	6	42.9	12192	17	US-10-212-872-629	Sequence 629, App	c 614	6	42.9	126872	19	US-10-741-600-17885	Sequence 17885, A
542	6	42.9	13635	17	US-10-464-368-30	Sequence 30, Appl	c 615	6	42.9	127238	13	US-10-087-192-787	Sequence 787, App
543	6	42.9	13635	17	US-10-210-175-13	Sequence 13, Appl	c 616	6	42.9	127238	18	US-10-775-169-82	Sequence 82, Appl
544	6	42.9	13638	17	US-10-464-368-29	Sequence 29, Appl	c 617	6	42.9	133955	13	US-10-087-192-1984	Sequence 1984, Ap
545	6	42.9	13836	13	US-10-087-192-671	Sequence 671, App	c 618	6	42.9	136338	15	US-10-741-600-17574	Sequence 17574, A
546	6	42.9	14538	18	US-10-741-601-49	Sequence 49, Appl	c 619	6	42.9	171936	15	US-10-265-071-24	Sequence 24, Appl
547	6	42.9	14745	18	US-10-741-601-48	Sequence 48, Appl	c 620	6	42.9	171936	15	US-10-025-966A-24	Sequence 24, Appl
548	6	42.9	14849	9	US-09-873-403-1	Sequence 1, Appli	c 621	6	42.9	172569	13	US-10-087-192-1366	Sequence 1366, Ap
549	6	42.9	14849	11	US-09-750-972-1	Sequence 1, Appli	c 622	6	42.9	179997	9	US-09-822-246-3	Sequence 3, Appli
550	6	42.9	14887	17	US-10-276-774-373	Sequence 373, App	c 623	6	42.9	179997	18	US-10-469-028-3	Sequence 3, Appli
551	6	42.9	14889	15	US-10-101-510-356	Sequence 356, App	c 624	6	42.9	203070	13	US-10-087-192-247	Sequence 247, App
552	6	42.9	14896	11	US-09-750-972-6	Sequence 6, Appli	c 625	6	42.9	207433	17	US-10-277-216-5	Sequence 5, Appli
553	6	42.9	14896	17	US-10-159-563-206	Sequence 206, App	c 626	6	42.9	207433	17	US-10-126-022-5	Sequence 5, Appli
554	6	42.9	14896	18	US-10-473-974-243	Sequence 243, App	c 627	6	42.9	210204	18	US-10-723-860-1746	Sequence 1746, Ap
555	6	42.9	15518	15	US-10-311-455-2145	Sequence 2145, Ap	c 628	6	42.9	219715	18	US-10-417-375-63	Sequence 63, Appl
556	6	42.9	15518	15	US-10-240-485-177	Sequence 177, App	c 629	6	42.9	240825	10	US-09-790-289-1	Sequence 1, Appli
c 557	6	42.9	16371	18	US-10-741-601-5618	Sequence 5618, Ap	c 630	6	42.9	240825	18	US-10-468-582-1	Sequence 1, Appli
c 558	6	42.9	16371	19	US-10-741-600-17823	Sequence 17823, A	c 631	6	42.9	254366	10	US-09-822-871-3	Sequence 3, Appli
559	6	42.9	16545	9	US-09-835-996A-32	Sequence 32, Appl	c 632	6	42.9	254366	17	US-10-673-885-3	Sequence 3, Appli
560	6	42.9	16559	14	US-10-198-846-12181	Sequence 12181, A	c 633	6	42.9	256190	18	US-10-322-281-320	Sequence 320, App
561	6	42.9	16842	17	US-10-221-613-298	Sequence 298, App	c 634	6	42.9	304905	17	US-10-271-416-1	Sequence 1, Appli
562	6	42.9	16842	17	US-10-221-714A-134	Sequence 134, App	c 635	6	42.9	318760	18	US-10-719-993-6755	Sequence 6755, Ap
563	6	42.9	17114	18	US-10-741-601-5770	Sequence 5770, Ap	c 636	6	42.9	321019	19	US-10-741-600-17566	Sequence 17566, A
564	6	42.9	17114	19	US-10-741-600-17982	Sequence 17982, A	c 637	6	42.9	326014	8	US-09-731-231A-3	Sequence 3, Appli
565	6	42.9	17200	9	US-09-764-877-3390	Sequence 3390, Ap	c 638	6	42.9	326014	18	US-10-751-985-3	Sequence 3, Appli
566	6	42.9	17200	17	US-10-242-515-3390	Sequence 3390, Ap	c 639	6	42.9	329019	18	US-10-388-838-48	Sequence 48, Appl
c 567	6	42.9	17492	18	US-10-719-993-6914	Sequence 6914, Ap	c 640	6	42.9	339234	18	US-10-322-696-73	Sequence 73, Appl
c 568	6	42.9	18364	15	US-10-243-243A-7	Sequence 7, Appli	c 641	6	42.9	339234	18	US-10-322-696-73	Sequence 73, Appl
c 569	6	42.9	18404	14	US-10-142-515-10	Sequence 10, Appl	c 642	6	42.9	3397001	18	US-10-319-908-16	Sequence 16, Appl
570	6	42.9	18966	9	US-09-764-877-3372	Sequence 3372, Ap	c 643	6	42.9	356803	18	US-10-719-993-6805	Sequence 6805, Ap
571	6	42.9	18966	17	US-10-242-515-3372	Sequence 3372, Ap	c 644	6	42.9	398287	19	US-10-741-601-5719	Sequence 5719, Ap
c 572	6	42.9	21721	17	US-10-650-507-41	Sequence 41, Appl	c 645	6	42.9	398287	19	US-10-741-600-17839	Sequence 17839, A
c 573	6	42.9	22976	17	US-10-650-507-19	Sequence 19, Appl	c 646	6	42.9	433631	13	US-10-087-192-205	Sequence 205, App
574	6	42.9	23107	11	US-09-997-722-28	Sequence 28, Appl	c 647	6	42.9	518360	18	US-10-367-094-125	Sequence 125, App
c 575	6	42.9	23187	16	US-10-214-684A-1	Sequence 1, Appli	c 648	6	42.9	561515	18	US-10-741-601-5662	Sequence 5682, Ap
c 576	6	42.9	27689	17	US-10-312-222-1	Sequence 1, Appli	c 649	6	42.9	561515	13	US-10-600-17730	Sequence 17730, A
577	6	42.9	27890	18	US-10-741-601-5686	Sequence 5686, Ap	c 650	6	42.9	653122	13	US-10-087-192-226	Sequence 226, App
578	6	42.9	27890	19	US-10-741-600-17751	Sequence 17751, A	c 651	6	42.9	684707	17	US-10-398-221-9	Sequence 9, Appli
579	6	42.9	30625	9	US-09-927-091-5	Sequence 5, Appli	c 652	6	42.9	713059	13	US-10-027-632-174581	Sequence 174581, A
580	6	42.9	30676	9	US-09-927-091-8	Sequence 8, Appli	c 653	6	42.9	713059	17	US-10-027-632-174581	Sequence 174581, A

654	6	42.9	744802	17	US-10-232-798-1369	Sequence 1369, Ap	c 727	5	35.7	25	19	US-10-719-900-43176	Sequence 43176, A
655	6	42.9	786452	18	US-10-719-993-6822	Sequence 6822, Ap	c 728	5	35.7	25	19	US-10-719-900-47542	Sequence 47542, A
656	6	42.9	1790242	18	US-10-719-993-6940	Sequence 6940, Ap	c 729	5	35.7	25	19	US-10-719-900-62178	Sequence 62178, A
657	6	42.9	2140405	13	US-10-027-632-76212	Sequence 76212, A	c 730	5	35.7	25	19	US-10-719-900-62964	Sequence 62964, A
658	6	42.9	2140405	17	US-10-027-632-76212	Sequence 76212, A	c 731	5	35.7	25	19	US-10-719-900-70403	Sequence 70403, A
659	6	42.9	2940917	13	US-10-027-633-174763	Sequence 174763, A	c 732	5	35.7	25	19	US-10-719-900-71951	Sequence 71951, A
660	6	42.9	2940917	17	US-10-027-633-174763	Sequence 174763, A	c 733	5	35.7	25	19	US-10-719-900-78832	Sequence 78832, A
661	6	42.9	3011208	17	US-10-398-221-2058	Sequence 2058, Ap	c 734	5	35.7	25	19	US-10-719-900-84811	Sequence 84811, A
662	6	42.9	3186778	13	US-10-027-633-174961	Sequence 174961, A	c 735	5	35.7	25	19	US-10-719-900-99092	Sequence 99092, A
663	6	42.9	3186778	17	US-10-027-633-174961	Sequence 174961, A	c 736	5	35.7	25	19	US-10-719-900-99092	Sequence 99092, A
664	6	42.9	3309400	9	US-09-738-626-1	Sequence 1, Appli	c 737	5	35.7	25	19	US-10-719-900-128662	Sequence 128662, A
665	6	42.9	9025608	15	US-10-156-761-1	Sequence 1, Appli	c 738	5	35.7	25	19	US-10-719-900-128777	Sequence 128777, A
666	6	42.9	9025608	15	US-10-156-761-1	Sequence 1, Appli	c 739	5	35.7	25	19	US-10-719-900-128778	Sequence 128778, A
667	5	35.7	17	15	US-10-060-895A-686	Sequence 686, App	c 740	5	35.7	25	19	US-10-719-900-130997	Sequence 130997, A
668	5	35.7	17	15	US-10-060-895A-687	Sequence 687, App	c 741	5	35.7	25	19	US-10-719-900-138295	Sequence 138295, A
669	5	35.7	17	15	US-10-060-895A-688	Sequence 688, App	c 742	5	35.7	25	19	US-10-719-900-147378	Sequence 147378, A
670	5	35.7	17	17	US-10-138-674-2043	Sequence 2043, Ap	c 743	5	35.7	25	19	US-10-719-900-154461	Sequence 154461, A
671	5	35.7	17	17	US-10-138-674-2043	Sequence 2043, Ap	c 744	5	35.7	25	19	US-10-719-900-162361	Sequence 162361, A
672	5	35.7	17	18	US-10-287-949A-2043	Sequence 9013, Ap	c 745	5	35.7	25	19	US-10-719-900-183494	Sequence 183494, A
673	5	35.7	17	18	US-10-287-949A-2043	Sequence 2043, Ap	c 746	5	35.7	25	19	US-10-719-900-205913	Sequence 205913, A
674	5	35.7	17	18	US-10-712-633-4246	Sequence 4246, Ap	c 747	5	35.7	25	19	US-10-719-900-206682	Sequence 206682, A
675	5	35.7	17	18	US-10-235-079B-19	Sequence 4246, Ap	c 748	5	35.7	25	19	US-10-719-900-235445	Sequence 235445, A
676	5	35.7	19	18	US-10-654-253-4	Sequence 19, Appli	c 749	5	35.7	25	19	US-10-719-900-234871	Sequence 234871, A
677	5	35.7	20	10	US-09-969-086A-3	Sequence 4, Appli	c 750	5	35.7	25	19	US-10-719-900-250128	Sequence 250128, A
678	5	35.7	20	16	US-10-369-378-50	Sequence 3, Appli	c 751	5	35.7	25	19	US-10-719-900-252724	Sequence 252724, A
679	5	35.7	21	18	US-10-786-720-3029	Sequence 3029, Ap	c 752	5	35.7	25	19	US-10-719-900-253673	Sequence 253673, A
680	5	35.7	21	18	US-10-751-736-49153	Sequence 49153, A	c 753	5	35.7	25	19	US-10-719-900-253769	Sequence 253769, A
681	5	35.7	21	18	US-10-751-736-49154	Sequence 49154, A	c 754	5	35.7	25	19	US-10-719-900-253770	Sequence 253770, A
682	5	35.7	23	9	US-09-520-538-15	Sequence 15, Appli	c 755	5	35.7	25	19	US-10-719-900-281405	Sequence 281405, A
683	5	35.7	25	14	US-10-215-112-6863	Sequence 6863, Ap	c 756	5	35.7	25	19	US-10-719-900-296256	Sequence 296256, A
684	5	35.7	25	14	US-10-215-112-10262	Sequence 10262, A	c 757	5	35.7	25	19	US-10-719-900-303768	Sequence 303768, A
685	5	35.7	25	14	US-10-215-112-10388	Sequence 10388, A	c 758	5	35.7	25	19	US-10-719-900-303769	Sequence 303769, A
686	5	35.7	25	15	US-10-060-895A-1455	Sequence 1455, Ap	c 759	5	35.7	25	19	US-10-719-900-307034	Sequence 307034, A
687	5	35.7	25	15	US-10-060-895A-1456	Sequence 1455, Ap	c 760	5	35.7	25	19	US-10-719-900-307035	Sequence 307035, A
688	5	35.7	25	15	US-10-060-895A-1457	Sequence 1456, Ap	c 761	5	35.7	25	19	US-10-719-900-321725	Sequence 321725, A
689	5	35.7	25	15	US-10-060-895A-1458	Sequence 1457, Ap	c 762	5	35.7	25	19	US-10-719-900-330959	Sequence 330959, A
690	5	35.7	25	15	US-10-060-895A-1459	Sequence 1458, Ap	c 763	5	35.7	25	19	US-10-719-900-335330	Sequence 335330, A
691	5	35.7	25	15	US-10-060-895A-1460	Sequence 1459, Ap	c 764	5	35.7	25	19	US-10-719-900-343584	Sequence 343584, A
692	5	35.7	25	15	US-10-060-895A-1461	Sequence 1460, Ap	c 765	5	35.7	25	19	US-10-719-900-362511	Sequence 362511, A
693	5	35.7	25	15	US-10-060-895A-1462	Sequence 1461, Ap	c 766	5	35.7	25	19	US-10-719-900-362513	Sequence 362513, A
694	5	35.7	25	15	US-10-060-895A-1463	Sequence 1462, Ap	c 767	5	35.7	25	19	US-10-719-900-373409	Sequence 373409, A
695	5	35.7	25	15	US-10-060-895A-1464	Sequence 1463, Ap	c 768	5	35.7	25	19	US-10-719-900-396244	Sequence 396244, A
696	5	35.7	25	15	US-10-060-895A-1465	Sequence 1464, Ap	c 769	5	35.7	25	19	US-10-719-900-404281	Sequence 404281, A
697	5	35.7	25	15	US-10-098-263B-2915	Sequence 1465, Ap	c 770	5	35.7	25	19	US-10-719-900-406234	Sequence 406234, A
698	5	35.7	25	15	US-10-098-263B-3551	Sequence 2915, Ap	c 771	5	35.7	25	19	US-10-719-900-417601	Sequence 417601, A
699	5	35.7	25	15	US-10-098-263B-9733	Sequence 3551, Ap	c 772	5	35.7	25	19	US-10-719-900-432978	Sequence 432978, A
700	5	35.7	25	15	US-10-098-263B-13257	Sequence 9733, Ap	c 773	5	35.7	25	19	US-10-719-900-433971	Sequence 433971, A
701	5	35.7	25	15	US-10-098-263B-13268	Sequence 13257, A	c 774	5	35.7	25	19	US-10-719-900-454720	Sequence 454720, A
702	5	35.7	25	15	US-10-098-263B-13268	Sequence 13268, A	c 775	5	35.7	25	19	US-10-719-900-455098	Sequence 455098, A
703	5	35.7	25	15	US-10-098-263B-24248	Sequence 24248, A	c 776	5	35.7	25	19	US-10-719-900-455734	Sequence 455734, A
704	5	35.7	25	15	US-10-098-263B-31469	Sequence 31469, A	c 777	5	35.7	25	19	US-10-719-900-467323	Sequence 467323, A
705	5	35.7	25	15	US-10-098-263B-42172	Sequence 42172, A	c 778	5	35.7	25	19	US-10-719-900-479181	Sequence 479181, A
706	5	35.7	25	15	US-10-098-263B-44754	Sequence 44754, A	c 779	5	35.7	25	19	US-10-719-900-507371	Sequence 507371, A
707	5	35.7	25	15	US-10-098-263B-53338	Sequence 53338, A	c 780	5	35.7	25	19	US-10-719-900-507490	Sequence 507490, A
708	5	35.7	25	15	US-10-098-263B-56978	Sequence 56978, A	c 781	5	35.7	25	19	US-10-719-900-507491	Sequence 507491, A
709	5	35.7	25	15	US-10-098-263B-58431	Sequence 58431, A	c 782	5	35.7	25	19	US-10-719-900-509731	Sequence 509731, A
710	5	35.7	25	15	US-10-098-263B-58432	Sequence 58432, A	c 783	5	35.7	25	19	US-10-719-900-529244	Sequence 529244, A
711	5	35.7	25	15	US-10-098-263B-79483	Sequence 79483, A	c 784	5	35.7	25	19	US-10-719-900-529245	Sequence 529245, A
712	5	35.7	25	15	US-10-098-263B-79964	Sequence 79964, A	c 785	5	35.7	25	19	US-10-719-900-530460	Sequence 530460, A
713	5	35.7	25	15	US-10-098-263B-82696	Sequence 82696, A	c 786	5	35.7	25	19	US-10-719-900-530461	Sequence 530461, A
714	5	35.7	25	15	US-10-098-263B-84184	Sequence 84184, A	c 787	5	35.7	25	19	US-10-719-900-537546	Sequence 537546, A
715	5	35.7	25	15	US-10-098-263B-94185	Sequence 94185, A	c 788	5	35.7	25	19	US-10-719-900-545787	Sequence 545787, A
716	5	35.7	25	15	US-10-098-263B-94186	Sequence 94186, A	c 789	5	35.7	25	19	US-10-719-900-568399	Sequence 568399, A
717	5	35.7	25	15	US-10-098-263B-98476	Sequence 98476, A	c 790	5	35.7	25	19	US-10-719-900-576321	Sequence 576321, A
718	5	35.7	25	15	US-10-098-263B-98830	Sequence 98830, A	c 791	5	35.7	25	19	US-10-719-900-607820	Sequence 607820, A
719	5	35.7	25	15	US-10-098-263B-103628	Sequence 103628, A	c 792	5	35.7	25	19	US-10-719-900-634123	Sequence 634123, A
720	5	35.7	25	15	US-10-098-263B-126214	Sequence 126214, A	c 793	5	35.7	25	19	US-10-719-900-635696	Sequence 635696, A
721	5	35.7	25	15	US-10-098-263B-125710	Sequence 125710, A	c 794	5	35.7	25	19	US-10-719-900-678174	Sequence 678174, A
722	5	35.7	25	15	US-10-098-263B-126285	Sequence 126285, A	c 795	5	35.7	25	19	US-10-719-900-693294	Sequence 693294, A
723	5	35.7	25	15	US-10-098-263B-137241	Sequence 127241, A	c 796	5	35.7	25	19	US-10-719-900-694113	Sequence 694113, A
724	5	35.7	25	18	US-10-717-597-492	Sequence 130715, A	c 797	5	35.7	25	19	US-10-719-900-709662	Sequence 709662, A
725	5	35.7	25	19	US-10-719-900-6000	Sequence 492, App	c 798	5	35.7	25	19	US-10-719-900-712003	Sequence 712003, A
726	5	35.7	25	19	US-10-719-900-36500	Sequence 6000, Ap	c 799	5	35.7	25	19	US-10-719-900-714936	Sequence 714936, A
						Sequence 36500, A	c 799	5	35.7	25	19	US-10-719-900-717597	Sequence 717597, A

C 800	5	35.7	25	19	US-10-719-900-726334	Sequence 726334,	C 873	5	35.7	60	10	US-09-908-975-17531	Sequence 17531, A
C 801	5	35.7	25	19	US-10-719-900-729972	Sequence 729972,	C 874	5	35.7	60	10	US-09-908-975-31505	Sequence 31505, A
C 802	5	35.7	25	19	US-10-719-900-752750	Sequence 752750,	C 875	5	35.7	65	10	US-09-908-975-11350	Sequence 11350, Ap
C 803	5	35.7	25	19	US-10-719-900-754258	Sequence 754258,	C 876	5	35.7	65	10	US-09-908-975-36407	Sequence 3640, Ap
C 804	5	35.7	25	19	US-10-719-900-755859	Sequence 755859,	C 877	5	35.7	65	10	US-09-908-975-26807	Sequence 26807, A
C 805	5	35.7	25	19	US-10-719-900-763636	Sequence 763636,	C 878	5	35.7	65	10	US-09-908-975-27013	Sequence 27013, A
C 806	5	35.7	25	19	US-10-719-900-772731	Sequence 772731,	C 879	5	35.7	65	10	US-09-908-975-29561	Sequence 29561, A
C 807	5	35.7	25	19	US-10-719-900-778496	Sequence 778496,	C 880	5	35.7	76	17	US-10-388-360-126	Sequence 126, App
C 808	5	35.7	25	19	US-10-719-900-782800	Sequence 782800,	C 881	5	35.7	77	9	US-09-449-204-15	Sequence 15, Appl
C 809	5	35.7	25	19	US-10-719-900-783131	Sequence 783131,	C 882	5	35.7	77	10	US-09-860-474-38	Sequence 38, Appl
C 810	5	35.7	25	19	US-10-719-900-795817	Sequence 795817,	C 883	5	35.7	77	16	US-10-409-565-38	Sequence 38, Appl
C 811	5	35.7	25	19	US-10-719-900-798884	Sequence 798884,	C 884	5	35.7	77	16	US-10-729-581-128	Sequence 128, App
C 812	5	35.7	25	19	US-10-719-900-806667	Sequence 806667,	C 885	5	35.7	79	16	US-10-029-386-21442	Sequence 21442, A
C 813	5	35.7	25	19	US-10-719-900-816908	Sequence 816908,	C 886	5	35.7	80	10	US-09-817-748-2	Sequence 2, Appli
C 814	5	35.7	25	19	US-10-719-900-820675	Sequence 820675,	C 887	5	35.7	84	9	US-09-880-821-7	Sequence 7, Appli
C 815	5	35.7	25	19	US-10-719-900-821711	Sequence 821711,	C 888	5	35.7	85	10	US-09-817-748-1	Sequence 1, Appli
C 816	5	35.7	25	19	US-10-719-900-831369	Sequence 831369,	C 889	5	35.7	87	9	US-09-880-821-6	Sequence 6, Appli
C 817	5	35.7	25	19	US-10-719-900-883895	Sequence 883895,	C 890	5	35.7	89	10	US-09-803-454-17	Sequence 17, Appl
C 818	5	35.7	25	19	US-10-719-900-890027	Sequence 890027,	C 891	5	35.7	90	10	US-09-747-377-381	Sequence 381, App
C 819	5	35.7	25	19	US-10-719-900-890028	Sequence 890028,	C 892	5	35.7	90	14	US-10-105-613-381	Sequence 381, App
C 820	5	35.7	25	19	US-10-719-900-894815	Sequence 894815,	C 893	5	35.7	90	17	US-10-296-734-1363	Sequence 1363, Ap
C 821	5	35.7	25	19	US-10-719-900-927001	Sequence 927001,	C 894	5	35.7	100	8	US-08-781-986A-4860	Sequence 4860, Ap
C 822	5	35.7	25	19	US-10-719-900-927801	Sequence 927801,	C 895	5	35.7	100	17	US-10-329-624-4860	Sequence 4860, Ap
C 823	5	35.7	25	19	US-10-719-900-937486	Sequence 937486,	C 896	5	35.7	101	17	US-10-674-124A-1784	Sequence 1784, Ap
C 824	5	35.7	25	19	US-10-719-900-940515	Sequence 940515,	C 897	5	35.7	101	18	US-10-674-124A-24968	Sequence 24968, A
C 825	5	35.7	25	19	US-10-719-900-952915	Sequence 952915,	C 898	5	35.7	101	18	US-10-425-115-155546	Sequence 155546,
C 826	5	35.7	25	19	US-10-719-900-974891	Sequence 974891,	C 899	5	35.7	102	17	US-08-781-986A-4831	Sequence 4831, Ap
C 827	5	35.7	27	9	US-09-815-656-25	Sequence 25, Appl	C 900	5	35.7	102	17	US-10-329-624-4831	Sequence 4831, Ap
C 828	5	35.7	27	9	US-09-815-656-39	Sequence 39, Appl	C 901	5	35.7	103	9	US-09-867-701-3640	Sequence 3640, Ap
C 829	5	35.7	28	17	US-10-621-758A-49	Sequence 49, Appl	C 902	5	35.7	103	9	US-09-983-965-4695	Sequence 4695, Ap
C 830	5	35.7	28	18	US-10-663-208A-49	Sequence 49, Appl	C 903	5	35.7	104	16	US-10-029-386-21407	Sequence 21407, A
C 831	5	35.7	28	18	US-10-646-308A-49	Sequence 49, Appl	C 904	5	35.7	106	17	US-10-242-535A-13819	Sequence 13819, A
C 832	5	35.7	28	18	US-10-736-769-49	Sequence 49, Appl	C 905	5	35.7	106	17	US-10-085-783A-13819	Sequence 13819, A
C 833	5	35.7	30	17	US-10-394-388A-20	Sequence 20, Appl	C 906	5	35.7	110	18	US-10-674-124A-18460	Sequence 18460, A
C 834	5	35.7	31	14	US-10-062-848-20	Sequence 20, Appl	C 907	5	35.7	110	18	US-10-674-124A-21187	Sequence 21187, A
C 835	5	35.7	31	14	US-10-776-104-20	Sequence 20, Appl	C 908	5	35.7	114	17	US-10-373-802-3	Sequence 3, Appli
C 836	5	35.7	32	10	US-09-330-169-6	Sequence 6, Appli	C 909	5	35.7	114	18	US-10-674-124A-16304	Sequence 16304, A
C 837	5	35.7	32	18	US-10-676-248B-132	Sequence 132, App	C 910	5	35.7	115	18	US-10-425-115-47986	Sequence 47986, A
C 838	5	35.7	32	18	US-10-823-730-6	Sequence 6, Appli	C 911	5	35.7	116	17	US-10-424-599-29703	Sequence 29703, A
C 839	5	35.7	33	9	US-09-834-109-1	Sequence 1, Appli	C 912	5	35.7	117	18	US-10-437-963-75653	Sequence 75653, A
C 840	5	35.7	34	9	US-09-829-381A-6	Sequence 6, Appli	C 913	5	35.7	118	9	US-09-864-761-29408	Sequence 29408, A
C 841	5	35.7	34	17	US-10-681-972-6	Sequence 6, Appli	C 914	5	35.7	119	15	US-10-189-916A-3	Sequence 3, Appli
C 842	5	35.7	35	10	US-09-860-474-56	Sequence 56, Appl	C 915	5	35.7	124	9	US-09-923-876-1731	Sequence 1731, Ap
C 843	5	35.7	35	16	US-10-409-565-56	Sequence 56, Appl	C 916	5	35.7	124	9	US-09-864-761-22846	Sequence 22846, A
C 844	5	35.7	35	18	US-10-363-552-45	Sequence 45, Appl	C 917	5	35.7	124	10	US-09-923-876-1731	Sequence 1731, Ap
C 845	5	35.7	37	9	US-09-834-109-3	Sequence 3, Appli	C 918	5	35.7	124	18	US-10-437-963-38624	Sequence 38624, A
C 846	5	35.7	38	10	US-09-997-623-17	Sequence 17, Appl	C 919	5	35.7	127	18	US-10-674-124A-4142	Sequence 4142, Ap
C 847	5	35.7	38	10	US-09-997-623-18	Sequence 18, Appl	C 920	5	35.7	128	9	US-09-864-761-26927	Sequence 26927, A
C 848	5	35.7	38	10	US-09-978-917A-17	Sequence 17, Appl	C 921	5	35.7	129	17	US-10-296-115-308	Sequence 308, App
C 849	5	35.7	39	17	US-10-423-688A-21	Sequence 21, Appl	C 922	5	35.7	129	18	US-10-852-973-2	Sequence 2, Appli
C 850	5	35.7	39	17	US-10-423-688A-21	Sequence 21, Appl	C 923	5	35.7	130	9	US-09-864-761-19929	Sequence 19929, A
C 851	5	35.7	40	15	US-10-008-960-33	Sequence 33, Appl	C 924	5	35.7	130	9	US-09-864-761-24378	Sequence 24378, A
C 852	5	35.7	41	10	US-09-969-086A-6	Sequence 6, Appli	C 925	5	35.7	130	9	US-09-864-761-24703	Sequence 24703, A
C 853	5	35.7	41	10	US-09-969-086A-6	Sequence 6, Appli	C 926	5	35.7	132	16	US-10-029-386-21062	Sequence 21062, A
C 854	5	35.7	41	17	US-10-035-833A-2469	Sequence 2469, Ap	C 927	5	35.7	132	18	US-10-674-124A-20958	Sequence 20958, A
C 855	5	35.7	41	17	US-10-035-833A-4804	Sequence 4804, Ap	C 928	5	35.7	135	9	US-09-998-598-2385	Sequence 2385, Ap
C 856	5	35.7	41	17	US-10-035-833A-4843	Sequence 4843, Ap	C 929	5	35.7	137	17	US-10-424-599-114909	Sequence 114909, A
C 857	5	35.7	47	17	US-10-349-143-733	Sequence 733, App	C 930	5	35.7	138	9	US-09-815-242-3667	Sequence 3667, Ap
C 858	5	35.7	47	17	US-10-333-829-118	Sequence 118, App	C 931	5	35.7	138	16	US-10-029-386-17105	Sequence 17105, A
C 859	5	35.7	50	17	US-10-131-827-2775	Sequence 2775, Ap	C 932	5	35.7	138	17	US-10-282-122A-4910	Sequence 4910, Ap
C 860	5	35.7	50	17	US-10-131-827-3611	Sequence 3611, Ap	C 933	5	35.7	141	9	US-09-864-761-21454	Sequence 21454, A
C 861	5	35.7	54	18	US-10-008-960-35	Sequence 35, Appl	C 934	5	35.7	141	18	US-10-425-115-177538	Sequence 177538, A
C 862	5	35.7	59	8	US-08-781-986A-4956	Sequence 4956, Ap	C 935	5	35.7	144	18	US-10-437-963-39237	Sequence 39237, A
C 863	5	35.7	59	9	US-09-797-410-11	Sequence 11, Appl	C 936	5	35.7	145	18	US-10-767-701-16206	Sequence 16206, A
C 864	5	35.7	59	17	US-10-329-624-4956	Sequence 4956, Ap	C 937	5	35.7	146	9	US-09-783-590-4109	Sequence 4109, Ap
C 865	5	35.7	59	17	US-10-362-263-11	Sequence 11, Appl	C 938	5	35.7	147	9	US-09-880-821-8	Sequence 8, Appli
C 866	5	35.7	60	10	US-09-908-975-5414	Sequence 5414, Ap	C 939	5	35.7	148	17	US-10-242-535A-37555	Sequence 37555, A
C 867	5	35.7	60	10	US-09-908-975-5778	Sequence 5778, Ap	C 940	5	35.7	148	17	US-10-085-783A-37555	Sequence 37555, A
C 868	5	35.7	60	10	US-09-908-975-8123	Sequence 8123, Ap	C 941	5	35.7	148	18	US-10-425-115-104591	Sequence 104591, A
C 869	5	35.7	60	10	US-09-908-975-12229	Sequence 12229, A	C 942	5	35.7	149	18	US-10-425-115-126133	Sequence 126133, A
C 870	5	35.7	60	10	US-09-908-975-12446	Sequence 12446, A	C 943	5	35.7	150	13	US-10-027-632-175656	Sequence 175656, A
C 871	5	35.7	60	10	US-09-908-975-14060	Sequence 14060, A	C 944	5	35.7	150	14	US-10-198-846-10346	Sequence 10346, A
C 872	5	35.7	60	10	US-09-908-975-14372	Sequence 14372, A	C 945	5	35.7	150	16	US-10-029-386-22305	Sequence 22305, A

Sequence 175656, A
Sequence 50954, A
Sequence 27689, A
Sequence 31975, A
Sequence 24, Appl
Sequence 61849, A
Sequence 12342, A
Sequence 50540, A
Sequence 3163, Ap
Sequence 29591, A
Sequence 21179, A
Sequence 6070, Ap
Sequence 6667, Ap
Sequence 22134, A
Sequence 9649, Ap
Sequence 24593, A
Sequence 11939, A
Sequence 11939, A
Sequence 34971, A
Sequence 123487, A
Sequence 44679, A
Sequence 109841, A
Sequence 4666, Ap
Sequence 102364, A
Sequence 3927, Ap
Sequence 21665, A
Sequence 6274, Ap
Sequence 23529, A
Sequence 4953, Ap
Sequence 8521, Ap
Sequence 42184, A
Sequence 2134, Ap
Sequence 14, Appl
Sequence 43522, A
Sequence 17338, A
Sequence 131630, A
Sequence 1898, Ap
Sequence 37128, A
Sequence 1122, Ap
Sequence 80578, A
Sequence 3076, Ap
Sequence 39739, A
Sequence 27156, A
Sequence 156610, A
Sequence 31, Appl
Sequence 11787, A
Sequence 26615, A
Sequence 173424, A
Sequence 180260, A
Sequence 17043, A
Sequence 132, App
Sequence 334, App

ALIGNMENTS

RESULT 1
US-10-242-535A-57578
; Sequence 57578, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340

Sequence 175656, A
Sequence 50954, A
Sequence 27689, A
Sequence 31975, A
Sequence 24, Appl
Sequence 61849, A
Sequence 12342, A
Sequence 50540, A
Sequence 3163, Ap
Sequence 29591, A
Sequence 21179, A
Sequence 6070, Ap
Sequence 6667, Ap
Sequence 22134, A
Sequence 9649, Ap
Sequence 24593, A
Sequence 11939, A
Sequence 11939, A
Sequence 34971, A
Sequence 123487, A
Sequence 44679, A
Sequence 109841, A
Sequence 4666, Ap
Sequence 102364, A
Sequence 3927, Ap
Sequence 21665, A
Sequence 6274, Ap
Sequence 23529, A
Sequence 4953, Ap
Sequence 8521, Ap
Sequence 42184, A
Sequence 2134, Ap
Sequence 14, Appl
Sequence 43522, A
Sequence 17338, A
Sequence 131630, A
Sequence 1898, Ap
Sequence 37128, A
Sequence 1122, Ap
Sequence 80578, A
Sequence 3076, Ap
Sequence 39739, A
Sequence 27156, A
Sequence 156610, A
Sequence 31, Appl
Sequence 11787, A
Sequence 26615, A
Sequence 173424, A
Sequence 180260, A
Sequence 17043, A
Sequence 132, App
Sequence 334, App

US-09-736-250-5 (1-14) x US-10-242-535A-57578 (1-288)
Pred. No.: 3,15e-06 Length: 288
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-10-085-783A-57578
; Sequence 57578, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57578
; LENGTH: 288
; TYPE: DNA
; ORGANISM: Human

US-10-085-783A-57578
Alignment Scores:
Pred. No.: 3,15e-06 Length: 288
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-09-736-250-5 (1-14) x US-10-085-783A-57578 (1-288)
Pred. No.: 3,15e-06 Length: 288
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-10-242-535A-20816
; Sequence 20816, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.

; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis

; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242.535A
; CURRENT FILING DATE: 2002-09-12
; PATENT NO. US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20816
; LENGTH: 350
; TYPE: DNA
; ORGANISM: Human
US-10-242-535A-20816

Alignment Scores:
Pred. No.: 3.69e-06 Length: 350
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-09-736-250-5 (1-14) x US-10-242-535A-20816 (1-350)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 129 GAAGATAATGTCAGAAAATGCGGTCTCTGTGTGGCACT 170

RESULT 4

US-10-085-783A-20816
; Sequence 20816, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liaw, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20816
; LENGTH: 350
; TYPE: DNA
; ORGANISM: Human
US-10-085-783A-20816

Alignment Scores:
Pred. No.: 3.69e-06 Length: 350
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-09-736-250-5 (1-14) x US-10-085-783A-20816 (1-350)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 129 GAAGATAATGTCAGAAAATGCGGTCTCTGTGTGGCACT 170

RESULT 5

US-09-920-300A-1413/c
; Sequence 1413, Application US/09920300A
; Patent No. US20020136728A1
; GENERAL INFORMATION:
; APPLICANT: King, Gordon E.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.547
; CURRENT APPLICATION NUMBER: US/09/920,300A
; CURRENT FILING DATE: 2001-07-31
; NUMBER OF SEQ ID NOS: 1789
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1413
; LENGTH: 444
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-920-300A-1413

Alignment Scores:
Pred. No.: 4.47e-06 Length: 444
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-736-250-5 (1-14) x US-09-920-300A-1413 (1-444)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 436 GAAGATAATGTCAGAAAATGCGGTCTCTGTGTGGCACT 395

RESULT 6

US-10-033-528-1413/c
; Sequence 1413, Application US/10033528
; Publication No. US20020131971A1
; GENERAL INFORMATION:
; APPLICANT: King, Gordon E.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.547C1
; CURRENT APPLICATION NUMBER: US/10/033,528
; CURRENT FILING DATE: 2001-12-26
; NUMBER OF SEQ ID NOS: 1896
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1413
; LENGTH: 444
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-528-1413

Alignment Scores:
Pred. No.: 4.47e-06 Length: 444
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-09-736-250-5 (1-14) x US-10-033-528-1413 (1-444)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 436 GAAGATAATGTCAGAAAATGCGGTCTCTGTGTGGCACT 395

RESULT 7

US-10-099-926-1413/c
; Sequence 1413, Application US/10099926
; Publication No. US20030166064A1
; GENERAL INFORMATION:
; APPLICANT: King, Gordon E.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; APPLICANT: Jiang, Yugu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.547C2
; CURRENT APPLICATION NUMBER: US/10/099,926
; CURRENT FILING DATE: 2002-03-17
; NUMBER OF SEQ ID NOS: 1982
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1413
; LENGTH: 444
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-099-926-1413

Alignment Scores:
Pred. No.: 4,47e-06 Length: 444
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 16 Gaps: 0

US-09-736-250-5 (1-14) x US-10-099-926-1413 (1-444)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 436 GAAGATAATGCTCAGAAAATGGGTTCTGTGTGGCACT 395

RESULT 8
US-09-777-564-1252
; Sequence 1252, Application US/09777564
; Patent No. US20020022591A1
; GENERAL INFORMATION:
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.493
; CURRENT APPLICATION NUMBER: US/09/777,564
; CURRENT FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 1730
; SOFTWARE: FastSeq for Window Version 4.0
; SEQ ID NO 1252
; LENGTH: 447
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(447)
; OTHER INFORMATION: n = A,T,C or G
US-09-777-564-1252

Alignment Scores:
Pred. No.: 4,49e-06 Length: 447
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-736-250-5 (1-14) x US-09-777-564-1252 (1-447)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 93 GAAGATAATGCTCAGAAAATGGGTTCTGTGTGGCACT 134

RESULT 9
US-10-015-219-1252
; Sequence 1252, Application US/10015219
; Publication No. US20030008299A1
; GENERAL INFORMATION:
; APPLICANT: Algate, Paul A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.493C1
; CURRENT APPLICATION NUMBER: US/10/015,219
; CURRENT FILING DATE: 2002-03-02
; NUMBER OF SEQ ID NOS: 1739
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1252
; LENGTH: 447
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 424, 428, 437, 440
; OTHER INFORMATION: n = A,T,C or G
US-10-015-219-1252

Alignment Scores:
Pred. No.: 4,49e-06 Length: 447
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-09-736-250-5 (1-14) x US-10-015-219-1252 (1-447)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 93 GAAGATAATGCTCAGAAAATGGGTTCTGTGTGGCACT 134

RESULT 10
US-09-736-250-2
; Sequence 2, Application US/09736250
; Publication No. US20050014139A1
; GENERAL INFORMATION:
; APPLICANT: SUMITOMO ELECTRIC INDUSTRIES, LTD.
; APPLICANT: NAKAMURA, Takeshi
; TITLE OF INVENTION: HUMAN CYCLIN I AND GENES ENCODING THE SAME
; FILE REFERENCE: 050212-0278
; CURRENT APPLICATION NUMBER: US/09/736,250
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 09/054,492
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: PCT/JP96/02905
; PRIOR FILING DATE: 1996-10-07
; PRIOR APPLICATION NUMBER: 284663/1995
; PRIOR FILING DATE: 1995-10-05
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 1134
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-736-250-2

Alignment Scores:
Pred. No.: 9,5e-06 Length: 1134
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-09-736-250-5 (1-14) x US-09-736-250-2 (1-1134)

Qy 1 GluAspAsnValSerGluAsnValClySerValCysGlyThr 14
Db 1027 GAAGATAATGTCAGAAAATGTGGTTCTGTGTGGCACT 1068

RESULT 11

US-10-172-118-1326
; Sequence 1326, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 1326
; LENGTH: 1260
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM_006835
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-1326

Alignment Scores:
Pred. No.: 1.03e-05 Length: 1260
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-09-736-250-5 (1-14) x US-10-172-118-1326 (1-1260)

Qy 1 GluAspAsnValSerGluAsnValClySerValCysGlyThr 14
Db 1027 GAAGATAATGTCAGAAAATGTGGTTCTGTGTGGCACT 1068

RESULT 12

US-10-342-887-1326
; Sequence 1326, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10/342,887
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 1326
; LENGTH: 1260

; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-342-887-1326

Alignment Scores:
Pred. No.: 1.03e-05 Length: 1260
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-09-736-250-5 (1-14) x US-10-342-887-1326 (1-1260)

Qy 1 GluAspAsnValSerGluAsnValClySerValCysGlyThr 14
Db 1027 GAAGATAATGTCAGAAAATGTGGTTCTGTGTGGCACT 1068

RESULT 13

US-10-641-643-899
; Sequence 899, Application US/10641643
; Publication No. US20040077003A1
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
; GENE EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/641,643
; FILING DATE: 14-Aug-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 899:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1260 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g1183161
; SEQUENCE DESCRIPTION: SEQ ID NO: 899 :

US-10-641-643-899
Alignment Scores:
Pred. No.: 1.03e-05 Length: 1260
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

```
DB: 17 Gaps: 0
US-09-736-250-5 (1-14) x US-10-641-643-899 (1-1260)
Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 1027 GAAGATAATGCTCAGAAAAATGCGGTCTCTGTGTGGCACT 1068
RESULT 14
US-09-867-701-10907
; Sequence 10907, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10907
; LENGTH: 1889
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-867-701-10907
Alignment Scores:
Pred. No.: 1.43e-05 Length: 1889
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
US-09-736-250-5 (1-14) x US-09-867-701-10907 (1-1889)
Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 1570 GAAGATAATGCTCAGAAAAATGCGGTCTCTGTGTGGCACT 1611
RESULT 15
US-09-814-353-21294
; Sequence 21294, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21294
; LENGTH: 2146
```

```
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-814-353-21294
Alignment Scores:
Pred. No.: 1.59e-05 Length: 2146
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0
US-09-736-250-5 (1-14) x US-09-814-353-21294 (1-2146)
Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 1213 GAAGATAATGCTCAGAAAAATGCGGTCTCTGTGTGGCACT 1254
Search completed: February 11, 2005, 17:09:44
Job time : 75.665 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 11, 2005, 07:42:20 ; Search time 218.164 Seconds
(without alignments)
2442.660 Million cell updates/sec

Title: US-09-736-250-5

Perfect score: 14

Sequence: 1 EDVSENVGVCVT 14

Scoring table:

OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Word size: 1

Total number of hits satisfying chosen parameters: 68471176

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=cgcn2 1/USPTO.spool/US09736250/runat_07022005 154942 20659/app query.fasta_1.718
-DB=EST -OFMT=fastap -SUFFIX=oligo.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi -LIST=1000
-DNCALIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc
-NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09736250.qcgn 1 4385 @runat_07022005 154942 20659 -NCPU=6 -ICPU=3
-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

EST:
1: gb_est1.*
2: gb_est2.*
3: gb_hc.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_gsa1.*
9: gb_gsa2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	14	100.0	136	7	Z20123
2	14	100.0	139	1	AA678060
3	14	100.0	139	1	AA094874
4	14	100.0	197	1	AA659220
5	14	100.0	234	1	AA058781
6	14	100.0	246	4	BG180306
7	14	100.0	251	5	B0327548
8	14	100.0	251	5	BQ327560
9	14	100.0	265	7	R85184

AA680208	ac82d11.s	1	AA680208	269	14	100.0	14	100.0
AA011113	ze34d03.r	275	AA011113	275	14	100.0	14	100.0
AA778982	ac37f07.s	278	AA778982	278	14	100.0	14	100.0
F32546	HSPD25369.H	296	F32546	296	14	100.0	14	100.0
BI493342	df100a06.	302	BI493342	302	14	100.0	14	100.0
R84129	KK6088F.Hum	302	R84129	302	14	100.0	14	100.0
R87368	ym8808.r1	321	R87368	321	14	100.0	14	100.0
BE245492	TCBAP1D22	323	BE245492	323	14	100.0	14	100.0
BI383113	tc22g10.x	328	BI383113	328	14	100.0	14	100.0
BE675114	7f02g08.x	335	BE675114	335	14	100.0	14	100.0
BF109323	7l61e07.x	331	BF109323	331	14	100.0	14	100.0
AW939307	RC3-BN003	340	AW939307	340	14	100.0	14	100.0
BI491010	df02d12.w	340	BI491010	340	14	100.0	14	100.0
R83731	yp15f12.f1	340	R83731	340	14	100.0	14	100.0
AA055821	z176h03.s	341	AA055821	341	14	100.0	14	100.0
AW019986	df02d12.y	341	AW019986	341	14	100.0	14	100.0
BM894061	ij62h08.x	341	BM894061	341	14	100.0	14	100.0
BF901867	IL5-MT021	343	BF901867	343	14	100.0	14	100.0
AI735109	as76a02.x	344	AI735109	344	14	100.0	14	100.0
H80782	y864a11.r1	346	H80782	346	14	100.0	14	100.0
AA248313	cs92469.s	347	AA248313	347	14	100.0	14	100.0
CB135564	K-EST0187	347	CB135564	347	14	100.0	14	100.0
AA018692	ze54f08.r	348	AA018692	348	14	100.0	14	100.0
BG943235	ax35c01.x	348	BG943235	348	14	100.0	14	100.0
BM894332	ij82h08.y	348	BM894332	348	14	100.0	14	100.0
AI857246	wj93h01.x	349	AI857246	349	14	100.0	14	100.0
AA730298	nw41c12.s	350	AA730298	350	14	100.0	14	100.0
R88164	ym90c07.r1	350	R88164	350	14	100.0	14	100.0
AW225340	T5C11.Br	351	AW225340	351	14	100.0	14	100.0
BE539946	601060692	352	BE539946	352	14	100.0	14	100.0
H38301	yp70a04.r1	352	H38301	352	14	100.0	14	100.0
AA558174	nl27d12.s	353	AA558174	353	14	100.0	14	100.0
H84151	yt02h10.r1	357	H84151	357	14	100.0	14	100.0
N45919	YV34801.r1	357	N45919	357	14	100.0	14	100.0
AW408405	UI-HF-BK0	358	AW408405	358	14	100.0	14	100.0
CD678566	hp09h12.y	358	CD678566	358	14	100.0	14	100.0
F36711	HSPD34599.H	359	F36711	359	14	100.0	14	100.0
D52300	HUM073H12A	363	D52300	363	14	100.0	14	100.0
BS300959	bb10h11.x	367	BS300959	367	14	100.0	14	100.0
AD172737	AGENCOURT	367	AD172737	367	14	100.0	14	100.0
AJ573253	AJ573253	368	AJ573253	368	14	100.0	14	100.0
AA225844	nc27b04.s	370	AA225844	370	14	100.0	14	100.0
AW020950	df16g08.y	370	AW020950	370	14	100.0	14	100.0
T36202	EST98394.Hu	370	T36202	370	14	100.0	14	100.0
AA053242	z172b09.s	373	AA053242	373	14	100.0	14	100.0
T30429	EST16545.Hu	376	T30429	376	14	100.0	14	100.0
AW403319	UI-HF-BK0	378	AW403319	378	14	100.0	14	100.0
BU566150	AGENCOURT	378	BU566150	378	14	100.0	14	100.0
R84342	yq23e04.r1	379	R84342	379	14	100.0	14	100.0
H86624	yt04d07.r1	381	H86624	381	14	100.0	14	100.0
AA088582	zk64b06.r	382	AA088582	382	14	100.0	14	100.0
R87605	ym91e01.r1	382	R87605	382	14	100.0	14	100.0
BI063463	IL3-UT011	383	BI063463	383	14	100.0	14	100.0
BI063812	IL3-UT011	384	BI063812	384	14	100.0	14	100.0
BI064006	IL3-UT011	384	BI064006	384	14	100.0	14	100.0
BI490970	df01h03.w	384	BI490970	384	14	100.0	14	100.0
BM666783	UI-E-Cl1	384	BM666783	384	14	100.0	14	100.0
BI063994	IL3-UT011	388	BI063994	388	14	100.0	14	100.0
F25987	HSPD13241.H	388	F25987	388	14	100.0	14	100.0
N78101	yv72f08.r1	389	N78101	389	14	100.0	14	100.0
AW403398	UI-HF-BK0	390	AW403398	390	14	100.0	14	100.0
BI063816	IL3-UT011	392	BI063816	392	14	100.0	14	100.0
BI063832	IL3-UT011	395	BI063832	395	14	100.0	14	100.0
W03594	za02b11.r1	395	W03594	395	14	100.0	14	100.0
R86879	ym86h08.r1	398	R86879	398	14	100.0	14	100.0
AI492331	ti23b03.x	402	AI492331	402	14	100.0	14	100.0
AA505973	ni01h04.s	402	AA505973	402	14	100.0	14	100.0
AA018037	ze51d04.r	403	AA018037	403	14	100.0	14	100.0
H25604	y148e05.r1	403	H25604	403	14	100.0	14	100.0
AI797547	we54h06.x	406	AI797547	406	14	100.0	14	100.0
BI063810	IL3-UT011	406	BI063810	406	14	100.0	14	100.0
AA146795	zo35h12.s	407	AA146795	407	14	100.0	14	100.0
BE090015	RC6-BT070	407	BE090015	407	14	100.0	14	100.0

C 83	14	100.0	408	1	AA057087	AA057087 zfs9d06.r	C 156	14	100.0	449	1	AA864947	AA864947 oh36b04.s
C 84	14	100.0	408	4	BI063454	BI063454 IL3-UT011	C 157	14	100.0	450	1	AI795935	AI795935 wh40c11.x
C 85	14	100.0	409	1	AA021333	AA021333 z68b08.r	C 158	14	100.0	450	1	AI158006	AI158006 zo53h03.s
C 86	14	100.0	409	2	AW387725	AW387725 MR4-ST011	C 159	14	100.0	451	1	AI301708	AI301708 gn36h05.x
C 87	14	100.0	409	2	AW401698	AW401698 UI-HF-BK0	C 160	14	100.0	451	7	H86415	H86415 ys93e05.r1
C 88	14	100.0	409	2	AW438598	AW438598 xu37a07.x	C 161	14	100.0	452	1	AA411127	AA411127 zc29g02.r
C 89	14	100.0	411	6	CA868145	CA868145 i-78e02.y	C 162	14	100.0	452	1	AA101887	AA101887 zk85b06.r
C 90	14	100.0	411	7	TI5517	TI5517 IB1478 Infa	C 163	14	100.0	453	2	AA406913	AA406913 UI-HF-BK0
C 91	14	100.0	413	7	N24351	N24351 yx14a05.r1	C 164	14	100.0	454	2	AW135630	AW135630 UI-H-B11-
C 92	14	100.0	414	1	AI370280	AI370280 qv76a01.x	C 165	14	100.0	454	2	BI063988	BI063988 IL3-UT011
C 93	14	100.0	414	2	BE168324	BE168324 QV3-HA051	C 166	14	100.0	455	7	CN403769	CN403769 170006001
C 94	14	100.0	414	1	BI063807	BI063807 IL3-UT011	C 167	14	100.0	456	7	N91218	N91218 zal3f01.r1
C 95	14	100.0	415	1	AA018940	AA018940 ze56a07.r	C 168	14	100.0	457	7	N32671	N32671 yx77e10.r1
C 96	14	100.0	415	2	BP222344	BP222344 7p51f01.x	C 169	14	100.0	459	1	AA001081	AA001081 ze47a01.r
C 97	14	100.0	417	1	AI085425	AI085425 oW82h01.s	C 170	14	100.0	459	1	AI032951	AI032951 ox06h03.s
C 98	14	100.0	417	7	H01313	H01313 y199c04.s1	C 171	14	100.0	459	1	AI347777	AI347777 qO96c05.x
C 99	14	100.0	417	7	R89574	R89574 yp97b03.s1	C 172	14	100.0	459	2	AA403463	AA403463 UI-HF-BK0
C 100	14	100.0	417	7	RA857209	RA857209 of63d04.s	C 173	14	100.0	459	7	N29011	N29011 yx40b06.r1
C 101	14	100.0	418	1	AA226929	AA226929 zr21b11.s	C 174	14	100.0	460	1	AA021650	AA021650 ze69d06.r
C 102	14	100.0	418	1	BI063848	BI063848 IL3-UT011	C 175	14	100.0	461	1	AA054388	AA054388 zf54f01.r
C 103	14	100.0	419	1	AA158818	AA158818 z047c01.r	C 176	14	100.0	461	1	AA057851	AA057851 z195f08.s
C 104	14	100.0	420	1	AA704015	AA704015 ag80b04.r	C 177	14	100.0	461	7	N25815	N25815 yx22b02.r1
C 105	14	100.0	420	4	BI063843	BI063843 IL3-UT011	C 178	14	100.0	461	7	R87382	R87382 ym88f06.r1
C 106	14	100.0	420	7	H84867	H84867 ys90h07.r1	C 179	14	100.0	462	1	AI499883	AI499883 tn97c04.x
C 107	14	100.0	421	1	AI952335	AI952335 wx72c10.x	C 180	14	100.0	462	1	AJ708106	AJ708106 AJ708106
C 108	14	100.0	421	1	AA157562	AA157562 z068g05.s	C 181	14	100.0	463	1	AA773958	AA773958 ab67d05.r
C 109	14	100.0	422	4	BI063835	BI063835 IL3-UT011	C 182	14	100.0	463	2	BE326321	BE326321 hw01f10.x
C 110	14	100.0	423	1	AI002297	AI002297 qO86f06.s	C 183	14	100.0	463	4	BI850226	BI850226 ima9qc.1
C 111	14	100.0	423	1	AA223161	AA223161 zr06b10.s	C 184	14	100.0	465	5	BU069467	BU069467 im22f05.x
C 112	14	100.0	424	1	BF197808	BF197808 7p29g06.x	C 185	14	100.0	466	1	AI274874	AI274874 qk61e11.x
C 113	14	100.0	424	2	AA043972	AA043972 zk58e02.s	C 186	14	100.0	466	1	AI306635	AI306635 qn45h11.x
C 114	14	100.0	426	1	AA146787	AA146787 z035g12.s	C 187	14	100.0	466	7	W21065	W21065 z5b5a09.r1
C 115	14	100.0	426	1	BF852263	BF852263 MR3-EN009	C 188	14	100.0	467	5	BQ302769	BQ302769 CN1-BT059
C 116	14	100.0	426	2	AA767578	AA767578 oa1b12.s	C 189	14	100.0	468	1	AA134108	AA134108 z129c01.s
C 117	14	100.0	427	1	AA767578	AA767578 oq92c10.s	C 190	14	100.0	468	1	AI879492	AI879492 au53b06.x
C 118	14	100.0	427	1	AA961959	AA961959 qz92c10.s	C 191	14	100.0	468	2	BF927593	BF927593 CM2-NT019
C 119	14	100.0	427	7	N68425	N68425 zal3e08.s1	C 192	14	100.0	468	4	BI063827	BI063827 IL3-UT011
C 120	14	100.0	428	1	AA525244	AA525244 ni52f05.s	C 193	14	100.0	468	7	NA3869	NA3869 yy43c12.r1
C 121	14	100.0	431	7	H82548	H82548 yv77a05.r1	C 194	14	100.0	470	1	AA837513	AA837513 oS31b11.s
C 122	14	100.0	432	7	CN645730	CN645730 ILLUMIGEN	C 195	14	100.0	470	2	AA213687	AA213687 zq92h06.r
C 123	14	100.0	433	1	AA150672	AA150672 z146b02.s	C 196	14	100.0	470	2	AW062552	AW062552 ILO-CT007
C 124	14	100.0	433	2	BF431566	BF431566 na445f09.	C 197	14	100.0	472	1	AA861414	AA861414 ak34b06.s
C 125	14	100.0	433	4	BI063839	BI063839 IL3-UT011	C 198	14	100.0	474	2	BE675931	BE675931 7f18f07.x
C 126	14	100.0	434	1	AA503477	AA503477 nh59e05.s	C 199	14	100.0	475	1	AI046124	AI046124 TENU1210
C 127	14	100.0	435	1	AA021376	AA021376 ze68c10.r	C 200	14	100.0	475	1	AI801762	AI801762 z095d05.x
C 128	14	100.0	435	1	AA121968	AA121968 zm25c09.s	C 201	14	100.0	475	1	AA459535	AA459535 zx89c08.r
C 129	14	100.0	435	7	W96274	W96274 ze42e02.r1	C 202	14	100.0	475	5	BQ548661	BQ548661 ik93h12.x
C 130	14	100.0	436	1	AA021071	AA021071 ze85e08.r	C 203	14	100.0	476	1	AA954106	AA954106 oq65d12.s
C 131	14	100.0	436	5	BQ379929	BQ379929 IL3-UT011	C 204	14	100.0	476	4	BI063844	BI063844 IL3-UT011
C 132	14	100.0	437	1	AA758948	AA758948 ah77e07.s	C 205	14	100.0	477	6	CA445832	CA445832 UI-H-E10-
C 133	14	100.0	437	1	AA121443	AA121443 zm23g08.s	C 206	14	100.0	478	1	AA456153	AA456153 zx74a01.r
C 134	14	100.0	437	1	AA159531	AA159531 z072g08.s	C 207	14	100.0	478	4	BI063991	BI063991 IL3-UT011
C 135	14	100.0	437	4	BI063825	BI063825 IL3-UT011	C 208	14	100.0	478	4	BI491939	BI491939 df17c01.w
C 136	14	100.0	438	1	AA128673	AA128673 zo04b02.s	C 209	14	100.0	478	4	BI906154	BI906154 603062603
C 137	14	100.0	440	1	AA164577	AA164577 zo92d11.s	C 210	14	100.0	479	2	BF942472	BF942472 n3e95a03.
C 138	14	100.0	441	1	AI635372	AI635372 ts94c11.x	C 211	14	100.0	479	2	AW020980	AW020980 df17c01.y
C 139	14	100.0	441	2	AW299224	AW299224 zx48a02.x	C 212	14	100.0	480	2	BE205841	BE205841 Bp46h01.x
C 140	14	100.0	441	2	BF109033	BF109033 7l49d03.x	C 213	14	100.0	482	4	BI063983	BI063983 IL3-UT011
C 141	14	100.0	441	7	H30847	H30847 y078e09.r1	C 214	14	100.0	482	5	BX280952	BX280952 BX280952
C 142	14	100.0	441	7	W46581	W46581 zc32e09.s1	C 215	14	100.0	482	7	R90752	R90752 ym02a05.r1
C 143	14	100.0	442	1	AA157272	AA157272 z0s2d07.s	C 216	14	100.0	483	1	AA586757	AA586757 nm71c04.s
C 144	14	100.0	442	2	BE295596	BE295596 y103c05.s1	C 217	14	100.0	483	1	AJ707455	AJ707455 AJ707455
C 145	14	100.0	443	2	BI063807	BI063807 601176557	C 218	14	100.0	484	1	AW403704	AW403704 UI-HF-BK0
C 146	14	100.0	444	1	AI342973	AI342973 qo27c04.x	C 219	14	100.0	485	2	AA157999	AA157999 z057d09.s
C 147	14	100.0	444	1	AA130255	AA130255 z129c01.r	C 220	14	100.0	485	1	AA17175	AA17175 zu13b07.r
C 148	14	100.0	445	1	AA102742	AA102742 zn75c10.s	C 221	14	100.0	485	2	AW264664	AW264664 xg33d03.x
C 149	14	100.0	445	5	BU740183	BU740183 tx40b07.x	C 222	14	100.0	485	2	BE206087	BE206087 bq37c12.x
C 150	14	100.0	446	1	AI680686	AI680686 t040b07.x	C 223	14	100.0	486	2	BF842750	BF842750 QV3-HT101
C 151	14	100.0	446	1	BI063833	BI063833 IL3-UT011	C 224	14	100.0	486	4	BI063468	BI063468 IL3-UT011
C 152	14	100.0	446	5	BU785406	BU785406 in45c04.x	C 225	14	100.0	487	1	AI813543	AI813543 wtj03d01.x
C 153	14	100.0	447	1	AI636109	AI636109 tr92h04.x	C 226	14	100.0	487	1	AA291445	AA291445 z44d09.r
C 154	14	100.0	447	6	CA943599	CA943599 lr82d01.x	C 227	14	100.0	487	1	AA291445	AA291445 z44d09.r
C 155	14	100.0	448	1	AA027118	AA027118 zk04h06.s	C 228	14	100.0	487	4	BI063801	BI063801 IL3-UT011

C 229	14	100.0	488	1	A1149667	A1149667	QF37D07.X	302	14	100.0	541	4	BM312319	BM312319	ig41h09.Y
C 230	14	100.0	488	1	AU712254	AU712254	QV37HT101	C 303	14	100.0	544	2	AW236763	AW236763	xm4f08.X
C 231	14	100.0	488	2	BF836252	BF836252	QV37HT101	C 304	14	100.0	549	1	AU160225	AU160225	xm4f08.X
C 232	14	100.0	489	1	AA937188	AA937188	ok13c10.S	C 305	14	100.0	549	1	AA599293	AA599293	ag35c03.S
C 233	14	100.0	489	1	AI580775	AI580775	ta04f05.X	C 306	14	100.0	550	5	BP306529	BP306529	BP306529
C 234	14	100.0	489	2	AW473016	AW473016	x827e00.X	C 307	14	100.0	552	2	AW176627	AW176627	IL4-CT007
C 235	14	100.0	492	4	BI063842	BI063842	IL3-UT011	C 308	14	100.0	554	2	AW515055	AW515055	xu83b04.X
C 236	14	100.0	492	4	BM509658	BM509658	ig92e01.Y	C 309	14	100.0	555	1	AA211288	AA211288	zp49l1.S
C 237	14	100.0	493	2	AW873472	AW873472	hm01h04.X	C 310	14	100.0	556	4	AA523356	AA523356	ni67b10.S
C 238	14	100.0	494	1	A1268435	A1268435	qm03h09.X	C 311	14	100.0	556	4	BG656173	BG656173	ib37h12.Y
C 239	14	100.0	495	4	BM707945	BM707945	UI-E-C11-	C 312	14	100.0	557	2	BF319112	BF319112	6018h189
C 240	14	100.0	497	1	AA088548	AA088548	z189c07.X	C 313	14	100.0	558	1	A1419541	A1419541	tf22d08.X
C 241	14	100.0	498	1	AW714067	AW714067	nw18g11.S	C 314	14	100.0	558	1	AU159472	AU159472	AU159472
C 242	14	100.0	498	2	AW302456	AW302456	xw04c02.X	C 315	14	100.0	559	1	AA521260	AA521260	aa75e06.S
C 243	14	100.0	499	1	AA827740	AA827740	ob54h11.S	C 316	14	100.0	559	4	BG684675	BG684675	602635957
C 244	14	100.0	499	1	AA612651	AA612651	no42f02.S	C 317	14	100.0	561	4	BF975395	BF975395	602245924
C 245	14	100.0	500	2	BF093118	BF093118	PM1-TN012	C 318	14	100.0	562	1	AA664175	AA664175	ac04h04.S
C 246	14	100.0	500	5	BU731805	BU731805	UI-E-C11-	C 319	14	100.0	562	2	BF437208	BF437208	767h12.X
C 247	14	100.0	501	1	A1340077	A1340077	QV44b07.X	C 320	14	100.0	562	4	EG686057	EG686057	602638626
C 248	14	100.0	501	1	AA533127	AA533127	nj46902.S	C 321	14	100.0	563	2	AW612687	AW612687	hh30e12.X
C 249	14	100.0	501	5	BU430243	BU430243	UI-HF-BN0	C 322	14	100.0	564	1	AA088443	AA088443	z189c07.S
C 250	14	100.0	502	1	A1126969	A1126969	QB96d02.X	C 323	14	100.0	564	1	A1755086	A1755086	cr35c06.X
C 251	14	100.0	502	2	AW772789	AW772789	h196h02.X	C 324	14	100.0	564	1	BP259087	BP259087	BP259087
C 252	14	100.0	502	4	BM687893	BM687893	UI-E-CK1-	C 325	14	100.0	568	1	A1144511	A1144511	qb73h04.X
C 253	14	100.0	504	1	A156184	A156184	z047c01.S	C 326	14	100.0	568	2	AW409690	AW409690	fh01d06.Y
C 254	14	100.0	504	4	BI063658	BI063658	IL3-UT011	C 327	14	100.0	569	1	AA595249	AA595249	no33b07.S
C 255	14	100.0	504	4	BI063676	BI063676	IL3-UT011	C 328	14	100.0	570	1	AA525154	AA525154	ni51a08.S
C 256	14	100.0	504	4	BI063677	BI063677	IL3-UT011	C 329	14	100.0	572	1	AU146040	AU146040	AU146040
C 257	14	100.0	504	4	BI063980	BI063980	IL3-UT011	C 330	14	100.0	576	5	BM996837	BM996837	UI-H-DH0-
C 258	14	100.0	504	4	BI063987	BI063987	IL3-UT011	C 331	14	100.0	577	4	BI869952	BI869952	603394102
C 259	14	100.0	505	4	BI063693	BI063693	IL3-UT011	C 332	14	100.0	578	5	BP258271	BP258271	BP258271
C 260	14	100.0	505	4	BI063815	BI063815	IL3-UT011	C 333	14	100.0	580	1	A1598247	A1598247	cn15d02.X
C 261	14	100.0	505	4	BI063845	BI063845	IL3-UT011	C 334	14	100.0	580	2	AW009156	AW009156	aw78b05.X
C 262	14	100.0	505	4	BI063973	BI063973	IL3-UT011	C 335	14	100.0	581	1	AA056104	AA056104	zf55c03.X
C 263	14	100.0	505	4	BI063998	BI063998	IL3-UT011	C 336	14	100.0	581	2	AW162274	AW162274	aw75h05.X
C 264	14	100.0	506	1	AA456187	AA456187	x74d06.X	C 337	14	100.0	581	5	BP258977	BP258977	BP258977
C 265	14	100.0	506	4	BI063678	BI063678	IL3-UT011	C 338	14	100.0	582	1	AU147052	AU147052	AU147052
C 266	14	100.0	506	4	BI063687	BI063687	IL3-UT011	C 339	14	100.0	582	2	AW411227	AW411227	fh11b01.Y
C 267	14	100.0	506	6	CA868199	CA868199	ir79e01.Y	C 340	14	100.0	587	1	AA496420	AA496420	zv37c03.X
C 268	14	100.0	507	2	BF837876	BF837876	QV37HT101	C 341	14	100.0	587	5	BP205055	BP205055	BP205055
C 269	14	100.0	507	4	BI063663	BI063663	IL3-UT011	C 342	14	100.0	588	5	BU078719	BU078719	im69c04.X
C 270	14	100.0	507	4	BI063665	BI063665	IL3-UT011	C 343	14	100.0	589	5	BU620209	BU620209	UI-H-PH1-
C 271	14	100.0	508	4	BI063990	BI063990	IL3-UT011	C 344	14	100.0	594	1	AU145099	AU145099	AU145099
C 272	14	100.0	509	4	BI063979	BI063979	IL3-UT011	C 345	14	100.0	596	1	AA434521	AA434521	zw31d12.X
C 273	14	100.0	511	1	BG656485	BG656485	z37h12.X	C 346	14	100.0	596	6	CA868387	CA868387	ir78e02.Y
C 274	14	100.0	513	1	AA443651	AA443651	zw35b10.X	C 347	14	100.0	597	6	CA868387	CA868387	ir78e02.Y
C 275	14	100.0	514	4	BI063978	BI063978	df01h03.Y	C 348	14	100.0	597	7	N58511	N58511	yy72f08.s1
C 276	14	100.0	515	2	AW019937	AW019937	df01h03.Y	C 349	14	100.0	598	1	AA053834	AA053834	zf53b06.X
C 277	14	100.0	515	6	CA948213	CA948213	iq19c12.Y	C 350	14	100.0	599	1	AA595432	AA595432	no34a11.S
C 278	14	100.0	516	1	AA968669	AA968669	qg76d05.S	C 351	14	100.0	601	1	AA846727	AA846727	aj99a10.S
C 279	14	100.0	516	1	AA310922	AA310922	EST181758	C 352	14	100.0	601	1	AA593789	AA593789	nm55d01.S
C 280	14	100.0	517	1	AI288797	AI288797	qm06g10.X	C 353	14	100.0	601	2	BE891426	BE891426	601434883
C 281	14	100.0	517	2	BE207846	BE207846	bb06a09.X	C 354	14	100.0	603	5	BQ272152	BQ272152	ij90a09.X
C 282	14	100.0	520	2	BF110854	BF110854	7n41b06.X	C 355	14	100.0	603	7	CN805010	CN805010	IL4UMIGEN
C 283	14	100.0	521	1	AA417071	AA417071	zul3b07.S	C 356	14	100.0	605	1	AA664102	AA664102	ac06a03.S
C 284	14	100.0	524	1	BI063679	BI063679	IL3-UT011	C 357	14	100.0	606	5	BU579739	BU579739	im50a11.X
C 285	14	100.0	524	4	BI912257	BI912257	60368487	C 358	14	100.0	607	1	AA044648	AA044648	DKE2p434P
C 286	14	100.0	526	1	AA758596	AA758596	ah58a08.S	C 359	14	100.0	607	1	AA629751	AA629751	ae63c01.S
C 287	14	100.0	526	1	AA604363	AA604363	no79g10.S	C 360	14	100.0	608	4	BM015005	BM015005	603640960
C 288	14	100.0	526	2	BE549514	BE549514	7b39e01.X	C 361	14	100.0	610	2	BF243478	BF243478	6018h79503
C 289	14	100.0	527	2	BF843136	BF843136	MR2-HT104	C 362	14	100.0	610	2	AW151319	AW151319	x947h08.X
C 290	14	100.0	531	1	A1601273	A1601273	ar99b01.X	C 363	14	100.0	611	1	AA188001	AA188001	zp67h10.S
C 291	14	100.0	531	5	BQ653339	BQ653339	AGENCOURT	C 364	14	100.0	611	2	BE223082	BE223082	hu47a07.X
C 292	14	100.0	532	1	AA018843	AA018843	ze57h10.X	C 365	14	100.0	611	4	BM690806	BM690806	UI-E-CK0-
C 293	14	100.0	532	1	AA0707260	AA0707260	ag84d03.X	C 366	14	100.0	612	1	A1420758	A1420758	tf02h11.X
C 294	14	100.0	534	2	AW051330	AW051330	wy89d03.X	C 367	14	100.0	612	2	AW612458	AW612458	hh02e09.X
C 295	14	100.0	534	6	CA867868	CA867868	ir82d01.Y	C 368	14	100.0	614	1	AA053911	AA053911	zf52f06.X
C 296	14	100.0	535	1	AA215707	AA215707	zr97h07.X	C 369	14	100.0	614	1	A1436613	A1436613	t103h01.X
C 297	14	100.0	537	2	AW290919	AW290919	UI-H-B12-	C 370	14	100.0	617	2	AW249490	AW249490	2821433.3
C 298	14	100.0	538	1	AA487524	AA487524	ab20e06.S	C 371	14	100.0	619	4	BI063996	BI063996	IL3-UT011
C 299	14	100.0	538	4	BM505258	BM505258	ig92e01.X	C 372	14	100.0	619	4	BM857651	BM857651	ij69c03.X
C 300	14	100.0	540	1	AA225516	AA225516	nc25b10.X	C 373	14	100.0	619	4	BM857651	BM857651	ij69c03.X
C 301	14	100.0	541	2	AW265239	AW265239	xq54a01.X	C 374	14	100.0	624	4	EG482778	EG482778	602502564

C 375	14	100.0	626	1	AA057586	AA057586 z62g09.r	448	14	100.0	750	4	BG428886	BG428886 602494673
C 376	14	100.0	628	2	BE220798	BE220798 hu18h03.x	449	14	100.0	751	5	BA422046	BA422046 BX422046
C 377	14	100.0	629	6	CB381894	CB381894 TGESTzyh2	450	14	100.0	754	4	BM479270	BM479270 AGENCOURT
C 378	14	100.0	632	6	CA947959	CA947959 iql19c12.x	C 451	14	100.0	756	2	AW073133	AW073133 wy94b02.x
C 379	14	100.0	633	5	BM991335	BM991335 UI-H-D10-	C 452	14	100.0	757	4	BG211683	BG211683 RST31252
C 380	14	100.0	634	1	AA053839	AA053839 zif53c08.r	C 453	14	100.0	757	4	BG777885	BG777885 602665623
C 381	14	100.0	635	2	BF594792	BF594792 z055d03.x	C 454	14	100.0	760	4	BI906096	BI906096 603062484
C 382	14	100.0	636	1	AA205570	AA205570 zq68b08.s	C 455	14	100.0	764	6	CB962746	CB962746 AGENCOURT
C 383	14	100.0	636	7	CN483826	CN483826 hw38g08.y	C 456	14	100.0	765	7	CF135787	CF135787 UI-HF-BNO
C 384	14	100.0	640	5	BQ429097	BQ429097 AGENCOURT	C 457	14	100.0	766	4	BG767215	BG767215 602740208
C 385	14	100.0	642	1	AS573290	AS573290 nk98c09.s	C 458	14	100.0	767	6	CD520815	CD520815 AGENCOURT
C 386	14	100.0	642	5	BU784337	BU784337 tn13g08.x	C 459	14	100.0	770	2	BF036200	BF036200 601458271
C 387	14	100.0	643	1	AI679428	AI679428 tu63f12.x	C 460	14	100.0	775	4	BG219146	BG219146 RST38899
C 388	14	100.0	644	5	BF794011	BF794011 602254657	C 461	14	100.0	778	4	BG213882	BG213882 RST33504
C 389	14	100.0	644	5	BU689348	BU689348 UI-CF-EC1	C 462	14	100.0	782	1	AI018633	AI018633 ou47h04.x
C 390	14	100.0	645	2	AW152399	AW152399 xg64a01.x	C 463	14	100.0	784	5	BU176897	BU176897 AGENCOURT
C 391	14	100.0	645	4	BM12236	BM12236 i941h09.x	C 464	14	100.0	801	2	BE620803	BE620803 601483387
C 392	14	100.0	647	2	BF435610	BF435610 nac33h11.	C 465	14	100.0	801	5	BQ645542	BQ645542 AGENCOURT
C 393	14	100.0	653	7	CN403762	CN403762 170004245	C 466	14	100.0	803	5	BQ071740	BQ071740 AGENCOURT
C 394	14	100.0	654	4	BG759588	BG759588 602712170	C 467	14	100.0	806	2	BF669925	BF669925 602118429
C 395	14	100.0	654	1	AI765328	AI765328 at73f10.x	C 468	14	100.0	810	5	BA461980	BA461980 BX461980
C 396	14	100.0	654	1	AI832325	AI832325 at73e05.x	C 469	14	100.0	828	5	BU566387	BU566387 AGENCOURT
C 397	14	100.0	654	2	BF792283	BF792283 602252801	C 470	14	100.0	829	1	AI523625	AI523625 t995c02.x
C 398	14	100.0	655	2	AW467341	AW467341 ue09e10.x	C 471	14	100.0	833	5	BU532129	BU532129 AGENCOURT
C 399	14	100.0	657	5	BQ773620	BQ773620 UI-H-E21-	C 472	14	100.0	834	2	BF698561	BF698561 602130766
C 400	14	100.0	661	1	AI719868	AI719868 as47a04.x	C 473	14	100.0	849	2	BF577160	BF577160 602135454
C 401	14	100.0	662	2	BF925989	BF925989 MR2-NT013	C 474	14	100.0	852	7	CF243019	CF243019 AGENCOURT
C 402	14	100.0	662	1	AI928836	AI928836 au65b11.x	C 475	14	100.0	853	2	BF666533	BF666533 602123987
C 403	14	100.0	663	2	BG613480	BG613480 603504247	C 476	14	100.0	854	4	BG182134	BG182134 RST998 AC
C 404	14	100.0	663	4	B1917454	B1917454 603185118	C 477	14	100.0	856	2	BF130818	BF130818 601818484
C 405	14	100.0	664	5	BU603028	BU603028 AGENCOURT	C 478	14	100.0	872	5	BU542568	BU542568 AGENCOURT
C 406	14	100.0	666	5	BU679866	BU679866 UI-CF-DU1	C 479	14	100.0	873	4	BG531994	BG531994 602561020
C 407	14	100.0	666	1	AA218918	AA218918 z102c03.s	C 480	14	100.0	889	6	CD517935	CD517935 AGENCOURT
C 408	14	100.0	667	6	CA441829	CA441829 UI-H-ED0-	C 481	14	100.0	893	4	BI257270	BI257270 602967201
C 409	14	100.0	668	5	BQ002431	BQ002431 UI-H-E11-	C 482	14	100.0	899	6	CD358716	CD358716 AGENCOURT
C 410	14	100.0	670	5	BM997732	BM997732 UI-H-D10-	C 483	14	100.0	899	6	CD522597	CD522597 AGENCOURT
C 411	14	100.0	671	5	BM980581	BM980581 UI-CF-EN1	C 484	14	100.0	911	2	BE747713	BE747713 601578166
C 412	14	100.0	671	5	BQ016234	BQ016234 UI-H-DT1-	C 485	14	100.0	913	5	BQ221930	BQ221930 AGENCOURT
C 413	14	100.0	671	5	BQ773013	BQ773013 UI-H-PE0-	C 486	14	100.0	920	2	BE300217	BE300217 600944220
C 414	14	100.0	672	5	BM970544	BM970544 UI-CF-EC1	C 487	14	100.0	921	5	BQ230170	BQ230170 AGENCOURT
C 415	14	100.0	672	5	BU615980	BU615980 UI-H-DF0-	C 488	14	100.0	921	7	CF264864	CF264864 AGENCOURT
C 416	14	100.0	672	6	CD640858	CD640858 AGENCOURT	C 489	14	100.0	927	2	BF575348	BF575348 602134082
C 417	14	100.0	673	1	AI928349	AI928349 w96c03.x	C 490	14	100.0	938	5	BQ710910	BQ710910 AGENCOURT
C 418	14	100.0	673	5	BQ182277	BQ182277 UI-H-EU0-	C 491	14	100.0	946	4	BG031336	BG031336 602299031
C 419	14	100.0	673	5	BU738049	BU738049 UI-E-DW1-	C 492	14	100.0	959	5	BQ230627	BQ230627 AGENCOURT
C 420	14	100.0	674	5	BM994615	BM994615 UI-H-DH0-	C 493	14	100.0	960	5	BQ30674	BQ30674 AGENCOURT
C 421	14	100.0	674	6	CA448476	CA448476 UI-H-ET0-	C 494	14	100.0	967	7	CN647834	CN647834 ILLUMGEN
C 422	14	100.0	674	6	CD366863	CD366863 UI-H-F12-	C 495	14	100.0	968	2	BE789168	BE789168 601476292
C 423	14	100.0	676	4	BG762543	BG762543 602734406	C 496	14	100.0	973	5	BQ650937	BQ650937 AGENCOURT
C 424	14	100.0	679	4	BG188438	BG188438 RST7456 A	C 497	14	100.0	975	2	BF570206	BF570206 602185591
C 425	14	100.0	680	4	BG661032	BG661032 N335 SSH	C 498	14	100.0	976	4	BG392121	BG392121 602410213
C 426	14	100.0	681	6	CD642085	CD642085 AGENCOURT	C 499	14	100.0	978	4	BM463752	BM463752 AGENCOURT
C 427	14	100.0	682	2	BF220183	BF220183 601296732	C 500	14	100.0	979	2	BF344340	BF344340 602014715
C 428	14	100.0	690	7	CF135924	CF135924 UI-HF-BNO	C 501	14	100.0	982	5	BQ708698	BQ708698 AGENCOURT
C 429	14	100.0	691	2	BF337048	BF337048 602034442	C 502	14	100.0	983	2	BF795121	BF795121 602256456
C 430	14	100.0	692	2	BE887738	BE887738 601486303	C 503	14	100.0	986	4	BG392783	BG392783 602410158
C 431	14	100.0	694	1	AA703243	AA703243 z170e05.s	C 504	14	100.0	1024	2	BE613274	BE613274 601452513
C 432	14	100.0	694	6	CA441689	CA441689 UI-H-ED0-	C 505	14	100.0	1029	4	BM454583	BM454583 AGENCOURT
C 433	14	100.0	695	1	AA910671	AA910671 ok84a04.s	C 506	14	100.0	1041	4	BM555910	BM555910 AGENCOURT
C 434	14	100.0	700	2	BF055443	BF055443 7j80b08.x	C 507	14	100.0	1059	4	BG254346	BG254346 602368913
C 435	14	100.0	701	1	AI568713	AI568713 th14g08.x	C 508	14	100.0	1068	5	BM923007	BM923007 AGENCOURT
C 436	14	100.0	716	2	BE888060	BE888060 601511562	C 509	14	100.0	1078	4	BM454194	BM454194 AGENCOURT
C 437	14	100.0	723	1	AI740926	AI740926 w918d08.x	C 510	14	100.0	1091	2	BE894125	BE894125 601438253
C 438	14	100.0	724	2	BF667981	BF667981 602122225	C 511	14	100.0	1109	4	BF980373	BF980373 602288255
C 439	14	100.0	724	7	CF135985	CF135985 UI-HF-BNO	C 512	14	100.0	1109	4	BM462171	BM462171 AGENCOURT
C 440	14	100.0	728	2	BE620268	BE620268 601483387	C 513	14	100.0	1126	4	BG119682	BG119682 602349304
C 441	14	100.0	731	2	BF241617	BF241617 601878943	C 514	14	100.0	1134	9	AY412158	AY412158 Homo sap1
C 442	14	100.0	731	5	BU632784	BU632784 UI-H-FE1-	C 515	14	100.0	1142	4	BM466858	BM466858 AGENCOURT
C 443	14	100.0	743	2	BF797400	BF797400 602257046	C 516	14	100.0	1241	4	BG746028	BG746028 602723467
C 444	14	100.0	744	6	CD522104	CD522104 AGENCOURT	C 517	14	100.0	1458	4	BM473295	BM473295 AGENCOURT
C 445	14	100.0	745	5	BQ000493	BQ000493 UI-H-DF0-	C 518	13	92.9	277	2	AW299229	AW299229 x848b02.x
C 446	14	100.0	746	4	BG912921	BG912921 602807320	C 519	13	92.9	298	2	BF902812	BF902812 CM2-MT019
C 447	14	100.0	748	6	CB963441	CB963441 AGENCOURT	C 520	13	92.9	298	2	AW409656	AW409656 FH01B09.Y

C 521 13 92.9 315 2 AW410809 Fh08e04.y
C 522 13 92.9 383 4 B1063819 IL3-UT011
C 523 13 92.9 408 1 AA578724 nh23h11.s
C 524 13 92.9 418 1 A1392905 tg10f04.x
C 525 13 92.9 437 7 H30719 yo78h08.r1
C 526 13 92.9 525 1 A1742970 w976e06.x
C 527 13 92.9 643 4 B1197962 602761927
C 528 13 92.9 703 4 BG616164 602642744
C 529 13 92.9 753 4 B1859488 60338338
C 530 13 92.9 839 4 BG397722 602438783
C 531 13 92.9 889 4 BF979086 602147596
C 532 13 92.9 915 4 BG682664 602626956
C 533 12 85.7 145 1 AA701610 zi41e11.s
C 534 12 85.7 348 5 BQ334196 FM4-WT010
C 535 12 85.7 388 1 AA099355 zk85b06.s
C 536 12 85.7 474 1 AA053977 zf47c02.r
C 537 12 85.7 714 2 BR294585 601176160
C 538 11 78.6 295 6 CB107619 K-EST0146
C 539 11 78.6 364 4 B1063837 IL3-UT011
C 540 11 78.6 395 2 AW780047 hm96g06.x
C 541 11 78.6 431 1 AA054181 zfi5lb08.r
C 542 11 78.6 455 2 BF837869 QV3-HT101
C 543 11 78.6 465 4 B1063666 IL3-UT011
C 544 11 78.6 504 2 AW402651 UI-HF-BK0
C 545 11 78.6 550 6 CB554966 MMSF0031
C 546 11 78.6 627 1 AA044936 zfi5lh09.f
C 547 11 78.6 857 2 BB962804 601656513
C 548 11 78.6 1425 4 BG429088 602494124
C 549 10 71.4 212 7 C0582535 ILLUMIGEN
C 550 10 71.4 253 4 B1036115 RCS-NT026
C 551 10 71.4 283 4 B1036116 RCS-NT026
C 552 10 71.4 291 6 CB710245 AMGNNUC:N
C 553 10 71.4 294 2 BF800842 CMA-CI006
C 554 10 71.4 296 6 C75090 C75090 Huma
C 555 10 71.4 319 7 C0692628 DG11-5011
C 556 10 71.4 331 1 A1502600 UI-R-C2-n
C 557 10 71.4 336 7 Z28780 HSB94D042 S
C 558 10 71.4 350 4 BM422610 RSA08.29
C 559 10 71.4 354 7 C0692475 DG11-48n6
C 560 10 71.4 350 6 CB779646 AMGNNUC:C
C 561 10 71.4 363 4 B1063847 IL3-UT011
C 562 10 71.4 373 1 AA483892 ne76d08.s
C 563 10 71.4 377 7 C0711948 DG14-179p
C 564 10 71.4 378 7 C0690584 DG11-277d
C 565 10 71.4 382 7 H25558 Y148C05.s1
C 566 10 71.4 384 7 R76787 Y162B02.s1
C 567 10 71.4 389 7 C0681704 DG11-132g
C 568 10 71.4 391 4 B1064004 IL3-UT011
C 569 10 71.4 398 1 AA013295 ze28c04.r
C 570 10 71.4 403 7 CN542715 UI-R-DQ1-
C 571 10 71.4 404 7 H43440 YP09h09.s1
C 572 10 71.4 404 7 H43440 YP09h09.s1
C 573 10 71.4 409 1 AA657275 v27e03.r
C 574 10 71.4 416 1 AA879848 v99f05.r
C 575 10 71.4 420 7 H81583 YU73G02.s1
C 576 10 71.4 427 1 AA012968 B10612968
C 577 10 71.4 421 4 B1063824 IL3-UT011
C 578 10 71.4 426 7 C0656112 DG22-1g1
C 579 10 71.4 427 7 C0684251 DG11-180g
C 580 10 71.4 438 7 C0679953 DG11-108p
C 581 10 71.4 440 7 R34642 YJ78f06.s1
C 582 10 71.4 442 7 H65038 Yf69a12.s1
C 583 10 71.4 454 7 C0712346 B10612346
C 584 10 71.4 459 7 C0683345 DG11-168C
C 585 10 71.4 463 2 BF525036 BPS25036
C 586 10 71.4 493 7 C0689602 BPS25036
C 587 10 71.4 512 7 C0691805 BPS25036
C 588 10 71.4 513 1 A1154993 A1154993 ud8e01.r
C 589 10 71.4 521 7 C0692089 DG11-41o1
C 590 10 71.4 523 7 C0711872 DG14-178j
C 591 10 71.4 524 2 BF082717 PM2-BT072
C 592 10 71.4 528 7 C0680564 DG11-117k
C 593 10 71.4 549 7 C0684316 DG11-181e

C 594 10 71.4 552 7 C0587851 DG2-17j6
C 595 10 71.4 556 7 C0690076 DG11-269p
C 596 10 71.4 557 7 C0711347 DG14-1671
C 597 10 71.4 558 7 C0688565 DG11-2470
C 598 10 71.4 561 7 C0689123 DG11-2540
C 599 10 71.4 565 7 C0694756 DG11-75k2
C 600 10 71.4 571 7 C0686546 DG11-218d
C 601 10 71.4 574 7 C0701431 DG32-2030
C 602 10 71.4 575 7 C0701622 DG32-209a
C 603 10 71.4 576 7 C0700099 DG32-1700
C 604 10 71.4 577 7 C0690551 DG11-2761
C 605 10 71.4 578 4 BG664994 DRABWFO3
C 606 10 71.4 582 7 C0693161 DG11-59a1
C 607 10 71.4 585 7 C0683945 DG11-176p
C 608 10 71.4 585 7 C0686061 DG11-210b
C 609 10 71.4 586 7 C0589769 DG3-30f10
C 610 10 71.4 586 7 C0689003 DG11-253d
C 611 10 71.4 591 7 C0695929 DG11-91h7
C 612 10 71.4 592 7 C0681686 DG11-132c
C 613 10 71.4 593 7 C0684897 DG11-192m
C 614 10 71.4 595 7 C0691112 DG11-286d
C 615 10 71.4 599 7 C0687411 DG11-231b
C 616 10 71.4 599 7 C0716739 DG14-2619
C 617 10 71.4 603 7 C0697636 DG32-115n
C 618 10 71.4 607 7 C0693827 DG11-68e2
C 619 10 71.4 609 7 C0693559 DG11-64f1
C 620 10 71.4 610 7 C0687549 DG11-233f
C 621 10 71.4 611 7 C0683741 DG11-174e
C 622 10 71.4 616 7 C0669306 DG33-4912
C 623 10 71.4 619 7 C0686845 DG11-222d
C 624 10 71.4 624 7 C0710722 DG14-1551
C 625 10 71.4 627 7 C0696053 DG11-93d4
C 626 10 71.4 628 7 C0656534 DG32-2c12
C 627 10 71.4 628 7 C0680061 DG11-110a
C 628 10 71.4 628 7 C0693506 DG11-63b8
C 629 10 71.4 628 7 C0717778 DG14-56k1
C 630 10 71.4 629 4 B1295794 UI-R-DK0-
C 631 10 71.4 629 7 C0684311 DG11-181d
C 632 10 71.4 635 7 CF109609 Shultzomi
C 633 10 71.4 644 2 AW972885 AW972885 EST384980
C 634 10 71.4 645 7 C0681575 DG11-131a
C 635 10 71.4 649 7 C0712475 DG14-18g1
C 636 10 71.4 653 7 C0690561 DG11-276n
C 637 10 71.4 655 7 C0686288 DG11-213m
C 638 10 71.4 665 7 CN004557 ip20b09.g
C 639 10 71.4 667 7 CN003894 ip40b06.g
C 640 10 71.4 668 7 C0671525 DG33-7k4
C 641 10 71.4 668 7 C0712839 DG14-197a
C 642 10 71.4 670 7 C0688812 DG11-250m
C 643 10 71.4 671 7 C0693103 DG11-58f1
C 644 10 71.4 676 7 C0689890 DG11-266p
C 645 10 71.4 677 7 C0711476 DG14-1690
C 646 10 71.4 679 7 C0685962 DG11-208p
C 647 10 71.4 679 7 C0686619 DG11-219f
C 648 10 71.4 681 7 C0714386 DG14-2250
C 649 10 71.4 686 7 C0687190 DG11-2280
C 650 10 71.4 691 7 C0570359 AGENCOURT
C 651 10 71.4 692 7 C0718367 DG14-63j8
C 652 10 71.4 693 7 C0711358 DG14-167m
C 653 10 71.4 695 7 C0692001 DG11-40d2
C 654 10 71.4 698 7 C0683294 DG11-167g
C 655 10 71.4 699 7 C0682968 DG11-162a
C 656 10 71.4 704 7 C0714359 DG14-225c
C 657 10 71.4 706 7 C069501 DG11-99m2
C 658 10 71.4 707 7 C0610170 DG8-90b24
C 659 10 71.4 713 7 C0693213 DG11-59k5
C 660 10 71.4 720 7 C0715438 DG14-2511
C 661 10 71.4 741 7 CK477989 AGENCOURT
C 662 10 71.4 748 7 CV077745 AGENCOURT
C 663 10 71.4 759 7 C0654666 DG15-1c6
C 664 10 71.4 796 7 C0558058 AGENCOURT
C 665 10 71.4 803 2 BF794848 60256720
C 666 10 71.4 826 7 C0571802 AGENCOURT

667	10	71.4	852	7	C0569279	COS69279	AGENCOURT	740	9	64.3	646	5	BQ264702	BO264702	NISC ff01
668	10	71.4	936	5	BU501311	BU501311	AGENCOURT	741	9	64.3	659	2	BE675818	BE675818	7f16f08.x
669	10	71.4	1048	7	CR755552	CR755552	AGENCOURT	742	9	64.3	663	2	BF536616	BF536616	602048784
670	10	71.4	1194	2	BF381715	BF381715	601815930	743	9	64.3	666	1	AA869420	AA869420	q2048784
671	10	71.4	1247	7	CF111004	CF111004	Shultzoni	744	9	64.3	669	6	BE370288	BE370288	601222543
672	9	64.3	67	1	AA085041	AA085041	zn14d06.s	745	9	64.3	669	6	CD769922	CD769922	AGENCOURT
673	9	64.3	100	5	AA237743	AA237743	mx77a06.r	746	9	64.3	681	2	BE381020	BE381020	601271560
674	9	64.3	205	5	BQ566775	BQ566775	gi69b06.y	747	9	64.3	681	4	BQ088190	BQ088190	H3149005
675	9	64.3	214	1	AA230786	AA230786	va67h05.x	748	9	64.3	682	5	BM950543	BM950543	UI-M-EHOP
676	9	64.3	229	1	AI242510	AI242510	qu35g12.x	749	9	64.3	693	1	AU134091	AU134091	AU134091
677	9	64.3	258	7	TI16055	TI16055	IB3060.infa	750	9	64.3	702	4	BI664158	BI664158	603289276
678	9	64.3	283	1	AI060810	AI060810	ub44b08.r	751	9	64.3	713	6	CA318826	CA318826	UI-M-EW0-
679	9	64.3	306	1	AA636862	AA636862	vr20g02.r	752	9	64.3	715	6	BA433441	BA433441	BB433441
680	9	64.3	312	4	BI491309	BI491309	df16g08.w	753	9	64.3	716	4	BI109437	BI109437	602897241
681	9	64.3	313	7	T36303	T36303	EST99874.Hu	754	9	64.3	725	4	BI693243	BI693243	603343544
682	9	64.3	321	7	W1646	W1646	me42d07.r1	755	9	64.3	730	5	BQ444485	BQ444485	UI-M-ERO-
683	9	64.3	321	7	W62085	W62085	me42d07.r1	756	9	64.3	731	6	CD578866	CD578866	UI-M-GMO-
684	9	64.3	334	7	D58262	D58262	HUM359G06B	757	9	64.3	742	4	BG918577	BG918577	602818361
685	9	64.3	338	7	AA032813	AA032813	mi36g09.r	758	9	64.3	744	7	CO425473	CO425473	UI-M-HU0-
686	9	64.3	363	1	AW227828	AW227828	up14g06.y	759	9	64.3	750	4	BI109427	BI109427	602897329
687	9	64.3	388	2	BE285868	BE285868	601096037	760	9	64.3	756	4	BI159253	BI159253	602922778
688	9	64.3	391	2	BE651680	BE651680	UI-M-AJO-	761	9	64.3	758	2	AW212638	AW212638	u010f05.x
689	9	64.3	396	1	AI286726	AI286726	ub84e02.r	762	9	64.3	774	6	CB573199	CB573199	AGENCOURT
690	9	64.3	406	7	W41289	W41289	mc44d07.r1	763	9	64.3	775	7	CO386590	CO386590	AGENCOURT
691	9	64.3	408	6	CD565437	CD565437	B0494H08-	764	9	64.3	776	7	CO425463	CO425463	UI-M-HU0-
692	9	64.3	410	2	BE284815	BE284815	601091130	765	9	64.3	798	7	CF950351	CF950351	UI-M-HU0-
693	9	64.3	418	7	N41846	N41846	yw72b06.r1	766	9	64.3	810	9	CL634334	CL634334	CH243-8F3
694	9	64.3	420	7	W83977	W83977	me35e06.r1	767	9	64.3	812	4	BI684148	BI684148	603306554
695	9	64.3	423	6	CD561781	CD561781	B0436C12-	768	9	64.3	817	4	BG919010	BG919010	602819195
696	9	64.3	425	1	AA260499	AA260499	mz81g11.r	769	9	64.3	836	4	BG862364	BG862364	602796251
697	9	64.3	427	2	BE624952	BE624952	u28e08.y	770	9	64.3	836	4	BI155031	BI155031	602902555
698	9	64.3	453	4	BG095222	BG095222	uu85a03.x	771	9	64.3	858	4	BG112293	BG112293	60292442
699	9	64.3	456	1	AA794632	AA794632	vu66h11.r	772	9	64.3	866	4	BI646132	BI646132	603276342
700	9	64.3	464	1	AA933799	AA933799	ol84a01.s	773	9	64.3	869	4	BI247958	BI247958	602938745
701	9	64.3	466	1	AA682145	AA682145	u13d01.r	774	9	64.3	890	4	BI858571	BI858571	603389075
702	9	64.3	469	2	AW913458	AW913458	uf53c01.y	775	9	64.3	898	2	BF124038	BF124038	601760121
703	9	64.3	470	1	AA833452	AA833452	ub8f08.r	776	9	64.3	917	5	BQ934917	BQ934917	AGENCOURT
704	9	64.3	474	7	CF982140	CF982140	maj78c11.	777	9	64.3	924	5	BQ876232	BQ876232	AGENCOURT
705	9	64.3	477	2	BE305396	BE305396	60109989	778	9	64.3	933	2	BF099265	BF099265	601752439
706	9	64.3	477	5	BP753934	BP753934	BP753934	779	9	64.3	933	4	BI695196	BI695196	603346642
707	9	64.3	478	7	CK382069	CK382069	laq31e11.	780	9	64.3	937	2	BF580447	BF580447	602097215
708	9	64.3	479	1	AI152814	AI152814	ud31d10.r	781	9	64.3	994	1	AV254915	AV254915	AV254915
709	9	64.3	479	4	EM069425	EM069425	id73g09.y	782	9	64.3	1008	4	BI649944	BI649944	603296592
710	9	64.3	479	5	BU756426	BU756426	UI-1-CF0-	783	9	64.3	1064	4	BG495262	BG495262	602542926
711	9	64.3	490	4	BG148619	BG148619	uu85a03.y	784	9	64.3	1110	9	AY412160	AY412160	Mus muscu
712	9	64.3	503	1	AI060433	AI060433	ub40c01.r	785	9	64.3	2045	3	AK050465	AK050465	Mus muscu
713	9	64.3	507	7	R88891	R88891	yp97b03.r1	786	9	64.3	2348	3	BC029328	BC029328	Mus muscu
714	9	64.3	513	1	AI851548	AI851548	UI-M-EH0-	787	9	64.3	2739	3	AK079476	AK079476	Mus muscu
715	9	64.3	522	5	BX516226	BX516226	EX516226	788	9	57.1	208	2	AW901060	AW901060	CM0-NN101
716	9	64.3	530	2	BE381296	BE381296	601271173	789	8	57.1	221	7	CO685194	CO685194	DG11-198k
717	9	64.3	532	2	BE381296	BE381296	DG11-277b	790	8	57.1	221	7	CO685194	CO685194	mm0329.se
718	9	64.3	543	2	BB821460	BB821460	BB821460	791	8	57.1	232	1	AA091845	AA091845	Y2985F.Huma
719	9	64.3	547	1	AI050464	AI050464	uc86e08.y	792	8	57.1	247	2	N55813	N55813	J2985F.Huma
720	9	64.3	547	1	AI050464	AI050464	uc86e08.y	793	8	57.1	280	2	BF433379	BF433379	7q69f12.x
721	9	64.3	569	7	CR757452	CR757452	uw26b02.x	794	8	57.1	284	1	AI681819	AI681819	tx39a03.x
722	9	64.3	571	2	BE852627	BE852627	CR757452	795	8	57.1	284	2	BE856106	BE856106	7f88a08.x
723	9	64.3	571	5	BQ566670	BQ566670	g166a09.y	796	8	57.1	286	7	T64661	T64661	YC25g10.s1
724	9	64.3	587	2	BE198998	BE198998	ur99c08.x	797	8	57.1	315	7	H38381	H38381	VP50f06.r1
725	9	64.3	593	4	BI082686	BI082686	602877713	798	8	57.1	328	4	BI493343	BI493343	df100a06
726	9	64.3	596	1	AA870528	AA870528	vg22g09.r	799	8	57.1	330	5	BP432781	BP432781	60332781
727	9	64.3	600	7	CR757454	CR757454	CR757454	800	8	57.1	390	7	F33267	F33267	HSPD26583.H
728	9	64.3	601	4	EG339944	EG339944	602441485	801	8	57.1	412	1	AA661682	AA661682	AJ661682
729	9	64.3	604	1	AA869591	AA869591	vg09h10.r	802	8	57.1	421	7	AA076644	AA076644	zm20c04.s
730	9	64.3	605	1	AA870443	AA870443	vg21f12.r	803	8	57.1	421	7	H56074	H56074	Yq97e04.s1
731	9	64.3	605	2	AA870528	AA870528	vg22g09.r	804	8	57.1	437	4	BI063826	BI063826	IL3-UT011
732	9	64.3	605	2	AW763774	AW763774	ur65e01.x	805	8	57.1	469	8	BE286652	BE286652	CH230-39N
733	9	64.3	608	7	CR757421	CR757421	CR757421	806	8	57.1	475	1	AA213581	AA213581	zq93b06.r
734	9	64.3	611	2	BE285099	BE285099	601097741	807	8	57.1	506	4	BI063982	BI063982	IL3-UT011
735	9	64.3	616	5	EM877227	EM877227	if95g09.x	808	8	57.1	520	7	N23823	N23823	Yx36h11.r1
736	9	64.3	624	6	CD771754	CD771754	AGENCOURT	809	8	57.1	560	4	BI404450	BI404450	MI-P-CPI-
737	9	64.3	627	6	BP428443	BP428443	BP428443	810	8	57.1	578	5	CA264293	CA264293	NC5BLB204
738	9	64.3	635	5	BI154726	BI154726	602904518	811	8	57.1	589	6	CA264293	CA264293	NC5BLB204
739	9	64.3	643	4	BI154726	BI154726	602904518	812	8	57.1	594	1	AA622254	AA622254	NC43F05.B

813	8	57.1	601	5	BP464377	BP464377 BP464377	C886	7	50.0	416	1	AA018089
814	8	57.1	640	1	AJ658836	AJ658836 AJ658836	C887	7	50.0	420	6	CD743630
815	8	57.1	650	8	AZ991285	AZ991285 2M0275H21	C888	7	50.0	419	7	R87366
816	8	57.1	695	9	CE139522	tigr-g8g-	C889	7	50.0	424	3	CNS33809
817	8	57.1	711	9	CE684361	tigr-g8g-	C890	7	50.0	430	3	CNS08RWA
818	8	57.1	737	7	CN166334	CNI66334 99T597 MA	C891	7	50.0	431	4	EI022886
819	8	57.1	759	7	CNI60762	CNI60762 949971 MA	C892	7	50.0	431	6	CB758501
820	8	57.1	796	7	CNI158846	CNI158846 947667 MA	C893	7	50.0	440	1	AA150796
821	8	57.1	841	7	CF552849	AGENCOURT	C894	7	50.0	445	1	AA670695
822	8	57.1	866	4	BG393996	BG393996 602A16B93	C895	7	50.0	446	4	BM584288
823	8	57.1	913	5	BO674754	AGENCOURT	C896	7	50.0	449	8	AQ667591
824	8	57.1	932	5	BO669046	AGENCOURT	C897	7	50.0	450	1	AAO74469
825	8	57.1	1083	4	EA460353	AGENCOURT	C898	7	50.0	450	4	BG316274
826	7	50.0	76	1	AA085832	zn13g01.s	C899	7	50.0	454	2	CO896984
827	7	50.0	107	3	CNS08RG6	AX024994 Single re	C900	7	50.0	455	2	BF424999
828	7	50.0	115	2	BF942477	nae95b04.	C901	7	50.0	455	4	BM031082
829	7	50.0	135	7	CV398108	CV398108 QV4-BN009	C902	7	50.0	456	8	BH033718
830	7	50.0	135	7	Z20407	HSAACBKPT P	C903	7	50.0	459	4	BM656418
831	7	50.0	174	5	BM956062	EST0999 H	C904	7	50.0	461	1	AI966777
832	7	50.0	179	4	BG315593	sab82b10.	C905	7	50.0	461	4	BM650863
833	7	50.0	183	7	Z20260	HGAATFTF P	C906	7	50.0	463	4	BM631318
834	7	50.0	194	4	BG315856	sab86c03.	C907	7	50.0	464	4	BM597973
835	7	50.0	221	7	CV192584	SNESTbab1	C908	7	50.0	465	6	CD745135
836	7	50.0	241	5	BU666756	NaL3_42B	C909	7	50.0	467	4	BM658125
837	7	50.0	250	6	CD743633	IRB21_CB3	C910	7	50.0	470	4	BM610572
838	7	50.0	257	7	CK927310	p3fmgC_01	C911	7	50.0	472	4	BM619172
839	7	50.0	261	3	CNS09QB7	Single re	C912	7	50.0	472	8	AZ762430
840	7	50.0	267	3	CNS08ZX	Single re	C913	7	50.0	475	6	CD743632
841	7	50.0	279	6	CD746492	S21_E05_S	C914	7	50.0	476	3	CNS08EU7
842	7	50.0	281	2	B2219458	hvS8d03_x	C915	7	50.0	476	6	CD745137
843	7	50.0	293	1	A3321649	EST24157	C916	7	50.0	477	4	BM639794
844	7	50.0	298	3	CNS08LBZ	Single re	C917	7	50.0	479	4	BM597967
845	7	50.0	306	4	BI494153	dfl08a12.	C918	7	50.0	479	6	CD743628
846	7	50.0	306	4	BI496000	dfl22b08.	C919	7	50.0	480	4	BM592404
847	7	50.0	307	4	BI494152	dfl08a12.	C920	7	50.0	480	6	CD745136
848	7	50.0	309	5	BU693912	SYD0997 S	C921	7	50.0	480	7	CF543445
849	7	50.0	310	8	AQ515925	HS_5235_A	C922	7	50.0	481	2	AW271202
850	7	50.0	313	6	CD743627	IRB1Q1_C0	C923	7	50.0	481	9	CE355174
851	7	50.0	320	1	AA281791	zt09b11.s	C924	7	50.0	481	9	CE355174
852	7	50.0	320	4	BI495999	dfl22b08.	C925	7	50.0	482	4	BM590863
853	7	50.0	320	6	CD743626	IRB15_B10	C926	7	50.0	482	7	CF541875
854	7	50.0	323	9	CE113499	tigr-g8g-	C927	7	50.0	483	6	CD746490
855	7	50.0	329	6	CD743638	IRB3_E02	C928	7	50.0	484	3	CNS08MLD
856	7	50.0	330	3	CNS09145	Single re	C929	7	50.0	485	4	BM584425
857	7	50.0	332	8	AO675313	HS_2145_A	C930	7	50.0	485	6	CD745133
858	7	50.0	333	6	CD743636	IRB11_F02	C931	7	50.0	485	7	CF929901
859	7	50.0	333	7	CR383299	CR383299 CR383299	C932	7	50.0	485	9	CE748006
860	7	50.0	336	1	A1887000	w195c04.x	C933	7	50.0	487	4	BG042891
861	7	50.0	336	4	BI015424	PM0-ET020	C934	7	50.0	488	4	BM605729
862	7	50.0	338	1	AU189657	AU189657 AU189657	C935	7	50.0	488	5	BQ133279
863	7	50.0	341	7	CR467553	CR467553	C936	7	50.0	489	7	CN637172
864	7	50.0	346	6	CB405932	CB405932 OSTF059G2	C937	7	50.0	492	4	BM610012
865	7	50.0	361	6	CD743634	IRB2Q1_D1	C938	7	50.0	492	7	CR527973
866	7	50.0	366	2	BB677894	BB677894 BB677894	C939	7	50.0	493	7	CR527974
867	7	50.0	370	6	CD743637	IRB3Q4_D0	C940	7	50.0	494	4	BM578604
868	7	50.0	382	2	BE005517	CML-BN011	C941	7	50.0	495	4	BI892857
869	7	50.0	385	7	CR575838	CR575838	C942	7	50.0	495	4	BM616017
870	7	50.0	387	3	CNS08UVK	Single re	C943	7	50.0	495	4	BM627059
871	7	50.0	390	3	CNS08LBY	Single re	C944	7	50.0	495	6	CD743629
872	7	50.0	391	3	CNS08X94	Single re	C945	7	50.0	497	2	BE080822
873	7	50.0	394	7	CO381419	FRA1039 S	C946	7	50.0	497	4	BM610736
874	7	50.0	396	2	AWB04253	PM3-UM008	C947	7	50.0	497	4	BM618338
875	7	50.0	398	4	BI702291	sag44g01.	C948	7	50.0	497	4	BM625709
876	7	50.0	405	2	AW572759	hd31a10.x	C949	7	50.0	498	4	BM631386
877	7	50.0	408	6	CD743635	IRB4Q4_B0	C950	7	50.0	499	4	BM624554
878	7	50.0	409	4	BM643095	BM643095 170006873	C951	7	50.0	499	6	CD746488
879	7	50.0	410	1	AA689586	nv66a05.s	C952	7	50.0	500	3	CNS09ATC
880	7	50.0	411	2	BF323814	BF323814 SNEST4a20	C953	7	50.0	500	6	CD746491
881	7	50.0	411	4	BI063688	IL3-UT011	C954	7	50.0	501	6	CD743624
882	7	50.0	411	5	BQ327547	CM0-RT001	C955	7	50.0	501	6	CD743625
883	7	50.0	411	5	BQ327559	CM0-RT001	C956	7	50.0	501	8	AQ185130
884	7	50.0	413	2	BE178859	PM1-HT060	C957	7	50.0	502	4	BM606472
885	7	50.0	415	8	B80366	CJT-H5P-204	C958	7	50.0	503	4	BM600909

C 959	7	50.0	505	1	AU240406
C 960	7	50.0	505	4	BM617315
C 961	7	50.0	506	3	BMX08JB9
C 962	7	50.0	506	4	BM593189
C 963	7	50.0	506	4	BM601862
C 964	7	50.0	506	4	BM629418
C 965	7	50.0	506	4	BM637119
C 966	7	50.0	506	6	CD745134
C 967	7	50.0	507	4	BM576728
C 968	7	50.0	507	4	BM642509
C 969	7	50.0	507	4	BM655807
C 970	7	50.0	508	3	CNS08MW9
C 971	7	50.0	508	4	BM606937
C 972	7	50.0	508	7	CO687010
C 973	7	50.0	509	5	BP132926
C 974	7	50.0	510	5	BP112779
C 975	7	50.0	510	6	CD743623
C 976	7	50.0	511	5	BU763570
C 977	7	50.0	514	3	CNS09AYB
C 978	7	50.0	515	3	CNS08DSV
C 979	7	50.0	515	4	BI064007
C 980	7	50.0	516	3	CNS091SN
C 981	7	50.0	516	4	BM604463
C 982	7	50.0	516	4	BM646452
C 983	7	50.0	517	3	CNS08ODU
C 984	7	50.0	517	8	AQ556413
C 985	7	50.0	520	1	BM6165628
C 986	7	50.0	520	4	BM610442
C 987	7	50.0	521	3	CNS08UJV
C 988	7	50.0	521	5	BP180275
C 989	7	50.0	522	3	CNS08RVA
C 990	7	50.0	523	3	CNS08KSN
C 991	7	50.0	526	3	CNS091A4
C 992	7	50.0	526	8	AZ970711
C 993	7	50.0	527	3	CNS08XXK
C 994	7	50.0	530	3	CNS08MLE
C 995	7	50.0	531	3	CNS08HX4
C 996	7	50.0	532	6	CA950720
C 997	7	50.0	536	4	BI427623
C 998	7	50.0	538	3	CNS08EUE
C 999	7	50.0	539	1	AL925224
C1000	7	50.0	540	3	CNS08NDC

/note="Vector: Bluescript; clone library=P, Human foetal Brain Whole tissue; cloning vector is Bluescript."

ORIGIN

Alignment Scores:
 Pred. No.: 9,24e-06 Length: 136
 Score: 14.00 Matches: 14
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 7 Gaps: 0

US-09-736-250-5 (1-14) x Z20123 (1-136)

QY 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
 |||||
 Db 24 GAAGATAAGTCTCAGAAATGTGGGTCTGTGTGGCACT 65
 |||||

RESULT 2
 AA678060/c
 LOCUS
 DEFINITION
 z125f08.s1 Soares fetal liver spleen INFLS S1 Homo sapiens cDNA
 clone IMAGE:431847 3' similar to RF:G1183162 G1183162 CYCLIN I. ;
 mRNA sequence.
 AA678060 139 bp mRNA linear EST 19-DEC-1997
 z125f08.s1 Soares fetal liver spleen INFLS S1 Homo sapiens cDNA
 clone IMAGE:431847 3' similar to RF:G1183162 G1183162 CYCLIN I. ;
 mRNA sequence.
 AA678060
 AA678060.1 GI:2658582
 EST.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 139)
 Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisels,G., Jost,S.,
 Kitzman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
 Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
 Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
 wasNU-NCI human EST Project
 Unpublished (1997)
 Contact: Wilton RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: estewatson.wustl.edu
 This clone is available royalty-free through LML; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Possible reversed clone: similarity on wrong strand
 Seq primer: -40m13 fwd. ET from Amersham
 High quality sequence stop: 1.
 Location/Qualifiers
 1. .139
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:431847"
 /sex="male"
 /dev_stage="20 week-post conception fetus"
 /lab_host="DH10B (ampicillin resistant)"
 /clone_lib="Soares fetal liver spleen INFLS S1"
 /note="Organ: Liver and Spleen; Vector: p7T3D (Pharmacina)
 with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
 This is a subtracted version of the original Soares fetal
 liver spleen INFLS library. 1st strand cDNA was primed
 with a Pac I - oligo(dT) primer [5,
 AACCTGGAAGATTAATTAAGATCTTTTTTTTTTTTTTTT 3'],
 double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacina), digested with Pac I and cloned into the Pac I
 and Eco RI sites of the modified p7T3 vector. Library
 went through one round of normalization. Library
 constructed by Bento Soares and M.Fatima Bonaldo."

TITLE
 JOURNAL
 COMMENT

FEATURES
 source

Pred. No.: 9.41e-06 Length: 139
 Score: 14.00 Matches: 14
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 1 Gaps: 0

US-09-736-250-5 (1-14) x AA678060 (1-139)

Qy 1 GluAspAenValSerGluAsnValGlySerValCysGlyThr 14
 Db 103 GAAGATAATGCTCAGAAATGTGGTTCTGTGTGGCACT 62

RESULT 3

AA094874

LOCUS

DEFINITION cp2090.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens
 CDNA 5', mRNA sequence.

ACCESSION AA094874

VERSION AA094874.1

KEYWORDS GI:1640491

SOURCE EST.

ORGANISM Homo sapiens (human)

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 139)

AUTHORS Liew, C.C.

JOURNAL CDNAS from fetal heart (1996)

COMMENT Unpublished (1996)

Contact: Liew CC

Brigham and Women's Hospital

Harvard Medical School

75 Francis St. Boston, MA 02115, USA

Tel: 6177328915

Fax: 6179750995

Email: cliw@rics.bwh.harvard.edu

PCR Primers

FORWARD: 5' GCCAGCTCGAATTAACCCCTCACTAAAGG 3'

BACKWARD: 5' CCAGTGAATTTAATACGACTCATATAGGCG 3'

Seq primer: 5' GAAATTAACCCCTCACTAAAGG 3'.

FEATURES

source

1. 139

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/lab_host="E. coli XL1-Blue"

/clone_lib="Human fetal heart, Lambda ZAP Express"

/note="Vector: Lambda ZAP Express; Site 1: EcoRI; Site 2:

XhoI; mRNA was purified from human fetal hearts (8-10

weeks). CDNA was synthesized using a XhoI-Oligo dr

adaptor-primer. EcoRI adaptors were ligated, followed by

digestion with XhoI, for directional cloning into

predigested lambda ZAP Express."

ORIGIN

Alignment Scores:

Pred. No.: 9.41e-06 Length: 139
 Score: 14.00 Matches: 14
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 1 Gaps: 0

US-09-736-250-5 (1-14) x AA094874 (1-139)

Qy 1 GluAspAenValSerGluAsnValGlySerValCysGlyThr 14
 Db 50 GAAGATAATGCTCAGAAATGTGGTTCTGTGTGGCACT 91

RESULT 4

AA659220

LOCUS

DEFINITION nt92c11.s1 NCI_CGAP_Pr12 Homo sapiens cDNA clone IMAGE:1205972
 EST 18-FEB-1998

similar to TR:G1183162 G1183162 CYCLIN I. ;, mRNA sequence.
 AA659220
 AA659220.1 GI:2595374
 EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 197)

REFERENCE NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgaps-remail.nih.gov

Tissue Procurement: W. Douglas Figg, Ph.D., Paul H. Dury, M.D.,

Rodrigo F. Chuai, M.D., Michael R. Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: David B. Krizman, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 288 Std Error: 0.00

Seq primer: -40m13 fwd. ET from Amersham

High quality sequence stop: 161.

FEATURES

source

1. 197

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clones="IMAGE:1205972"

/sex="male"

/tissue_type="metastatic prostate bone lesion"

/lab_host="NCI CGAP Pr12"

/note="Vector: pAMP10; mRNA made from metastatic prostate

lesion of the bone, CDNA made by oligo-dr priming.

Non-directionally cloned. Size-selected on agarose gel,

average insert size 600 bp. Library made by D. Krizman,

NIH."

Alignment Scores:

Pred. No.: 1.26e-05 Length: 197
 Score: 14.00 Matches: 14
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 1 Gaps: 0

US-09-736-250-5 (1-14) x AA659220 (1-197)

Qy 1 GluAspAenValSerGluAsnValGlySerValCysGlyThr 14
 Db 93 GAAGATAATGCTCAGAAATGTGGTTCTGTGTGGCACT 134

RESULT 5

AA058781/c

LOCUS

DEFINITION zf58f03.r1 Soares retina NZB4HR Homo sapiens cDNA clone
 IMAGE:381149 5', similar to TR:G1183162 G1183162 CYCLIN I. ;, mRNA
 sequence.

ACCESSION AA058781

VERSION AA058781.1

KEYWORDS GI:1551591

SOURCE EST.

ORGANISM Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 234)

REFERENCE Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiappelli, B.,

Chisoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W.,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM0&t2=CM0-RT0017-21100-702-e07&t3=2000-11-21&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 7

High quality sequence stop: 25.

FEATURES

source

Location/Qualifiers

1..251

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/dev_stage="Adult"

/clone_lib="RT0017"

/note="Organ: kidney tumor; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Alignment Scores:

Pred. No.: 1.53e-05 Length: 251
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0

US-09-736-250-5 (1-14) x BQ327548 (1-251)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14

|||||
Db 163 GAAGATAATGCTCAGAAATGCGGTCTGTGTGGCACT 204

RESULT 8

BQ327560

LOCUS BQ327560 251 bp mRNA linear EST 17-MAY-2002

DEFINITION CM0-RT0017-221100-705-e07 RT0017 Homo sapiens cDNA, mRNA sequence.

ACCESSION BQ327560

VERSION BQ327560.1 GI:20944806

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 251)

AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Negai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM0&t2=CM0-RT0017-221100-705-e07&t3=2000-11-22&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 7

High quality sequence stop: 25.

FEATURES

source

Location/Qualifiers

1..251

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/dev_stage="Adult"

/clone_lib="RT0017"

/note="Organ: kidney tumor; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Alignment Scores:
Pred. No.: 1.53e-05 Length: 251
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0

US-09-736-250-5 (1-14) x BQ327560 (1-251)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14

|||||
Db 163 GAAGATAATGCTCAGAAATGCGGTCTGTGTGGCACT 204

RESULT 9

R85184/c

LOCUS

DEFINITION

ACCESSION

R85184

VERSION

R85184.1

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

```

/mol_type="mRNA"
/db_xref="GDB:3827349"
/db_xref="taxon:9606"
/clone="IMAGE:180699"
/sex="Male"
/dev_stage="55-year old"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares adult brain N2b4HB55y"
/note="Organ: brain; Vector: pT7T3D (Pharmacia) with a
modified polylinker; Site 1: Not 1; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - Oligo (dR) primer [5',
TGGTACCAATCTGAAGTGGAGCGCCGCTTTTCTTTTCTTTTCTTTT 3'],
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 53. Library constructed by Bento
Soares and M. Fatima Donaldo. The adult brain RNA was
provided by Dr. Donald H. Gilden. Tissue was acquired
17-18 hours after death which occurred in consequence of a
ruptured aortic aneurysm. RNA was prepared from a pool of
tissues representing the following areas of the brain:
frontal, parietal, temporal and occipital cortex from the
left and right hemispheres, subcortical white matter,
basal ganglia, thalamus, cerebellum, midbrain, pons and
medulla."

Alignment Scores:
Pred. No.: 1.6e-05 Length: 265
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0

US-09-736-250-5 (1-14) x R85184 (1-265)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
|||||
Db 234 GAAGATAATGCTCAGAAAATGCGGTCTGTGTGGCACT 193

RESULT 10
AA680208/c
LOCUS
DEFINITION
IMAGE:869109 3' similar to TR:G1183162 G1183162 CYCLIN I.; mRNA
sequence.

ACCESSION
AA680208.1 GI:2656176
VERSION
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 269)
Hallier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le.N., Lennon,G., Marra,M.,
Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-NCI human EST Project
Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
Seq primer: -40n13 fwd. ET from Amersham
High quality sequence stop: 215.

FEATURES
source
Location/Qualifiers
1..269
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3827349"
/db_xref="taxon:9606"
/clone="IMAGE:180699"
/sex="Male"
/dev_stage="55-year old"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares adult brain N2b4HB55y"
/note="Organ: brain; Vector: pT7T3D (Pharmacia) with a
modified polylinker; Site 1: Not 1; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - Oligo (dR) primer [5',
TGGTACCAATCTGAAGTGGAGCGCCGCTTTTCTTTTCTTTTCTTTT 3'],
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 53. Library constructed by Bento
Soares and M. Fatima Donaldo. The adult brain RNA was
provided by Dr. Donald H. Gilden. Tissue was acquired
17-18 hours after death which occurred in consequence of a
ruptured aortic aneurysm. RNA was prepared from a pool of
tissues representing the following areas of the brain:
frontal, parietal, temporal and occipital cortex from the
left and right hemispheres, subcortical white matter,
basal ganglia, thalamus, cerebellum, midbrain, pons and
medulla."

US-09-736-250-5 (1-14) x AA680208 (1-269)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
|||||
Db 116 GAAGATAATGCTCAGAAAATGCGGTCTGTGTGGCACT 75

RESULT 11
AA011113/c
LOCUS
DEFINITION
IMAGE:360869 5', mRNA sequence.

ACCESSION
AA011113
VERSION
AA011113.1 GI:1472160
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 275)
Hallier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le.M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and
Wilson,R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: mob.REGA+5'
High quality sequence stop: 165.

FEATURES
source
Location/Qualifiers
1..275
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1277414"
/db_xref="taxon:9606"
/clone="IMAGE:360869"
/sex="male"
/tissue_type="retina"
/dev_stage="55 year old"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares retina N2b4HR"

```

/note="Organ: eye; Vector: pTT3D (Pharmacia) with a modified polylinker; Site_1: Not 1; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-TGTTACCAATCTGAAGTGGAGCGCGCTTTTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pTT3 vector (Pharmacia). The retinas were obtained from a 55 year old Caucasian and total cellular poly(A)⁺ RNA was extracted 6 hrs after their removal. The retina RNA was kindly provided by Roderick R. McInnes M.D. Ph.D. from the University of Toronto. Library constructed by Bento Soares and M.Fatima Bonaldo."

ORIGIN

Alignment Scores:

Pred. No.: 1.65e-05 Length: 275
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-09-736-250-5 (1-14) x AA011113 (1-275)

Qy 1 GluAspAenValSerGluAenValGlySerValCysGlyThr 14

Db 234 GAAGATAATGCTCAGAAATGTGGTCTCTGTGTGGCACT 193

RESULT 12

LOCUS

AA778982 278 bp mRNA linear EST 05-FEB-1998
ac37f07.s1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone
IMAGE:858661 3' similar to TR:Q14094 Q14094 CYCLIN I.; mRNA
sequence.

ACCESSION

AA778982

VERSION

AA778982.1 GI:2838313

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M.,
Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F.,
Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.
WashU-NCI human EST Project
Unpublished (1997)

TITLE

JOURNAL

COMMENT

Contact: Wilton RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: es@watson.wustl.edu

FEATURES

source

This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 177.
Location/Qualifiers
1..278
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:858661"
/dev_stages="hnt neurons"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="Stratagene hNT neuron (#937233)"
/note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
XhoI; Cloned unidirectionally. Primer: Oligo dT.
Differentiated, post mitotic hNT neurons. Average insert
size: 1.5 Kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5'

GAATTCGGCAGAG 3' ~3' adaptor sequence: 5'
CTCAGATTTTTTTTTTTTTTTT 3"

ORIGIN

Alignment Scores:

Pred. No.: 1.67e-05 Length: 278
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-09-736-250-5 (1-14) x AA778982 (1-278)

Qy 1 GluAspAenValSerGluAenValGlySerValCysGlyThr 14

Db 188 GAAGATAATGCTCAGAAATGTGGTCTCTGTGTGGCACT 147

RESULT 13

F32546

LOCUS

DEFINITION HSPD25369 HM3 Homo sapiens cDNA clone s3000040A06, mRNA sequence.

ACCESSION

F32546

VERSION

F32546.1 GI:4818172

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

AUTHORS

1 (bases 1 to 296)

TITLE

Identification of 4370 expressed sequence tags from a
3'-end-specific cDNA library of human skeletal muscle by DNA
sequencing and filter hybridization

JOURNAL

Genome Res. 6 (1), 35-42 (1996)

MEDLINE

98276048

COMMENT

8681137

CONTACT

Contact: Valle G.

CRIBI Biotechnology Centre

University of Padua

Via Trieste 75, 35121 Padua, Italy

ABI Chromatograms and other information are available on WWW at
http://grup.bio.unipd.it.

FEATURES

source

1..296

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clones="s3000040A06"

/sex="female"

/tissue_type="pectoral muscle (after mastectomy)"

/clone_lib="HM3"

/note="Vector: pcDNAII (Invitrogen); Site 1: BstXI;

Site 2: NotI; The library is not subtracted by G.

Lanfranchi. This library is not subtracted nor normalized.

The first strand cDNA was primed with a biotinylated

oligo-dT-NotI primer

(5'-biotin-AACCCGCTCGAGCGCGCTTTTTTTTTTTT-3'). The

ds cDNA was sonicated and size-selected in the range

350-550 bp. The 3' specific fragments were selected by

streptavidin coated magnetic beads, ligated to

non-palindromic BstXI adapters, NotI digested and

directionally cloned into BstXI-NotI cut pcDNAII vector."

ORIGIN

Alignment Scores:

Pred. No.: 1.76e-05 Length: 296

Score: 14.00 Matches: 14

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 7 Gaps: 0

US-09-736-250-5 (1-14) x F32546 (1-296)

Qy 1 GluAspAsnValSerGluAsnValCysGlyThr 14
Db 82 GAAGATAATGCTCAGAAAATGGGTCTGTGTGTGGCACT 123

RESULT 14
BI493342/c 302 bp mRNA linear EST 28-AUG-2001
LOCUS df100406.w1 Morton Fetal Cochlea Homo sapiens cDNA clone
DEFINITION IMAGE:2540459 3', mRNA sequence.

ACCESSION BI493342
VERSION BI493342.1 GI:15332686
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 302)
AUTHORS Robertson,N.G., Khetarpal,U., Gutierrez-Espeleta,G.A., Bieber,F.R.
and Morton,C.C.

TITLE Isolation of novel and known genes from a human fetal cochlear cDNA
library using subtractive hybridization and differential screening
JOURNAL Genomics 23, 42-50 (1994)
MEDLINE 95130111
PUBMED 7829101

COMMENT Contact: Morton, C. C.
Departments of Pathology and Obstetrics, Gynecology and
Reproductive Biology
Brigham and Women's Hospital
75 Francis Street, Harvard Medical School, Boston, MA 02115, USA
Tel: 617 732 7980
Fax: 617 738 6996
Email: cmorton@rics.bwh.harvard.edu
DNA sequencing and analyses were performed by National Institutes
of Health Intramural Sequencing Center (NISC; see
<http://www.nisc.nih.gov>).
This clone is available royalty-free through LLMU; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Plate: LHAM6328 row: B column: 12
Seq primer: T7 primer.

FEATURES

Location/Qualifiers
1..302
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2540459"
/tissue_type="cochlea"
/dev_stage="16-22 week fetus"
/lab_host="SOLR cells (kanamycin resistant)"
/clone_lib="Morton Fetal Cochlea"
/note="Organ: ear; Vector: pBluescript SK-; Site 1: EcoRI;
Site 2: XhoI; Reference: Genomics 23, 42-50 (1994) Cloned
unidirectionally. Primer: Oligo dt. Fetal cochlea, normal.
37% of inserts <0.5 kb, 56% 0.5-1.0 kb, 7% >1 kb. Uni-ZAP
XR Vector. Library constructed by N. Robertson, C. Morton.
-5' adaptor sequence: 5' GAATTCGGCAGCAG 3' -3' adaptor
sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3' "

ORIGIN

Alignment Scores:
Pred. No.: 1.79e-05 Length: 302
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-736-250-5 (1-14) x BI493342 (1-302)

Qy 1 GluAspAsnValSerGluAsnValCysGlyThr 14
Db |||||

Db 259 GAAGATAATGCTCAGAAAATGGGTCTGTGTGTGGCACT 218

RESULT 15

N84129

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 302)

Liew,C.C.

CDNAs from fetal heart (1996)

Unpublished (1996)

Contact: Liew CC

Brigham and Women's Hospital

Harvard Medical School

75 Francis St. Boston, MA 02115, USA

Tel: 6177328915

Fax: 6179750995

Email: cliew@rics.bwh.harvard.edu

Seq primer: GAAATTAACCTCACTAAAGGG.

FEATURES

Location/Qualifiers

1..302

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="KK6088"

/lab_host="E. coli XL1-Blue"

/note="Vector: Lambda ZAP Express; Site 1: EcoRI; Site 2:

XhoI; mRNA was purified from human fetal hearts (8-10

weeks). cDNA was synthesized using a XhoI-Oligo dT

adaptor-primer. EcoRI adaptors were ligated, followed by

digestion with XhoI, for directional cloning into

predigested lambda ZAP Express."

ORIGIN

Alignment Scores:

Pred. No.: 1.79e-05 Length: 302

Score: 14.00 Matches: 14

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 7 Gaps: 0

US-09-736-250-5 (1-14) x N84129 (1-302)

Qy 1 GluAspAsnValSerGluAsnValCysGlyThr 14

Db |||||

50 GAAGATAATGCTCAGAAAATGGGTCTGTGTGTGGCACT 91

Search completed: February 11, 2005, 12:22:00

Job time : 274.164 secs